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| (54) Title: <i>ENTEROCOCCUS FAECALIS</i> POLYNUCLEOTIDES AND POLYPEPTIDES | | |
| (57) Abstract The present invention relates to novel genes from <i>Enterococcus faecalis</i> and the polypeptides they encode. Also provided are vectors, host cells, antibodies and methods for producing the same. The invention additionally relates to diagnostic methods for detecting <i>Enterococcus</i> nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by <i>Enterococcus</i> . | | |

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Enterococcus faecalis polynucleotides and polypeptides

Field of the Invention

The present invention relates to novel *Enterococcus faecalis* genes (*E. faecalis*)
5 nucleic acids and polypeptides. Also provided are vectors, host cells and recombinant
methods for producing the same. Further provided are diagnostic methods for
detecting *Enterococcus faecalis* using probes, primers, and antibodies to the *E. faecalis*
nucleic acids and polypeptides of the present invention. The invention further relates
to screening methods for identifying agonists and antagonists of *E. faecalis*
10 polypeptide activity and to vaccines using *E. faecalis* nucleic acids and polypeptides.

Background of the Invention

Enterococci have been recognized as being pathogenic for humans since the
turn of the century when they were first described by Thiercelin in 1988 as
15 microscopic organisms. The genus *Enterococcus* includes the species *Enterococcus*
faecalis or *E. faecalis* which is the most common pathogen in the group, accounting for
80 - 90 percent of all enterococcal infections. See Lewis et al. (1990) Eur J. Clin
Microbiol Infect Dis.9:111-117.

The incidence of enterococcal infections has increased in recent years and
20 enterococci are now the second most frequently reported nosocomial pathogens.
Enterococcal infection is of particular concern because of its resistance to antibiotics.
Recent attention has focused on enterococci not only because of their increasing role in
nosocomial infections, but also because of their remarkable and increasing resistance to
antimicrobial agents. These factors are mutually reinforcing since resistance allows
25 enterococci to survive in an environment in which antimicrobial agents are heavily
used; the hospital setting provides the antibiotics which eliminate or suppress
susceptible bacteria, thereby providing a selective advantage for resistant organisms,
and the hospital also provides the potential for dissemination of resistant enterococci
via the usual routes of hand and environmental contamination.

Antimicrobial resistance can be divided into two general types, inherent or intrinsic property and that which is acquired. The genes for intrinsic resistance, like other species characteristics, appear to reside on the chromosome. Acquired resistance results from either a mutation in the existing DNA or acquisition of new DNA. The various inherent traits expressed by enterococci include resistance to semisynthetic penicillinase-resistant penicillins, cephalosporins, low levels of aminoglycosides, and low levels of clindamycin. Examples of acquired resistance include resistance to chloramphenicol, erythromycin, high levels of clindamycin, tetracycline, high levels of aminoglycosides, penicillin by means of penicillinase, fluoroquinolones, and vancomycin. Resistance to high levels of penicillin without penicillinase and resistance to fluoroquinolones are not known to be plasmid or transposon mediated and presumably are due to mutation(s).

Although the main reservoir for enterococci in humans is the gastrointestinal tract, the bacteria can also reside in the gallbladder, urethra and vagina.

E. faecalis has emerged as an important pathogen in endocarditis, bacteremia, urinary tract infections (UTIs), intraabdominal infections, soft tissue infections, and neonatal sepsis. See Lewis et al. (1990) *supra*.. In the 1970s and 1980s enterococci became firmly established as major nosocomial pathogens. They are now the fourth leading cause of hospital-acquired infection and the third leading cause of bacteremia in the United States. Fatality ratios for enterococcal bacteremia range from 12% to 68%, with death due to enterococcal sepsis in 4 to 50% of these cases. See T.G. Emori (1993) Clin. Microbiol. Rev. 6:428-442.

The ability of enterococci to colonize the gastrointestinal tract, plus the many intrinsic and acquired resistance traits, means that these organisms, which usually seem to have relatively low intrinsic virulence, are given an excellent opportunity to become secondary invaders. Since nosocomial isolates of enterococci have displayed resistance to essentially every useful antimicrobial agent, it will likely become increasingly difficult to successfully treat and control enterococcal infections.

Particularly when the various resistance genes come together in a single strain, an event almost certain to occur at some time in the future.

The etiology of diseases mediated or exacerbated by *Enterococcus faecalis*, involves the programmed expression of *E. faecalis* genes, and that characterizing these genes and their patterns of expression would dramatically add to our understanding of the organism and its host interactions. Knowledge of the *E. faecalis* gene and genomic organization would improve our understanding of disease etiology and lead to improved and new ways of preventing, treating and diagnosing diseases. Thus, there is a need to characterize the genome of *E. faecalis* and for polynucleotides of this organism.

Summary of the Invention

The present invention provides for isolated *E. faecalis* polynucleotides and polypeptides shown in Table 1 and SEQ ID NO:1 through SEQ ID NO:496 (polynucleotide sequences having odd SEQ ID NOs and polypeptide sequences having even SEQ ID NOs). One aspect of the invention provides isolated nucleic acid molecules comprising polynucleotides having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence shown in Table 1; (b) a nucleotide sequence encoding any of the amino acid sequences of the polypeptides shown in Table 1; and (c) a nucleotide sequence complementary to any of the nucleotide sequences in (a) or (b). The invention further provides for fragments of the nucleic acid molecules of (a), (b) & (c) above.

Further embodiments of the invention include isolated nucleic acid molecules that comprise a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to any of the nucleotide sequences in (a), (b) or (c) above, or a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide in (a), (b) or (c) above. Additional nucleic acid embodiments of the invention relate to isolated nucleic acid molecules comprising polynucleotides which encode the amino acid sequences of

epitope-bearing portions of a *E. faecalis* polypeptide having an amino acid sequence in (a) above.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells containing
5 the recombinant vectors, as well as to methods of making such vectors and host cells. The present invention further relates to the use of these vectors in the production of *E. faecalis* polypeptides or peptides by recombinant techniques.

The invention further provides isolated *E. faecalis* polypeptides having an amino acid sequence selected from the group consisting of an amino acid sequence of
10 any of the polypeptides described in Table 1 or fragments thereof.

The polypeptides of the present invention also include polypeptides having an amino acid sequence with at least 70% similarity, and more preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% similarity to those described in Table 1, as well as polypeptides having an amino acid sequence at least 70% identical, more
15 preferably at least 75% identical, and still more preferably 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to those above; as well as isolated nucleic acid molecules encoding such polypeptides.

The present invention further provides a single or multi-component vaccine comprising one or more of the *E. faecalis* polynucleotides or polypeptides described
20 in Table 1, or fragments thereof, together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the *E. faecalis* polypeptide(s) are present in an amount effective to elicit an immune response to members of the *Enterococcus* genus, or at least *E. faecalis*, in an animal. The *E. faecalis* polypeptides of the present invention may further be combined with one or more immunogens of one or more other
25 Enterococcal or non-Enterococcal organisms to produce a multi-component vaccine intended to elicit an immunological response against members of the *Enterococcus* genus and, optionally, one or more non-Enterococcal organisms.

The vaccines of the present invention can be administered in a DNA form, e.g., "naked" DNA, wherein the DNA encodes one or more Enterococcal polypeptides

and, optionally, one or more polypeptides of a non-Enterococcal organism. The DNA encoding one or more polypeptides may be constructed such that these polypeptides are expressed as fusion proteins.

The vaccines of the present invention may also be administered as a
5 component of a genetically engineered organism or host cell. Thus, a genetically engineered organism or host cell which expresses one or more *E. faecalis* polypeptides may be administered to an animal. For example, such a genetically engineered organism or host cell may contain one or more *E. faecalis* polypeptides of the present invention intracellularly, on its cell surface, or in its periplasmic space. Further, such
10 a genetically engineered organism or host cell may secrete one or more *E. faecalis* polypeptides. The vaccines of the present invention may also be co-administered to an animal with an immune system modulator (*e.g.*, CD86 and GM-CSF).

The invention also provides a method of inducing an immunological response in an animal to one or more members of the *Enterococcus* genus, preferably one or
15 more isolates of the *E. faecalis* species, comprising administering to the animal a vaccine as described above.

The invention further provides a method of inducing a protective immune response in an animal, sufficient to prevent, attenuate, or control an infection by members of the *Enterococcus* genus, preferably at least *E. faecalis* species,
20 comprising administering to the animal a composition comprising one or more of the polynucleotides or polypeptides described in Table 1, or fragments thereof. Further, these polypeptides, or fragments thereof, may be conjugated to another immunogen and/or administered in admixture with an adjuvant.

The invention further relates to antibodies elicited in an animal by the
25 administration of one or more *E. faecalis* polypeptides of the present invention and to methods for producing such antibodies and fragments thereof. The invention further relates to recombinant antibodies and fragments thereof and to methods for producing such antibodies and fragments thereof.

The invention also provides diagnostic methods for detecting the expression of

the polynucleotides of Table 1 by members of the *Enterococcus* genus in an animal. One such method involves assaying for the expression of a polynucleotide encoding *E. faecalis* polypeptides in a sample from an animal. This expression may be assayed either directly (e.g., by assaying polypeptide levels using antibodies elicited in response to amino acid sequences described in Table 1) or indirectly (e.g., by assaying for antibodies having specificity for amino acid sequences described in Table 1). The expression of polynucleotides can also be assayed by detecting the nucleic acids of Table 1. An example of such a method involves the use of the polymerase chain reaction (PCR) to amplify and detect *Enterococcus* nucleic acid sequences.

10 The present invention also relates to nucleic acid probes having all or part of a nucleotide sequence described in Table 1 (odd SEQ ID NOs) which are capable of hybridizing under stringent conditions to *Enterococcus* nucleic acids. The invention further relates to a method of detecting one or more *Enterococcus* nucleic acids in a biological sample obtained from an animal, said one or more nucleic acids encoding
15 *Enterococcus* polypeptides, comprising: (a) contacting the sample with one or more of the above-described nucleic acid probes, under conditions such that hybridization occurs, and (b) detecting hybridization of said one or more probes to the *Enterococcus* nucleic acid present in the biological sample.

Other uses of the polypeptides of the present invention include: *inter alia*, to
20 detect *E. faecalis* in immunoassays, as epitope tags, as molecular weight markers on SDS-PAGE gels, as molecular weight markers for molecular sieve gel filtration columns, to generate antibodies that specifically bind *E. faecalis* polypeptides of the present invention for the detection *E. faecalis* in immunoassays, to generate an immune response against *E. faecalis* and other *Enterococcus* species, and as vaccines
25 against *E. faecalis*, other *Enterococcus* species and other bacteria genres.

Isolated nucleic acid molecules of the present invention, particularly DNA molecules, are useful as probes for gene mapping and for identifying *E. faecalis* in a biological samples, for instance, by Southern and Northern blot analysis.

Polynucleotides of the present invention are also useful in detecting *E. faecalis* by

PCR using primers for a particular *E. faecalis* polynucleotide. Isolated polynucleotides of the present invention are also useful in making the polypeptides of the present invention.

5 Detailed Description

The present invention relates to recombinant *E. faecalis* nucleic acids and fragments thereof. The present invention further relates to recombinant *E. faecalis* polypeptides and fragments thereof. The invention also relates to methods for using these polypeptides to produce immunological responses and to confer immunological protection to disease caused by members of the genus *Enterococcus*, at least isolates of the *E. faecalis* genus. The invention further relates to nucleic acid sequences which encode antigenic *E. faecalis* polypeptides and to methods for detecting *E. faecalis* nucleic acids and polypeptides in biological samples. The invention also relates to antibodies specific for the polypeptides and peptides of the present invention and methods for detecting such antibodies produced in a host animal.

Definitions

The following definitions are provided to clarify the subject matter which the inventors consider to be the present invention.

As used herein, the phrase "pathogenic agent" means an agent which causes a disease state or affliction in an animal. Included within this definition, for examples, are bacteria, protozoans, fungi, viruses and metazoan parasites which either produce a disease state or render an animal infected with such an organism susceptible to a disease state (e.g., a secondary infection). Further included are species and strains of the genus *Enterococcus* which produce disease states in animals.

As used herein, the term "organism" means any living biological system, including viruses, regardless of whether it is a pathogenic agent.

As used herein, the term "*Enterococcus*" means any species or strain of bacteria which is members of the genus *Enterococcus*. Such species and strains are

known to those of skill in the art, and include those that are pathogenic and those that are not.

As used herein, the phrase "one or more *E. faecalis* polypeptides of the present invention" means polypeptides comprising the amino acid sequence of one or more of the *E. faecalis* polypeptides described in Table 1 (even SEQ ID NOs). These polypeptides may be expressed as fusion proteins wherein the *E. faecalis* polypeptides of the present invention are linked to additional amino acid sequences which may be of Enterococcal or non-Enterococcal origin. This phrase further includes polypeptide comprising fragments of the *E. faecalis* polypeptides of the present invention. Additional definitions are provided throughout the specification.

Explanation of Table 1

Table 1, below, provides information describing genes which encode polypeptides of *E. faecalis*. The table lists the gene identifier which consists of the letters EF, which denote *E. faecalis*, followed immediately by a three digit numeric code, which arbitrarily number the *E. faecalis* genes of the present invention. A number from 1 through 4 follows the three digit number. A number 1 represents the full length open reading frame of the gene specified by the preceeding three digit number. A number 2 represents the full length polypeptide encoded by the gene specified the preceeding three digit number. A number 3 represents a polynucleotide fragment, of the gene represented by the preceeding three digit number, used to produce an antigenic polypeptide. A number 4 represents an antigenic polypeptide fragment, of the gene represented by the preceeding three digit number, used to stimulate an immune response or as a vaccine. The nucleotide and amino acid sequences of each gene and fragment are also shown in the Sequence Listing under the SEQ ID NO listed in Table 1.

Explanation of Table 2

Table 2 lists accession numbers for the closest matching sequences between

the polypeptides of the present invention and those available through GenBank and Derwent databases. These reference numbers are the database entry numbers commonly used by those of skill in the art, who will be familiar with their denominations. The descriptions of the nomenclature for GenBank are available from the National Center for Biotechnology Information. Column 1 lists the gene or ORF of the present invention. Column 2 lists the accession number of a "match" gene sequence in GenBank or Derwent databases. Column 3 lists the description of the "match" gene sequence. Columns 4 and 5 are the high score and smallest sum probability, respectively, calculated by BLAST. Polypeptides of the present invention that do not share significant identity/similarity with any polypeptide sequences of GenBank and Derwent are not represented in Table 2. Polypeptides of the present invention that share significant identity/similarity with more than one of the polypeptides of GenBank and Derwent are represented more than once.

15 ***Explanation of Table 3.***

The *E. faecalis* polypeptides of the present invention may include one or more conservative amino acid substitutions from natural mutations or human manipulation as indicated in Table 3. Changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein. Residues from the following groups, as indicated in Table 3, may be substituted for one another: Aromatic, Hydrophobic, Polar, Basic, Acidic, and Small,

Explanation of Table 4

Table 4 lists residues comprising antigenic epitopes of antigenic epitope-bearing fragments present in each of the full length *E. faecalis* polypeptides described in Table 1 as predicted by the inventors using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power Macintosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). *E. faecalis*

polypeptide shown in Table 1 may one or more antigenic epitopes comprising residues described in Table 4. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. The residues and locations shown described in Table 4 correspond to the amino acid sequences for each full length gene sequence shown in Table 1 and in the Sequence Listing. Polypeptides of the present invention that do not have antigenic epitopes recognized by the Jameson-Wolf algorithm are not represented in Table 2.

10 *Selection of Nucleic Acid Sequences Encoding Antigenic E. faecalis Polypeptides*

Sequenced *E. faecalis* genomic DNA was obtained from the *E. faecalis* strain V586. The *E. faecalis* strain V586 was deposited 2 May 1997 at the ATCC, 10801 University Blvd. Manassas, VA 20110-2209, and given accession number 55969.

Some ORFs contained in the subset of fragments of the *E. faecalis* genome disclosed herein were derived through the use of a number of screening criteria detailed below. The ORFs are bounded at the amino terminus by a methionine or valine residue and usually at the carboxy terminus by a stop codon.

Most of the selected sequences consist of complete ORFs. The polypeptides that do not comprise a complete ORF can be determined by determining whether the corresponding polynucleotide sequence comprises a stop codon after the codon for the last amino acid residue in the polypeptide sequence. It is not always preferred to express a complete ORF in a heterologous system. It may be challenging to express and purify a highly hydrophobic protein by common laboratory methods. Some of the polypeptide vaccine candidates described herein have been modified slightly to simplify the production of recombinant protein. For example, nucleotide sequences which encode highly hydrophobic domains, such as those found at the amino terminal signal sequence, have been excluded from some constructs used for expression of the polypeptides. Furthermore, any highly hydrophobic amino acid sequences occurring at the carboxy terminus have also been excluded from the recombinant expression

constructs. Thus, in one embodiment, a polypeptide which represents a truncated or modified ORF may be used as an antigen.

While numerous methods are known in the art for selecting potentially immunogenic polypeptides, many of the ORFs disclosed herein were selected on the basis of screening *Enterococcus faecalis* ORFs for several aspects of potential immunogenicity. One set of selection criteria are as follows:

1. *Type I signal sequence*: An amino terminal type I signal sequence generally directs a nascent protein across the plasma and outer membranes to the exterior of the bacterial cell. Experimental evidence obtained from studies with *Escherichia coli* suggests that the typical type I signal sequence consists of the following biochemical and physical attributes (Izard, J. W. and Kendall, D. A. *Mol. Microbiol.* 13:765-773 (1994)). The length of the type I signal sequence is approximately 15 to 25 primarily hydrophobic amino acid residues with a net positive charge in the extreme amino terminus. In addition, the central region of the signal sequence adopts an alpha-helical conformation in a hydrophobic environment. Finally, the region surrounding the actual site of cleavage is ideally six residues long, with small side-chain amino acids in the -1 and -3 positions.

2. *Type IV signal sequence*: The type IV signal sequence is an example of the several types of functional signal sequences which exist in addition to the type I signal sequence detailed above. Although functionally related, the type IV signal sequence possesses a unique set of biochemical and physical attributes (Strom, M. S. and Lory, S., *J. Bacteriol.* 174:7345-7351 (1992)). These are typically six to eight amino acids with a net basic charge followed by an additional sixteen to thirty primarily hydrophobic residues. The cleavage site of a type IV signal sequence is typically after the initial six to eight amino acids at the extreme amino terminus. In addition, type IV signal sequences generally contain a phenylalanine residue at the +1 site relative to the cleavage site.

3. *Lipoprotein*: Studies of the cleavage sites of twenty-six bacterial lipoprotein precursors has allowed the definition of a consensus amino acid sequence

for lipoprotein cleavage. Nearly three-fourths of the bacterial lipoprotein precursors examined contained the sequence L-(A,S)-(G,A)-C at positions -3 to +1, relative to the point of cleavage (Hayashi, S. and Wu, H. C., *J. Bioenerg. Biomembr.* 22:451-471 (1990)).

- 5 4. *LPXTG motif*: It has been experimentally determined that most anchored proteins found on the surface of gram-positive bacteria possess a highly conserved carboxy terminal sequence. More than fifty such proteins from organisms such as *S. pyogenes*, *S. mutans*, *E. faecalis*, *S. pneumoniae*, and others, have been identified based on their extracellular location and carboxy terminal amino acid sequence (Fischetti, V. A., *ASM News* 62:405-410 (1996)). The conserved region consists of six charged
10 amino acids at the extreme carboxy terminus coupled to 15-20 hydrophobic amino acids presumed to function as a transmembrane domain. Immediately adjacent to the transmembrane domain is a six amino acid sequence conserved in nearly all proteins examined. The amino acid sequence of this region is L-P-X-T-G-X, where X is any
15 amino acid.

 An algorithm for selecting antigenic and immunogenic *Enterococcus faecalis* polypeptides including the foregoing criteria was developed. The algorithm is similar to that described in U.S. patent application 08/781,986, filed January 3, 1997, which is fully incorporated by reference herein. Use of the algorithm by the inventors to
20 select immunologically useful *Enterococcus faecalis* polypeptides resulted in the selection of a number of the disclosed ORFs. Polypeptides comprising the polypeptides identified in this group may be produced by techniques standard in the art and as further described herein.

25 *Nucleic Acid Molecules*

Sequenced *E. faecalis* genomic DNA was obtained from the *E. faecalis* strain V586. As discussed elsewhere herein, polynucleotides of the present invention readily may be obtained by routine application of well known and standard procedures for cloning and sequencing DNA. Detailed methods for obtaining libraries and for sequencing are

provided below, for instance. A wide variety of *Enterococcus faecalis* strains that can be used to prepare *E. faecalis* genomic DNA for cloning and for obtaining polynucleotides and polypeptides of the present invention. A wide variety of *Enterococcus faecalis* strains are available to the public from recognized depository institutions, such as the American Type Culture Collection (ATCC). It is recognized that minor variation in the nucleic acid and amino acid sequence may be expected from *E. faecalis* strain to strain. The present invention provides for genes, including both polynucleotides and polypeptides, of the of the present invention from all the *Enterococcus faecalis* strains.

Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer (such as the Model 373 from Applied Biosystems, Inc., Foster City, CA), and all amino acid sequences of polypeptides encoded by DNA molecules determined herein were predicted by translation of a DNA sequence determined as above. Therefore, as is known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 90% identical, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence will be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion. In case of conflict between Table 1 and either the nucleic acid sequence of the clones listed in Table 1 or the amino acid sequence of the protein expressed by the clones listed in Table 1, the clones listed in Table 1 are controlling. By "nucleotide sequence" of a nucleic acid molecule or

polynucleotide is intended to mean either a DNA or RNA sequence. Using the information provided herein, such as the nucleotide sequence in Table 1, a nucleic acid molecule of the present invention encoding a *E. faecalis* polypeptide may be obtained using standard cloning and screening procedures, such as those for cloning DNAs using genomic DNA as starting material. See, e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989). Illustrative of the invention, the nucleic acid molecule described in Table 1 was discovered in a DNA library derived from a *E. faecalis* genomic DNA.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, DNA and genomic DNA obtained by cloning or produced synthetically. The DNA may be double-stranded or single-stranded. Single-stranded DNA or RNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

By "isolated" nucleic acid molecule(s) is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. This includes segments of DNA comprising the *E. faecalis* polynucleotides of the present invention isolated from the native chromosome. These fragments include both isolated fragments consisting only of *E. faecalis* DNA and fragments comprising heterologous sequences such as vector sequences or other foreign DNA. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

In addition, isolated nucleic acid molecules of the invention include DNA molecules which comprise a sequence substantially different from those described above but which, due to the degeneracy of the genetic code, still encode a *E. faecalis* polypeptides and peptides of the present invention (e.g. polypeptides of Table 1).

5 That is, all possible DNA sequences that encode the *E. faecalis* polypeptides of the present invention. This includes the genetic code and species-specific codon preferences known in the art. Thus, it would be routine for one skilled in the art to generate the degenerate variants described above, for instance, to optimize codon expression for a particular host (e.g., change codons in the bacteria mRNA to those
10 preferred by a mammalian or other bacterial host such as *E. coli*).

The invention further provides isolated nucleic acid molecules having the nucleotide sequence shown in Table 1 or a nucleic acid molecule having a sequence complementary to one of the above sequences. Such isolated molecules, particularly DNA molecules, are useful as probes for gene mapping and for identifying *E. faecalis*
15 in a biological sample, for instance, by PCR, Southern blot, Northern blot, or other form of hybridization analysis.

The present invention is further directed to nucleic acid molecules encoding portions or fragments of the nucleotide sequences described herein. Fragments include portions of the nucleotide sequences of Table 1, or the *E. faecalis* nucleotide
20 sequences contained in the plasmid clones listed in Table 1, at least 10 contiguous nucleotides in length selected from any two integers, one of which representing a 5' nucleotide position and a second of which representing a 3' nucleotide position, where the first nucleotide for each nucleotide sequence in Table 1 is position 1. That is, every combination of a 5' and 3' nucleotide position that a fragment at least 10
25 contiguous nucleotides in length could occupy is included in the invention. At least means a fragment may be 10 contiguous nucleotide bases in length or any integer between 10 and the length of an entire nucleotide sequence of Table 1 minus 1. Therefore, included in the invention are contiguous fragments specified by any 5' and 3' nucleotide base positions of a nucleotide sequences of Table 1 wherein the

contiguous fragment is any integer between 10 and the length of an entire nucleotide sequence minus 1.

Further, the invention includes polynucleotides comprising fragments specified by size, in nucleotides, rather than by nucleotide positions. The invention includes
5 any fragment size, in contiguous nucleotides, selected from integers between 10 and the length of an entire nucleotide sequence minus 1. Preferred sizes of contiguous nucleotide fragments include 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides. Other preferred sizes of contiguous nucleotide fragments, which may be useful as diagnostic probes and primers, include fragments 50-300 nucleotides in
10 length which include, as discussed above, fragment sizes representing each integer between 50-300. Larger fragments are also useful according to the present invention corresponding to most, if not all, of the nucleotide sequences shown in Table 1 or of the *E. faecalis* nucleotide sequences of the plasmid clones listed in Table 1. The preferred sizes are, of course, meant to exemplify not limit the present invention as all
15 size fragments, representing any integer between 10 and the length of an entire nucleotide sequence minus 1, are included in the invention. Additional preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding epitope-bearing portions of *E. faecalis* polypeptides identified in Table 4.

The present invention also provides for the exclusion of any fragment,
20 specified by 5' and 3' base positions or by size in nucleotide bases as described above for any nucleotide sequence of Table 1 or the plasmid clones listed in Table 1. Any number of fragments of nucleotide sequences in Table 1 or the plasmid clones listed in Table 1, specified by 5' and 3' base positions or by size in nucleotides, as described above, may be excluded from the present invention.

25 In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to a portion of a polynucleotide in a nucleic acid molecules of the invention described above, for instance, nucleotide sequences of Table 1 or the *E. faecalis* sequences of the plasmid clones listed in Table 1. By "stringent hybridization

conditions" is intended overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

By a polynucleotide which hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides bases, and more preferably at least about 20 nucleotides bases, still more preferably at least about 30 nucleotides bases, and even more preferably about 30-70 (e.g., 50) nucleotides bases of the reference polynucleotide. These are useful as diagnostic probes and primers as discussed above. By a portion of a polynucleotide of "at least 20 nucleotides bases in length," for example, is intended 20 or more contiguous nucleotides bases nucleotides from the nucleotide sequence of the reference polynucleotide (e.g., the nucleotide sequence as shown in Table 1). Portions of a polynucleotide which hybridizes to a nucleotide sequence in Table 1, which can be used as probes and primers, may also be precisely specified by 5' and 3' base positions or by size in nucleotide bases as described above or precisely excluded in the same manner.

The nucleic acid molecules of the present invention include those encoding the full length *E. faecalis* polypeptides of Table 1 and portions of the *E. faecalis* polypeptides of Table 1. Also included in the present invention are nucleic acids encoding the above full length sequences and further comprise additional sequences, such as those encoding an added secretory leader sequence, such as a pre-, or pro- or prepro- protein sequence. Further included in the present invention are nucleic acids encoding the above full length sequences and portions thereof and further comprise additional heterologous amino acid sequences encoded by nucleic acid sequences from a different source.

Also included in the present invention are nucleic acids encoding the above protein sequences together with additional, non-coding sequences, including for

example, but not limited to non-coding 5' and 3' sequences. These sequences include transcribed, non-translated sequences that may play a role in transcription, and mRNA processing, for example, ribosome binding and stability of mRNA. Also included in the present invention are additional coding sequences which provide
5 additional functionalities.

Thus, a nucleotide sequence encoding a polypeptide may be fused to a marker sequence, such as a sequence encoding a peptide which facilitates purification of the fused polypeptide. In certain preferred embodiments of this aspect of the invention, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in
10 a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. For instance, hexa-histidine provides for convenient purification of the fusion protein. See Gentz et al. (1989) Proc. Natl. Acad. Sci. 86:821-24. The "HA" tag is another peptide useful for purification which corresponds to an epitope derived from the influenza hemagglutinin
15 protein. See Wilson et al. (1984) Cell 37:767. As discussed below, other such fusion proteins include the *E. faecalis* polypeptides of the present invention fused to Fc at the N- or C-terminus.

Variant and Mutant Polynucleotides

20 The present invention further relates to variants of the nucleic acid molecules which encode portions, analogs or derivatives of a *E. faecalis* polypeptides of Table 1 and variant polypeptides thereof including portions, analogs, and derivatives of the *E. faecalis* polypeptides. Variants may occur naturally, such as a natural allelic variant. By an "allelic variant" is intended one of several alternate forms of a gene occupying a
25 given locus on a chromosome of an organism. See, e.g., B. Lewin, Genes IV (1990). Non-naturally occurring variants may be produced using art-known mutagenesis techniques.

Such nucleic acid variants include those produced by nucleotide substitutions, deletions, or additions. The substitutions, deletions, or additions may involve one or

more nucleotides. The variants may be altered in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of a *E. faecalis* protein of the present invention or portions thereof. Also especially preferred in this regard are conservative substitutions.

Such polypeptide variants include those produced by amino acid substitutions, deletions or additions. The substitutions, deletions, or additions may involve one or more residues. Alterations may produce conservative or non-conservative amino acid substitutions, deletions, or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of a *E. faecalis* protein of the present invention or portions thereof. Also especially preferred in this regard are conservative substitutions.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells containing the recombinant vectors, as well as to methods of making such vectors and host cells and for using them for production of *E. faecalis* polypeptides or peptides by recombinant techniques.

The present application is directed to nucleic acid molecules at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleic acid sequence shown in Table 1. The above nucleic acid sequences are included irrespective of whether they encode a polypeptide having *E. faecalis* activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having *E. faecalis* activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having *E. faecalis* activity include, *inter alia*, isolating an *E. faecalis* gene or allelic variants thereof from a DNA library, and detecting *E. faecalis*

mRNA expression samples, environmental samples, suspected of containing *E. faecalis* by Northern Blot analysis.

Preferred, are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in Table 1, which do, in fact, encode a polypeptide having *E. faecalis* protein activity. By "a polypeptide having *E. faecalis* activity" is intended polypeptides exhibiting activity similar, but not necessarily identical, to an activity of the *E. faecalis* protein of the invention, as measured in a particular biological assay suitable for measuring activity of the specified protein.

Due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequences shown in Table 1 will encode a polypeptide having *E. faecalis* protein activity. In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having *E. faecalis* protein activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

The biological activity or function of the polypeptides of the present invention are expected to be similar or identical to polypeptides from other bacteria that share a high degree of structural identity/similarity. Tables 2 lists accession numbers and descriptions for the closest matching sequences of polypeptides available through Genbank and Derwent databases. It is therefore expected that the biological activity or function of the polypeptides of the present invention will be similar or identical to those polypeptides from other bacterial genres, species, or strains listed in Table 2.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the *E. faecalis* polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted, inserted, or substituted with another nucleotide. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. *See Brutlag et al. (1990) Comp. App. Biosci. 6:237-245.* In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by first converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3'

truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only nucleotides outside the 5' and 3' nucleotides of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 nucleotide subject sequence is aligned to a 100 nucleotide query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 nucleotides at 5' end. The 10 unpaired nucleotides represent 10% of the sequence (number of nucleotides at the 5' and 3' ends not matched/total number of nucleotides in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 nucleotides were perfectly matched the final percent identity would be 90%. In another example, a 90 nucleotide subject sequence is compared with a 100 nucleotide query sequence. This time the deletions are internal deletions so that there are no nucleotides on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only nucleotides 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

Vectors and Host Cell

The present invention also relates to vectors which include the isolated DNA molecules of the present invention, host cells comprising the recombinant vectors, and the production of *E. faecalis* polypeptides and peptides of the present invention expressed by the host cells.

5 Recombinant constructs may be introduced into host cells using well known techniques such as infection, transduction, transfection, transvection, electroporation and transformation. The vector may be, for example, a phage, plasmid, viral or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in
10 complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged *in vitro* using an appropriate packaging cell line
15 and then transduced into host cells.

Preferred are vectors comprising *cis*-acting control regions to the polynucleotide of interest. Appropriate *trans*-acting factors may be supplied by the host, supplied by a complementing vector or supplied by the vector itself upon introduction into the host.

20 In certain preferred embodiments in this regard, the vectors provide for specific expression, which may be inducible and/or cell type-specific. Particularly preferred among such vectors are those inducible by environmental factors that are easy to manipulate, such as temperature and nutrient additives.

Expression vectors useful in the present invention include chromosomal-,
25 episomal- and virus-derived vectors, *e.g.*, vectors derived from bacterial plasmids, bacteriophage, yeast episomes, yeast chromosomal elements, viruses such as baculoviruses, papova viruses, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as cosmids and phagemids.

The DNA insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the *E. coli lac*, *trp* and *tac* promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression
5 constructs will further contain sites for transcription initiation, termination and, in the transcribed region, a ribosome binding site for translation. The coding portion of the mature transcripts expressed by the constructs will preferably include a translation initiating site at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

10 As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin, or ampicillin resistance genes for culturing in *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*,
15 *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE9,
20 pQE10 available from Qiagen; pBS vectors, Phagescript vectors, Bluescript vectors, pNH8A, pNH16a, pNH18A, pNH46A available from Stratagene; pET series of vectors available from Novagen; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV,
25 pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Among known bacterial promoters suitable for use in the present invention include the *E. coli lacI* and *lacZ* promoters, the T3, T5 and T7 promoters, the *gpt* promoter, the lambda PR and PL promoters and the *trp* promoter. Suitable eukaryotic

promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, the early and late SV40 promoters, the promoters of retroviral LTRs, such as those of the Rous sarcoma virus (RSV), and metallothionein promoters, such as the mouse metallothionein-I promoter.

5 Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection or other methods. Such methods are described in many standard laboratory manuals (for example, Davis, *et al.*, *Basic Methods In Molecular Biology* (1986)).

10 Transcription of DNA encoding the polypeptides of the present invention by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are *cis*-acting elements of DNA, usually about from 10 to 300 nucleotides that act to increase transcriptional activity of a promoter in a given host cell-type. Examples of enhancers include the SV40 enhancer, which is located on the late side of
15 the replication origin at nucleotides 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

For secretion of the translated polypeptide into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment,
20 appropriate secretion signals may be incorporated into the expressed polypeptide, for example, the amino acid sequence KDEL. The signals may be endogenous to the polypeptide or they may be heterologous signals.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals, but also additional heterologous
25 functional regions. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence in the host cell, during purification, or during subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the

polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability and to facilitate purification, among others, are familiar and routine techniques in the art. A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize proteins. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is thoroughly advantageous for use in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified in the advantageous manner described. This is the case when Fc portion proves to be a hindrance to use in therapy and diagnosis, for example when the fusion protein is to be used as antigen for immunizations. In drug discovery, for example, human proteins, such as, hIL5-receptor has been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. See Bennett, D. et al. (1995) J. Molec. Recogn. 8:52-58 and Johanson, K. et al. (1995) J. Biol. Chem. 270 (16):9459-9471.

The *E. faecalis* polypeptides can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin chromatography and high performance liquid chromatography ("HPLC") is employed for purification. Polypeptides of the present invention include naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect and mammalian cells.

Polypeptides and Fragments

The invention further provides an isolated *E. faecalis* polypeptide having an amino acid sequence in Table 1, or a peptide or polypeptide comprising a portion of the above polypeptides.

5

Variant and Mutant Polypeptides

To improve or alter the characteristics of *E. faecalis* polypeptides of the present invention, protein engineering may be employed. Recombinant DNA technology known to those skilled in the art can be used to create novel mutant proteins or muteins including single or multiple amino acid substitutions, deletions, additions, or fusion proteins. Such modified polypeptides can show, e.g., enhanced activity or increased stability. In addition, they may be purified in higher yields and show better solubility than the corresponding natural polypeptide, at least under certain purification and storage conditions.

15

N-Terminal and C-Terminal Deletion Mutants

It is known in the art that one or more amino acids may be deleted from the N-terminus or C-terminus without substantial loss of biological function. For instance, Ron et al. J. Biol. Chem., 268:2984-2988 (1993), reported modified KGF proteins that had heparin binding activity even if 3, 8, or 27 N-terminal amino acid residues were missing. Accordingly, the present invention provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of the *E. faecalis* polypeptides shown in Table 1, and polynucleotides encoding such polypeptides.

25

Similarly, many examples of biologically functional C-terminal deletion muteins are known. For instance, Interferon gamma shows up to ten times higher activities by deleting 8-10 amino acid residues from the carboxy terminus of the protein *See, e.g.,* Dobeli, et al. (1988) J. Biotechnology 7:199-216. Accordingly, the present invention provides polypeptides having one or more residues from the

carboxy terminus of the amino acid sequence of the *E. faecalis* polypeptides shown in Table 1. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini as described below.

The present invention is further directed to polynucleotide encoding portions or fragments of the amino acid sequences described herein as well as to portions or fragments of the isolated amino acid sequences described herein. Fragments include portions of the amino acid sequences of Table 1, are at least 5 contiguous amino acid in length, are selected from any two integers, one of which representing a N-terminal position. The initiation codon of the polypeptides of the present inventions position 1. Every combination of a N-terminal and C-terminal position that a fragment at least 5 contiguous amino acid residues in length could occupy, on any given amino acid sequence of Table 1 is included in the invention. At least means a fragment may be 5 contiguous amino acid residues in length or any integer between 5 and the number of residues in a full length amino acid sequence minus 1. Therefore, included in the invention are contiguous fragments specified by any N-terminal and C-terminal positions of amino acid sequence set forth in Table 1 wherein the contiguous fragment is any integer between 5 and the number of residues in a full length sequence minus 1.

Further, the invention includes polypeptides comprising fragments specified by size, in amino acid residues, rather than by N-terminal and C-terminal positions. The invention includes any fragment size, in contiguous amino acid residues, selected from integers between 5 and the number of residues in a full length sequence minus 1. Preferred sizes of contiguous polypeptide fragments include about 5 amino acid residues, about 10 amino acid residues, about 20 amino acid residues, about 30 amino acid residues, about 40 amino acid residues, about 50 amino acid residues, about 100 amino acid residues, about 200 amino acid residues, about 300 amino acid residues, and about 400 amino acid residues. The preferred sizes are, of course, meant to exemplify, not limit, the present invention as all size fragments representing any integer between 5 and the number of residues in a full length sequence minus 1 are included in the invention. The present invention also provides for the exclusion of any

fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above. Any number of fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above may be excluded.

- 5 The above fragments need not be active since they would be useful, for example, in immunoassays, in epitope mapping, epitope tagging, to generate antibodies to a particular portion of the protein, as vaccines, and as molecular weight markers.

10 *Other Mutants*

- In addition to N- and C-terminal deletion forms of the protein discussed above, it also will be recognized by one of ordinary skill in the art that some amino acid sequences of the *E. faecalis* polypeptide can be varied without significant effect of the structure or function of the protein. If such differences in sequence are contemplated,
15 it should be remembered that there will be critical areas on the protein which determine activity.

- Thus, the invention further includes variations of the *E. faecalis* polypeptides which show substantial *E. faecalis* polypeptide activity or which include regions of *E. faecalis* protein such as the protein portions discussed below. Such mutants include
20 deletions, insertions, inversions, repeats, and type substitutions selected according to general rules known in the art so as to have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided. There are two main approaches for studying the tolerance of an amino acid sequence to change. See, Bowie, J. U. *et al.* (1990), Science 247:1306-1310. The first
25 method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality.

 These studies have revealed that proteins are surprisingly tolerant of amino

acid substitutions. The studies indicate which amino acid changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Other such phenotypically silent substitutions are described by

5 Bowie et al. (*supra*) and the references cited therein. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic

10 residues Phe, Tyr.

Thus, the fragment, derivative, analog, or homolog of the polypeptide of Table 1, or that encoded by the plaimds listed in Table 1, may be: (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted

15 amino acid residue may or may not be one encoded by the genetic code: or (ii) one in which one or more of the amino acid residues includes a substituent group: or (iii) one in which the *E. faecalis* polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol): or (iv) one in which the additional amino acids are fused to the above form of

20 the polypeptide, such as an IgG Fc fusion region peptide or leader or secretory sequence or a sequence which is employed for purification of the above form of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

Thus, the *E. faecalis* polypeptides of the present invention may include one or

25 more amino acid substitutions, deletions, or additions, either from natural mutations or human manipulation. As indicated, changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein (see Table 3).

Amino acids in the *E. faecalis* proteins of the present invention that are

essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis. *See, e.g.*, Cunningham et al. (1989) Science 244:1081-1085. The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then
5 tested for biological activity using assays appropriate for measuring the function of the particular protein.

Of special interest are substitutions of charged amino acids with other charged or neutral amino acids which may produce proteins with highly desirable improved characteristics, such as less aggregation. Aggregation may not only reduce activity but
10 also be problematic when preparing pharmaceutical formulations, because aggregates can be immunogenic. *See, e.g.*, Pinckard et al., (1967) Clin. Exp. Immunol. 2:331-340; Robbins, et al., (1987) Diabetes 36:838-845; Cleland, et al., (1993) Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377.

The polypeptides of the present invention are preferably provided in an
15 isolated form, and preferably are substantially purified. A recombinantly produced version of the *E. faecalis* polypeptide can be substantially purified by the one-step method described by Smith et al. (1988) Gene 67:31-40. Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies directed against the polypeptides of the invention in methods which are well known in
20 the art of protein purification.

The invention further provides for isolated *E. faecalis* polypeptides comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of a full-length *E. faecalis* polypeptide having the complete amino acid sequence shown in Table 1; (b) the amino acid sequence of a full-length *E.*
25 *faecalis* polypeptide having the complete amino acid sequence shown in Table 1 excepting the N-terminal methionine; (c) the complete amino acid sequence encoded by the plaimds listed in Table 1; and (d) the complete amino acid sequence excepting the N-terminal methionine encoded by the plaimds listed in Table 1. The polypeptides of the present invention also include polypeptides having an amino acid

sequence at least 80% identical, more preferably at least 90% identical, and still more preferably 95%, 96%, 97%, 98% or 99% identical to those described in (a), (b), (c), and (d) above.

Further polypeptides of the present invention include polypeptides which
5 have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above.

A further embodiment of the invention relates to a polypeptide which
comprises the amino acid sequence of a *E. faecalis* polypeptide having an amino acid
sequence which contains at least one conservative amino acid substitution, but not
10 more than 50 conservative amino acid substitutions, not more than 40 conservative
amino acid substitutions, not more than 30 conservative amino acid substitutions, and
not more than 20 conservative amino acid substitutions. Also provided are
polypeptides which comprise the amino acid sequence of a *E. faecalis* polypeptide,
having at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 conservative amino
15 acid substitutions.

By a polypeptide having an amino acid sequence at least, for example, 95%
"identical" to a query amino acid sequence of the present invention, it is intended that
the amino acid sequence of the subject polypeptide is identical to the query sequence
except that the subject polypeptide sequence may include up to five amino acid
20 alterations per each 100 amino acids of the query amino acid sequence. In other
words, to obtain a polypeptide having an amino acid sequence at least 95% identical
to a query amino acid sequence, up to 5% of the amino acid residues in the subject
sequence may be inserted, deleted, (indels) or substituted with another amino acid.
These alterations of the reference sequence may occur at the amino or carboxy
25 terminal positions of the reference amino acid sequence or anywhere between those
terminal positions, interspersed either individually among residues in the reference
sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%,
95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences

shown in Table 1 or to the amino acid sequence encoded by the plaimds listed in Table 1 can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al., (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the query and subject sequences are both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, the results, in percent identity, must be manually corrected. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query amino acid residues outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not match/align with the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected. No other manual corrections are to be made for the purposes of the present invention.

The above polypeptide sequences are included irrespective of whether they have their normal biological activity. This is because even where a particular polypeptide molecule does not have biological activity, one of skill in the art would still know how to use the polypeptide, for instance, as a vaccine or to generate antibodies. Other uses of the polypeptides of the present invention that do not have *E. faecalis* activity include, *inter alia*, as epitope tags, in epitope mapping, and as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods known to those of skill in the art.

As described below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting *E. faecalis* protein expression or as agonists and antagonists capable of enhancing or inhibiting *E. faecalis* protein function. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" *E. faecalis* protein binding proteins

which are also candidate agonists and antagonists according to the present invention.
See, e.g., Fields et al. (1989) Nature 340:245-246.

Epitope-Bearing Portions

5 In another aspect, the invention provides peptides and polypeptides comprising epitope-bearing portions of the *E. faecalis* polypeptides of the present invention. These epitopes are immunogenic or antigenic epitopes of the polypeptides of the present invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein or polypeptide is the
10 immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic determinant" or "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. *See, e.g.,* Geysen, et al. (1983) Proc. Natl. Acad. Sci. USA 81:3998- 4002.
15 Predicted antigenic epitopes are shown in Table 4, below. It is pointed out that Table 4 only lists amino acid residues comprising epitopes predicted to have the highest degree of antigenicity. The polypeptides not listed in Table 4 and portions of polypeptides not listed in Table 4 are not considered non-antigenic. This is because they may still be antigenic *in vivo* but merely not recognized as such by the particular
20 algorithm used. Thus, Table 4 lists the amino acid residues comprising preferred antigenic epitopes but not a complete list. Amino acid residues comprising other antigenic epitopes may be determined by algorithms similar to the Jameson-Wolf analysis or by *in vivo* testing for an antigenic response using the methods described herein or those known in the art.

25 As to the selection of peptides or polypeptides bearing an antigenic epitope (*i.e.*, that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. *See, e.g.,* Sutcliffe, et al., (1983) Science 219:660-666.

Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (*i.e.*, immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are
5 extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the mimicked protein; longer, peptides, especially those containing proline residues, usually are effective. *See*, Sutcliffe, et al., *supra*, p. 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1
10 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind
15 specifically to a polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. *See* Sutcliffe, et al., *supra*, p. 663. The antibodies raised by antigenic epitope-bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to
20 different peptides may be used for tracking the fate of various regions of a protein precursor which undergoes post-translational processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (*e.g.*, about 9 amino acids) can bind and displace the larger
25 peptides in immunoprecipitation assays. *See, e.g.*, Wilson, et al., (1984) Cell 37:767-778. The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for instance, by adsorption chromatography using methods known in the art.

Antigenic epitope-bearing peptides and polypeptides of the invention

designed according to the above guidelines preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (i.e. any integer between 7 and 50) contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide of the invention, containing about 50 to about 100 amino acids, or any length up to and including the entire amino acid sequence of a polypeptide of the invention, also are considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (*i.e.*, the sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); and sequences containing proline residues are particularly preferred.

Non-limiting examples of antigenic polypeptides or peptides that can be used to generate an enterococcal-specific immune response or antibodies include portions of the amino acid sequences identified in Table 1. More specifically, Table 4 discloses a list of non-limiting residues that are involved in the antigenicity of the epitope-bearing fragments of the present invention. Therefore, the present inventions provides for isolated and purified antigenic epitope-bearing fragments of the polypeptides of the present invention comprising a peptide sequences of Table 4. The antigenic epitope-bearing fragments comprising a peptide sequence of Table 4 preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (i.e. any integer between 7 and 50) of a polypeptide of the present invention. That is, included in the present invention are antigenic polypeptides between the integers of 7 and 50 amino acid in length comprising one or more of the sequences of Table 4. Therefore, in most cases, the polypeptides of Table 4 make up only a portion of the antigenic polypeptide. All combinations of sequences between the integers of 7 and 50 amino acid in length comprising one or more of the sequences of Table 4 are included. The antigenic epitope-bearing

fragements may be specified by either the number of contiguous amino acid residues or by specific N-terminal and C-terminal positions as described above for the polypeptide fragements of the present invention, wherein the initiation codon is residue 1. Any number of the described antigenic epitope-bearing fragements of the present invention may also be excluded from the present invention in the same manner.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, an epitope-bearing amino acid sequence of the present invention may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing single amino acid variants of a segment of the HA1 polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four weeks (Houghten, R. A. Proc. Natl. Acad. Sci. USA **82**:5131-5135 (1985)). This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten and coworkers (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps involved in solid-phase methods. A completely manual procedure allows 500-1000 or more syntheses to be conducted simultaneously (Houghten et al. (1985) Proc. Natl. Acad. Sci. **82**:5131-5135 at 5134.

Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. *See, e.g.,* Sutcliffe, et al., *supra*;; Wilson, et al., *supra*;; and Bittle, et al. (1985) J. Gen. Virol. **66**:2347-2354. Generally, animals may be immunized with free peptide; however, anti-peptide

antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker such as m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carrier using a more general linking agent such as glutaraldehyde.

Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg peptide or carrier protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

Immunogenic epitope-bearing peptides of the invention, *i.e.*, those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance, Geysen, *et al.*, *supra*, discloses a procedure for rapid concurrent synthesis on solid supports of hundreds of peptides of sufficient purity to react in an ELISA. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease virus was located by Geysen *et al.* *supra* with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the

reaction with antibody were determined. Thus, peptide analogs of the epitope-bearing peptides of the invention can be made routinely by this method. U.S. Patent No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

5 Further still, U.S. Patent No. 5,194,392, to Geysen (1990), describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (*i.e.*, a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092, also to Geysen (1989),
10 describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. *et al.* (1996) discloses linear C₁-C₇-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and
15 libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods. The entire disclosure of each document cited in this section on "Polypeptides and Fragments" is hereby incorporated herein by reference.

20 As one of skill in the art will appreciate, the polypeptides of the present invention and the epitope-bearing fragments thereof described above can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life *in vivo*. This has been shown, *e.g.*, for chimeric proteins consisting of the
25 first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EPA 0,394,827; Trauneker *et al.* (1988) *Nature* 331:84-86. Fusion proteins that have a disulfide-linked dimeric structure due to the IgG part can also be more efficient in binding and neutralizing other molecules than a monomeric *E. faecalis* polypeptide or

fragment thereof alone. *See* Fountoulakis et al. (1995) J. Biochem. 270:3958-3964. Nucleic acids encoding the above epitopes of *E. faecalis* polypeptides can also be recombined with a gene of interest as an epitope tag to aid in detection and purification of the expressed polypeptide.

5

Antibodies

E. faecalis protein-specific antibodies for use in the present invention can be raised against the intact *E. faecalis* protein or an antigenic polypeptide fragment thereof, which may be presented together with a carrier protein, such as an albumin, to
10 an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier.

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules, single chain whole antibodies, and antibody fragments. Antibody fragments of the present invention include Fab and F(ab')₂ and
15 other fragments including single-chain Fvs (scFv) and disulfide-linked Fvs (sdFv). Also included in the present invention are chimeric and humanized monoclonal antibodies and polyclonal antibodies specific for the polypeptides of the present invention. The antibodies of the present invention may be prepared by any of a variety of methods. For example, cells expressing a polypeptide of the present
20 invention or an antigenic fragment thereof can be administered to an animal in order to induce the production of sera containing polyclonal antibodies. For example, a preparation of *E. faecalis* polypeptide or fragment thereof is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific
25 activity.

In a preferred method, the antibodies of the present invention are monoclonal antibodies or binding fragments thereof. Such monoclonal antibodies can be prepared using hybridoma technology. *See, e.g.,* Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988);

Hammerling, et al., in: MONOCLONAL ANTIBODIES AND T-CELL HYBRIDOMAS 563-681 (Elsevier, N.Y., 1981). Fab and F(ab')₂ fragments may be produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, *E. faecalis* polypeptide-binding fragments, chimeric, and humanized antibodies can be produced through the application of recombinant DNA technology or through synthetic chemistry using methods known in the art.

Alternatively, additional antibodies capable of binding to the polypeptide antigen of the present invention may be produced in a two-step procedure through the use of anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and that, therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, *E. faecalis* polypeptide-specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the *E. faecalis* polypeptide-specific antibody can be blocked by the *E. faecalis* polypeptide antigen. Such antibodies comprise anti-idiotypic antibodies to the *E. faecalis* polypeptide-specific antibody and can be used to immunize an animal to induce formation of further *E. faecalis* polypeptide-specific antibodies.

Antibodies and fragments thereof of the present invention may be described by the portion of a polypeptide of the present invention recognized or specifically bound by the antibody. Antibody binding fragments of a polypeptide of the present invention may be described or specified in the same manner as for polypeptide fragments discussed above, i.e., by N-terminal and C-terminal positions or by size in contiguous amino acid residues. Any number of antibody binding fragments, of a polypeptide of the present invention, specified by N-terminal and C-terminal positions or by size in amino acid residues, as described above, may also be excluded from the present invention. Therefore, the present invention includes antibodies the specifically bind a particularly described fragment of a polypeptide of the present

invention and allows for the exclusion of the same.

Antibodies and fragments thereof of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies and fragments that do not bind polypeptides of any other species of *Enterococcus* other than *E.*

5 *faecalis* are included in the present invention. Likewise, antibodies and fragments that bind only species of *Enterococcus*, i.e. antibodies and fragments that do not bind bacteria from any genus other than *Enterococcus*, are included in the present invention.

10 ***Diagnostic Assays***

The present invention further relates to methods for assaying *staphylococcal* infection in an animal by detecting the expression of genes encoding *staphylococcal* polypeptides of the present invention. The methods comprise analyzing tissue or body fluid from the animal for *Enterococcus*-specific antibodies, nucleic acids, or
15 proteins. Analysis of nucleic acid specific to *Enterococcus* is assayed by PCR or hybridization techniques using nucleic acid sequences of the present invention as either hybridization probes or primers. See, e.g., Sambrook et al. Molecular cloning: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 2nd ed., 1989, page 54 reference); Eremeeva et al. (1994) J. Clin. Microbiol. 32:803-810 (describing
20 differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA) and Chen et al. 1994 J. Clin. Microbiol. 32:589-595 (detecting *B. burgdorferi* nucleic acids via PCR).

Where diagnosis of a disease state related to infection with *Enterococcus* has already been made, the present invention is useful for monitoring progression or
25 regression of the disease state whereby patients exhibiting enhanced *Enterococcus* gene expression will experience a worse clinical outcome relative to patients expressing these gene(s) at a lower level.

By "biological sample" is intended any biological sample obtained from an animal, cell line, tissue culture, or other source which contains *Enterococcus*

polypeptide, mRNA, or DNA. Biological samples include body fluids (such as saliva, blood, plasma, urine, mucus, synovial fluid, etc.) tissues (such as muscle, skin, and cartilage) and any other biological source suspected of containing *Enterococcus* polypeptides or nucleic acids. Methods for obtaining biological samples such as
5 tissue are well known in the art.

The present invention is useful for detecting diseases related to *Enterococcus* infections in animals. Preferred animals include monkeys, apes, cats, dogs, birds, cows, pigs, mice, horses, rabbits and humans. Particularly preferred are humans.

Total RNA can be isolated from a biological sample using any suitable
10 technique such as the single-step guanidinium-thiocyanate-phenol-chloroform method described in Chomczynski et al. (1987) Anal. Biochem. 162:156-159. mRNA encoding *Enterococcus* polypeptides having sufficient homology to the nucleic acid sequences identified in Table 1 to allow for hybridization between complementary sequences are then assayed using any appropriate method. These include Northern blot analysis, S1
15 nuclease mapping, the polymerase chain reaction (PCR), reverse transcription in combination with the polymerase chain reaction (RT-PCR), and reverse transcription in combination with the ligase chain reaction (RT-LCR).

Northern blot analysis can be performed as described in Harada et al. (1990) Cell 63:303-312. Briefly, total RNA is prepared from a biological sample as described
20 above. For the Northern blot, the RNA is denatured in an appropriate buffer (such as glyoxal/dimethyl sulfoxide/sodium phosphate buffer), subjected to agarose gel electrophoresis, and transferred onto a nitrocellulose filter. After the RNAs have been linked to the filter by a UV linker, the filter is prehybridized in a solution containing formamide, SSC, Denhardt's solution, denatured salmon sperm, SDS, and sodium
25 phosphate buffer. A *E. faecalis* polynucleotide sequence shown in Table 1 labeled according to any appropriate method (such as the ³²P-multiprimed DNA labeling system (Amersham)) is used as probe. After hybridization overnight, the filter is washed and exposed to x-ray film. DNA for use as probe according to the present invention is described in the sections above and will preferably at least 15 nucleotides

in length.

S1 mapping can be performed as described in Fujita et al. (1987) Cell 49:357-367. To prepare probe DNA for use in S1 mapping, the sense strand of an above-described *E. faecalis* DNA sequence of the present invention is used as a
5 template to synthesize labeled antisense DNA. The antisense DNA can then be digested using an appropriate restriction endonuclease to generate further DNA probes of a desired length. Such antisense probes are useful for visualizing protected bands corresponding to the target mRNA (*i.e.*, mRNA encoding *Enterococcus* polypeptides).

10 Levels of mRNA encoding *Enterococcus* polypeptides are assayed, for *e.g.*, using the RT-PCR method described in Makino et al. (1990) Technique 2:295-301. By this method, the radioactivities of the "amplicons" in the polyacrylamide gel bands are linearly related to the initial concentration of the target mRNA. Briefly, this method involves adding total RNA isolated from a biological sample in a reaction
15 mixture containing a RT primer and appropriate buffer. After incubating for primer annealing, the mixture can be supplemented with a RT buffer, dNTPs, DTT, RNase inhibitor and reverse transcriptase. After incubation to achieve reverse transcription of the RNA, the RT products are then subject to PCR using labeled primers. Alternatively, rather than labeling the primers, a labeled dNTP can be included in the
20 PCR reaction mixture. PCR amplification can be performed in a DNA thermal cycler according to conventional techniques. After a suitable number of rounds to achieve amplification, the PCR reaction mixture is electrophoresed on a polyacrylamide gel. After drying the gel, the radioactivity of the appropriate bands (corresponding to the mRNA encoding the *Enterococcus* polypeptides of the present invention) are
25 quantified using an imaging analyzer. RT and PCR reaction ingredients and conditions, reagent and gel concentrations, and labeling methods are well known in the art. Variations on the RT-PCR method will be apparent to the skilled artisan. Other PCR methods that can detect the nucleic acid of the present invention can be found in PCR PRIMER: A LABORATORY MANUAL (C.W. Dieffenbach et al. eds., Cold

Spring Harbor Lab Press, 1995).

The polynucleotides of the present invention, including both DNA and RNA, may be used to detect polynucleotides of the present invention or Enterococcal species including *E. faecalis* using bio chip technology. The present invention

5 includes both high density chip arrays (>1000 oligonucleotides per cm^2) and low density chip arrays (<1000 oligonucleotides per cm^2). Bio chips comprising arrays of polynucleotides of the present invention may be used to detect Enterococcal species, including *E. faecalis*, in biological and environmental samples and to diagnose an animal, including humans, with an *E. faecalis* or other Enterococcal infection. The bio

10 chips of the present invention may comprise polynucleotide sequences of other pathogens including bacteria, viral, parasitic, and fungal polynucleotide sequences, in addition to the polynucleotide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips can also be used to monitor an *E. faecalis* or other Enterococcal infections and to monitor the genetic

15 changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip technology comprising arrays of polynucleotides of the present invention may also be used to simultaneously monitor the expression of a multiplicity of genes, including those of the present invention. The polynucleotides used to comprise a selected array may be specified in

20 the same manner as for the fragments, i.e, by their 5' and 3' positions or length in contiguous base pairs and include from. Methods and particular uses of the polynucleotides of the present invention to detect Enterococcal species, including *E. faecalis*, using bio chip technology include those known in the art and those of: U.S. Patent Nos. 5510270, 5545531, 5445934, 5677195, 5532128, 5556752, 5527681,

25 5451683, 5424186, 5607646, 5658732 and World Patent Nos. WO/9710365, WO/9511995, WO/9743447, WO/9535505, each incorporated herein in their entireties.

Biosensors using the polynucleotides of the present invention may also be used to detect, diagnose, and monitor *E. faecalis* or other Enterococcal species and

infections thereof. Biosensors using the polynucleotides of the present invention may also be used to detect particular polynucleotides of the present invention. Biosensors using the polynucleotides of the present invention may also be used to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. Methods and particular uses of the polynucleotides of the present invention to detect Enterococcal species, including *E. faecalis*, using biosensors include those known in the art and those of: U.S. Patent Nos. 5721102, 5658732, 5631170, and World Patent Nos. WO97/35011, WO/9720203, each incorporated herein in their entireties.

Thus, the present invention includes both bio chips and biosensors comprising polynucleotides of the present invention and methods of their use.

Assaying *Enterococcus* polypeptide levels in a biological sample can occur using any art-known method, such as antibody-based techniques. For example, *Enterococcus* polypeptide expression in tissues can be studied with classical immunohistological methods. In these, the specific recognition is provided by the primary antibody (polyclonal or monoclonal) but the secondary detection system can utilize fluorescent, enzyme, or other conjugated secondary antibodies. As a result, an immunohistological staining of tissue section for pathological examination is obtained. Tissues can also be extracted, e.g., with urea and neutral detergent, for the liberation of *Enterococcus* polypeptides for Western-blot or dot/slot assay. See, e.g., Jalkanen, M. et al. (1985) J. Cell. Biol. 101:976-985; Jalkanen, M. et al. (1987) J. Cell. Biol. 105:3087-3096. In this technique, which is based on the use of cationic solid phases, quantitation of a *Enterococcus* polypeptide can be accomplished using an isolated *Enterococcus* polypeptide as a standard. This technique can also be applied to body fluids.

Other antibody-based methods useful for detecting *Enterococcus* polypeptide gene expression include immunoassays, such as the ELISA and the radioimmunoassay (RIA). For example, a *Enterococcus* polypeptide-specific monoclonal antibodies can be used both as an immunoabsorbent and as an enzyme-labeled probe to detect and

quantify a *Enterococcus* polypeptide. The amount of a *Enterococcus* polypeptide present in the sample can be calculated by reference to the amount present in a standard preparation using a linear regression computer algorithm. Such an ELISA is described in Iacobelli et al. (1988) Breast Cancer Research and Treatment 11:19-30. In
5 another ELISA assay, two distinct specific monoclonal antibodies can be used to detect *Enterococcus* polypeptides in a body fluid. In this assay, one of the antibodies is used as the immunoabsorbent and the other as the enzyme-labeled probe.

The above techniques may be conducted essentially as a "one-step" or "two-step" assay. The "one-step" assay involves contacting the *Enterococcus*
10 polypeptide with immobilized antibody and, without washing, contacting the mixture with the labeled antibody. The "two-step" assay involves washing before contacting the mixture with the labeled antibody. Other conventional methods may also be employed as suitable. It is usually desirable to immobilize one component of the assay system on a support, thereby allowing other components of the system to be
15 brought into contact with the component and readily removed from the sample. Variations of the above and other immunological methods included in the present invention can also be found in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

Suitable enzyme labels include, for example, those from the oxidase group,
20 which catalyze the production of hydrogen peroxide by reacting with substrate. Glucose oxidase is particularly preferred as it has good stability and its substrate (glucose) is readily available. Activity of an oxidase label may be assayed by measuring the concentration of hydrogen peroxide formed by the enzyme-labeled antibody/substrate reaction. Besides enzymes, other suitable labels include
25 radioisotopes, such as iodine (^{125}I , ^{121}I), carbon (^{14}C), sulphur (^{35}S), tritium (^3H), indium (^{112}In), and technetium ($^{99\text{m}}\text{Tc}$), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Further suitable labels for the *Enterococcus* polypeptide-specific antibodies of the present invention are provided below. Examples of suitable enzyme labels include

malate dehydrogenase, Enterococcal nuclease, delta-5-steroid isomerase, yeast-alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, and
5 acetylcholine esterase.

Examples of suitable radioisotopic labels include ^3H , ^{111}In , ^{125}I , ^{131}I , ^{32}P , ^{35}S , ^{14}C , ^{51}Cr , ^{57}Co , ^{58}Co , ^{59}Fe , ^{75}Se , ^{152}Eu , ^{90}Y , ^{67}Cu , ^{217}Bi , ^{211}At , ^{212}Pb , ^{47}Sc , ^{109}Pd , etc. ^{111}In is a preferred isotope where *in vivo* imaging is used since it avoids the problem of dehalogenation of the ^{125}I or ^{131}I -labeled monoclonal antibody by the liver. In
10 addition, this radionuclide has a more favorable gamma emission energy for imaging. See, e.g., Perkins et al. (1985) Eur. J. Nucl. Med. 10:296-301; Carasquillo et al. (1987) J. Nucl. Med. 28:281-287. For example, ^{111}In coupled to monoclonal antibodies with 1-(P-isothiocyanatobenzyl)-DPTA has shown little uptake in non-tumor tissues, particularly the liver, and therefore enhances specificity of tumor
15 localization. See, Esteban et al. (1987) J. Nucl. Med. 28:861-870.

Examples of suitable non-radioactive isotopic labels include ^{157}Gd , ^{55}Mn , ^{162}Dy , ^{52}Tr , and ^{56}Fe .

Examples of suitable fluorescent labels include an ^{152}Eu label, a fluorescein label, an isothiocyanate label, a rhodamine label, a phycoerythrin label, a phycocyanin
20 label, an allophycocyanin label, an o-phthaldehyde label, and a fluorescamine label.

Examples of suitable toxin labels include, *Pseudomonas* toxin, diphtheria toxin, ricin, and cholera toxin.

Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an
25 oxalate ester label, a luciferin label, a luciferase label, and an aequorin label.

Examples of nuclear magnetic resonance contrasting agents include heavy metal nuclei such as Gd, Mn, and iron.

Typical techniques for binding the above-described labels to antibodies are provided by Kennedy et al. (1976) Clin. Chim. Acta 70:1-31, and Schurs et al. (1977)

Clin. Chim. Acta 81:1-40. Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method, all of which methods are incorporated by reference herein.

5 In a related aspect, the invention includes a diagnostic kit for use in screening serum containing antibodies specific against *E. faecalis* infection. Such a kit may include an isolated *E. faecalis* antigen comprising an epitope which is specifically immunoreactive with at least one anti-*E. faecalis* antibody. Such a kit also includes means for detecting the binding of said antibody to the antigen. In specific
10 embodiments, the kit may include a recombinantly produced or chemically synthesized peptide or polypeptide antigen. The peptide or polypeptide antigen may be attached to a solid support.

In a more specific embodiment, the detecting means of the above-described kit includes a solid support to which said peptide or polypeptide antigen is attached.
15 Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the antibody to the *E. faecalis* antigen can be detected by binding of the reporter labeled antibody to the anti-*E. faecalis* polypeptide antibody.

In a related aspect, the invention includes a method of detecting *E. faecalis* infection in a subject. This detection method includes reacting a body fluid, preferably
20 serum, from the subject with an isolated *E. faecalis* antigen, and examining the antigen for the presence of bound antibody. In a specific embodiment, the method includes a polypeptide antigen attached to a solid support, and serum is reacted with the support. Subsequently, the support is reacted with a reporter-labeled anti-human antibody. The support is then examined for the presence of reporter-labeled
25 antibody.

The solid surface reagent employed in the above assays and kits is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plates or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or

covalent attachment of the protein, typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

5 The polypeptides and antibodies of the present invention, including fragments thereof, may be used to detect Enterococcal species including *E. faecalis* using bio chip and biosensor technology. Bio chip and biosensors of the present invention may comprise the polypeptides of the present invention to detect antibodies, which specifically recognize Enterococcal species, including *E. faecalis*. Bio chip and
10 biosensors of the present invention may also comprise antibodies which specifically recognize the polypeptides of the present invention to detect Enterococcal species, including *E. faecalis* or specific polypeptides of the present invention. Bio chips or biosensors comprising polypeptides or antibodies of the present invention may be used to detect Enterococcal species, including *E. faecalis*, in biological and
15 environmental samples and to diagnose an animal, including humans, with an *E. faecalis* or other Enterococcal infection. Thus, the present invention includes both bio chips and biosensors comprising polypeptides or antibodies of the present invention and methods of their use.

 The bio chips of the present invention may further comprise polypeptide
20 sequences of other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the polypeptide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips of the present invention may further comprise antibodies or fragments thereof specific for other pathogens including bacteria, viral, parasitic, and fungal polypeptide
25 sequences, in addition to the antibodies or fragments thereof of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips and biosensors of the present invention may also be used to monitor an *E. faecalis* or other Enterococcal infection and to monitor the genetic changes (amino acid deletions, insertions, substitutions, etc.) in response to drug therapy in the clinic and drug

development in the laboratory. The bio chip and biosensors comprising polypeptides or antibodies of the present invention may also be used to simultaneously monitor the expression of a multiplicity of polypeptides, including those of the present invention. The polypeptides used to comprise a bio chip or biosensor of the present invention
5 may be specified in the same manner as for the fragments, i.e, by their N-terminal and C-terminal positions or length in contiguous amino acid residue. Methods and particular uses of the polypeptides and antibodies of the present invention to detect Enterococcal species, including *E. faecalis*, or specific polypeptides using bio chip and biosensor technology include those known in the art, those of the U.S. Patent Nos.
10 and World Patent Nos. listed above for bio chips and biosensors using polynucleotides of the present invention, and those of: U.S. Patent Nos. 5658732, 5135852, 5567301, 5677196, 5690894 and World Patent Nos. WO9729366, WO9612957, each incorporated herein in their entireties.

15 ***Treatment:***

Agonists and Antagonists - Assays and Molecules

The invention also provides a method of screening compounds to identify those which enhance or block the biological activity of the *E. faecalis* polypeptides of the present invention. The present invention further provides where the compounds
20 kill or slow the growth of *E. faecalis*. The ability of *E. faecalis* antagonists, including *E. faecalis* ligands, to prophylactically or therapeutically block antibiotic resistance may be easily tested by the skilled artisan. See, e.g., Straden et al. (1997) J Bacteriol. 179(1):9-16.

An agonist is a compound which increases the natural biological function or
25 which functions in a manner similar to the polypeptides of the present invention, while antagonists decrease or eliminate such functions. Potential antagonists include small organic molecules, peptides, polypeptides, and antibodies that bind to a polypeptide of the invention and thereby inhibit or extinguish its activity.

The antagonists may be employed for instance to inhibit peptidoglycan cross

bridge formation. Antibodies against *E. faecalis* may be employed to bind to and inhibit *E. faecalis* activity to treat antibiotic resistance. Any of the above antagonists may be employed in a composition with a pharmaceutically acceptable carrier.

5 *Vaccines*

The present invention also provides vaccines comprising one or more polypeptides of the present invention. Heterogeneity in the composition of a vaccine may be provided by combining *E. faecalis* polypeptides of the present invention. Multi-component vaccines of this type are desirable because they are likely to be
10 more effective in eliciting protective immune responses against multiple species and strains of the *Enterococcus* genus than single polypeptide vaccines.

Multi-component vaccines are known in the art to elicit antibody production to numerous immunogenic components. See, e.g., Decker et al. (1996) J. Infect. Dis. 174:S270-275. In addition, a hepatitis B, diphtheria, tetanus, pertussis tetravalent
15 vaccine has recently been demonstrated to elicit protective levels of antibodies in human infants against all four pathogenic agents. See, e.g., Aristegui, J. et al. (1997) Vaccine 15:7-9.

The present invention in addition to single-component vaccines includes multi-component vaccines. These vaccines comprise more than one polypeptide,
20 immunogen or antigen. Thus, a multi-component vaccine would be a vaccine comprising more than one of the *E. faecalis* polypeptides of the present invention.

Further within the scope of the invention are whole cell and whole viral vaccines. Such vaccines may be produced recombinantly and involve the expression of one or more of the *E. faecalis* polypeptides described in Table 1. For example, the
25 *E. faecalis* polypeptides of the present invention may be either secreted or localized intracellular, on the cell surface, or in the periplasmic space. Further, when a recombinant virus is used, the *E. faecalis* polypeptides of the present invention may, for example, be localized in the viral envelope, on the surface of the capsid, or internally within the capsid. Whole cells vaccines which employ cells expressing

heterologous proteins are known in the art. *See, e.g.*, Robinson, K. et al. (1997) Nature Biotech. 15:653-657; Sirard, J. et al. (1997) Infect. Immun. 65:2029-2033; Chabalgoity, J. et al. (1997) Infect. Immun. 65:2402-2412. These cells may be administered live or may be killed prior to administration. Chabalgoity, J. et al., *supra*,
5 for example, report the successful use in mice of a live attenuated *Salmonella* vaccine strain which expresses a portion of a platyhelminth fatty acid-binding protein as a fusion protein on its cells surface.

A multi-component vaccine can also be prepared using techniques known in the art by combining one or more *E. faecalis* polypeptides of the present invention, or
10 fragments thereof, with additional non-Enterococcal components (*e.g.*, diphtheria toxin or tetanus toxin, and/or other compounds known to elicit an immune response). Such vaccines are useful for eliciting protective immune responses to both members of the *Enterococcus* genus and non-Enterococcal pathogenic agents.

The vaccines of the present invention also include DNA vaccines. DNA
15 vaccines are currently being developed for a number of infectious diseases. *See, et al.*, Boyer, et al. (1997) Nat. Med. 3:526-532; reviewed in Spier, R. (1996) Vaccine 14:1285-1288. Such DNA vaccines contain a nucleotide sequence encoding one or more *E. faecalis* polypeptides of the present invention oriented in a manner that allows for expression of the subject polypeptide. For example, the direct
20 administration of plasmid DNA encoding *B. burgdorferi* OspA has been shown to elicit protective immunity in mice against borrelial challenge. *See*, Luke et al. (1997) J. Infect. Dis. 175:91-97.

The present invention also relates to the administration of a vaccine which is co-administered with a molecule capable of modulating immune responses. Kim et al.
25 (1997) Nature Biotech. 15:641-646, for example, report the enhancement of immune responses produced by DNA immunizations when DNA sequences encoding molecules which stimulate the immune response are co-administered. In a similar fashion, the vaccines of the present invention may be co-administered with either nucleic acids encoding immune modulators or the immune modulators themselves.

These immune modulators include granulocyte macrophage colony stimulating factor (GM-CSF) and CD86.

The vaccines of the present invention may be used to confer resistance to Enterococcal infection by either passive or active immunization. When the vaccines of the present invention are used to confer resistance to Enterococcal infection through active immunization, a vaccine of the present invention is administered to an animal to elicit a protective immune response which either prevents or attenuates a Enterococcal infection. When the vaccines of the present invention are used to confer resistance to Enterococcal infection through passive immunization, the vaccine is provided to a host animal (*e.g.*, human, dog, or mouse), and the antisera elicited by this antisera is recovered and directly provided to a recipient suspected of having an infection caused by a member of the *Enterococcus* genus.

The ability to label antibodies, or fragments of antibodies, with toxin molecules provides an additional method for treating Enterococcal infections when passive immunization is conducted. In this embodiment, antibodies, or fragments of antibodies, capable of recognizing the *E. faecalis* polypeptides disclosed herein, or fragments thereof, as well as other *Enterococcus* proteins, are labeled with toxin molecules prior to their administration to the patient. When such toxin derivatized antibodies bind to *Enterococcus* cells, toxin moieties will be localized to these cells and will cause their death.

The present invention thus concerns and provides a means for preventing or attenuating a Enterococcal infection resulting from organisms which have antigens that are recognized and bound by antisera produced in response to the polypeptides of the present invention. As used herein, a vaccine is said to prevent or attenuate a disease if its administration to an animal results either in the total or partial attenuation (*i.e.*, suppression) of a symptom or condition of the disease, or in the total or partial immunity of the animal to the disease.

The administration of the vaccine (or the antisera which it elicits) may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically,

the compound(s) are provided in advance of any symptoms of Enterococcal infection. The prophylactic administration of the compound(s) serves to prevent or attenuate any subsequent infection. When provided therapeutically, the compound(s) is provided upon or after the detection of symptoms which indicate that an animal may
5 be infected with a member of the *Enterococcus* genus. The therapeutic administration of the compound(s) serves to attenuate any actual infection. Thus, the *E. faecalis* polypeptides, and fragments thereof, of the present invention may be provided either prior to the onset of infection (so as to prevent or attenuate an anticipated infection) or after the initiation of an actual infection.

10 The polypeptides of the invention, whether encoding a portion of a native protein or a functional derivative thereof, may be administered in pure form or may be coupled to a macromolecular carrier. Example of such carriers are proteins and carbohydrates. Suitable proteins which may act as macromolecular carrier for enhancing the immunogenicity of the polypeptides of the present invention include
15 keyhole limpet hemacyanin (KLH) tetanus toxoid, pertussis toxin, bovine serum albumin, and ovalbumin. Methods for coupling the polypeptides of the present invention to such macromolecular carriers are disclosed in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

20 A composition is said to be "pharmacologically or physiologically acceptable" if its administration can be tolerated by a recipient animal and is otherwise suitable for administration to that animal. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a
25 detectable change in the physiology of a recipient patient.

While in all instances the vaccine of the present invention is administered as a pharmacologically acceptable compound, one skilled in the art would recognize that the composition of a pharmacologically acceptable compound varies with the animal to which it is administered. For example, a vaccine intended for human use will

generally not be co-administered with Freund's adjuvant. Further, the level of purity of the *E. faecalis* polypeptides of the present invention will normally be higher when administered to a human than when administered to a non-human animal.

As would be understood by one of ordinary skill in the art, when the vaccine of the present invention is provided to an animal, it may be in a composition which may contain salts, buffers, adjuvants, or other substances which are desirable for improving the efficacy of the composition. Adjuvants are substances that can be used to specifically augment a specific immune response. These substances generally perform two functions: (1) they protect the antigen(s) from being rapidly catabolized after administration and (2) they nonspecifically stimulate immune responses.

Normally, the adjuvant and the composition are mixed prior to presentation to the immune system, or presented separately, but into the same site of the animal being immunized. Adjuvants can be loosely divided into several groups based upon their composition. These groups include oil adjuvants (for example, Freund's complete and incomplete), mineral salts (for example, $\text{AlK}(\text{SO}_4)_2$, $\text{AlNa}(\text{SO}_4)_2$, $\text{AlNH}_4(\text{SO}_4)$, silica, kaolin, and carbon), polynucleotides (for example, poly IC and poly AU acids), and certain natural substances (for example, wax D from *Mycobacterium tuberculosis*, as well as substances found in *Corynebacterium parvum*, or *Bordetella pertussis*, and members of the genus *Brucella*). Other substances useful as adjuvants are the saponins such as, for example, Quil A. (Superfos A/S, Denmark). Preferred adjuvants for use in the present invention include aluminum salts, such as $\text{AlK}(\text{SO}_4)_2$, $\text{AlNa}(\text{SO}_4)_2$, and $\text{AlNH}_4(\text{SO}_4)$. Examples of materials suitable for use in vaccine compositions are provided in REMINGTON'S PHARMACEUTICAL SCIENCES 1324-1341 (A. Osol, ed, Mack Publishing Co, Easton, PA, (1980) (incorporated herein by reference).

The therapeutic compositions of the present invention can be administered parenterally by injection, rapid infusion, nasopharyngeal absorption (intranasopharyngeally), dermoabsorption, or orally. The compositions may alternatively be administered intramuscularly, or intravenously. Compositions for parenteral administration include sterile aqueous or non-aqueous solutions,

suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Carriers or occlusive dressings can be used to increase skin permeability and enhance antigen absorption. Liquid dosage forms for oral administration may generally comprise a liposome solution containing the liquid dosage form. Suitable forms for suspending liposomes include emulsions, suspensions, solutions, syrups, and elixirs containing inert diluents commonly used in the art, such as purified water. Besides the inert diluents, such compositions can also include adjuvants, wetting agents, emulsifying and suspending agents, or sweetening, flavoring, or perfuming agents.

Therapeutic compositions of the present invention can also be administered in encapsulated form. For example, intranasal immunization using vaccines encapsulated in biodegradable microsphere composed of poly(DL-lactide-co-glycolide). *See*, Shahin, R. et al. (1995) Infect. Immun. 63:1195-1200. Similarly, orally administered encapsulated *Salmonella typhimurium* antigens can also be used. Allaoui-Attarki, K. et al. (1997) Infect. Immun. 65:853-857. Encapsulated vaccines of the present invention can be administered by a variety of routes including those involving contacting the vaccine with mucous membranes (e.g., intranasally, intracolonicly, intraduodenally).

Many different techniques exist for the timing of the immunizations when a multiple administration regimen is utilized. It is possible to use the compositions of the invention more than once to increase the levels and diversities of expression of the immunoglobulin repertoire expressed by the immunized animal. Typically, if multiple immunizations are given, they will be given one to two months apart.

According to the present invention, an "effective amount" of a therapeutic composition is one which is sufficient to achieve a desired biological effect. Generally, the dosage needed to provide an effective amount of the composition will vary depending upon such factors as the animal's or human's age, condition, sex, and extent of disease, if any, and other variables which can be adjusted by one of ordinary skill in

the art.

The antigenic preparations of the invention can be administered by either single or multiple dosages of an effective amount. Effective amounts of the compositions of the invention can vary from 0.01-1,000 µg/ml per dose, more
5 preferably 0.1-500 µg/ml per dose, and most preferably 10-300 µg/ml per dose.

Examples

Example 1: Isolation of a Selected DNA Clone From the Deposited Sample of E. faecalis

10 Three approaches can be used to isolate a *E. faecalis* clone comprising a polynucleotide of the present invention from any *E. faecalis* genomic DNA library. The *E. faecalis* strain V586 has been deposited as a convenient source for obtaining a *E. faecalis* strain although a wide variety of strains *E. faecalis* strains can be used which are known in the art.

15 *E. faecalis* genomic DNA is prepared using the following method. A 20ml overnight bacterial culture grown in a rich medium (e.g., Trypticase Soy Broth, Brain Heart Infusion broth or Super broth), pelleted, washed two times with TES (30mM Tris-pH 8.0, 25mM EDTA, 50mM NaCl), and resuspended in 5ml high salt TES (2.5M NaCl). Lysostaphin is added to final concentration of approx 50ug/ml and the
20 mixture is rotated slowly 1 hour at 37C to make protoplast cells. The solution is then placed in incubator (or place in a shaking water bath) and warmed to 55C. Five hundred micro liter of 20% sarcosyl in TES (final concentration 2%) is then added to lyse the cells. Next, guanidine HCl is added to a final concentration of 7M (3.69g in 5.5 ml). The mixture is swirled slowly at 55C for 60-90 min (solution should clear).
25 A CsCl gradient is then set up in SW41 ultra clear tubes using 2.0ml 5.7M CsCl and overlaying with 2.85M CsCl. The gradient is carefully overlayed with the DNA-containing GuHCl solution. The gradient is spun at 30,000 rpm, 20C for 24 hr and the lower DNA band is collected. The volume is increased to 5 ml with TE buffer. The DNA is then treated with protease K (10 ug/ml) overnight at 37 C, and

precipitated with ethanol. The precipitated DNA is resuspended in a desired buffer.

In the first method, a plasmid is directly isolated by screening a plasmid *E. faecalis* genomic DNA library using a polynucleotide probe corresponding to a polynucleotide of the present invention. Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ^{32}P - γ -ATP using T4 polynucleotide kinase and purified according to routine methods. (See, e.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The library is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art. See, e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989). The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening. See, e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989) or other techniques known to those of skill in the art.

Alternatively, two primers of 15-25 nucleotides derived from the 5' and 3' ends of a polynucleotide of Table 1 are synthesized and used to amplify the desired DNA by PCR using a *E. faecalis* genomic DNA prep as a template. PCR is carried out under routine conditions, for instance, in 25 μl of reaction mixture with 0.5 μg of the above DNA template. A convenient reaction mixture is 1.5-5 mM MgCl_2 , 0.01% (w/v) gelatin, 20 μM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a

Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

- 5 Finally, overlapping oligos of the DNA sequences of Table 1 can be chemically synthesized and used to generate a nucleotide sequence of desired length using PCR methods known in the art.

Example 2(a): Expression and Purification Enterococcal polypeptides in E. coli

- 10 The bacterial expression vector pQE60 was used for bacterial expression of some of the polypeptide fragments used in the soft tissue and systemic infection models discussed below. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Ampr") and contains a bacterial origin of replication ("ori"), an IPTG inducible promoter, a ribosome binding
15 site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin (QIAGEN, Inc., *supra*) and suitable single restriction enzyme cleavage sites. These elements are arranged such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the carboxyl
20 terminus of that polypeptide.

- The DNA sequence encoding the desired portion of a *E. faecalis* protein of the present invention was amplified from *E. faecalis* genomic DNA using PCR oligonucleotide primers which anneal to the 5' and 3' sequences coding for the portions of the *E. faecalis* polynucleotide shown in Table 1. Additional nucleotides
25 containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

 For cloning the mature protein, the 5' primer has a sequence containing an appropriate restriction site followed by nucleotides of the amino terminal coding sequence of the desired *E. faecalis* polynucleotide sequence in Table 1. One of

ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of the complete protein shorter or longer than the mature form.

The 3' primer has a sequence containing an appropriate restriction site followed by
5 nucleotides complementary to the 3' end of the polypeptide coding sequence of Table 1, excluding a stop codon, with the coding sequence aligned with the restriction site so as to maintain its reading frame with that of the six His codons in the pQE60 vector.

The amplified *E. faecalis* DNA fragment and the vector pQE60 were digested with restriction enzymes which recognize the sites in the primers and the digested
10 DNAs were then ligated together. The *E. faecalis* DNA was inserted into the restricted pQE60 vector in a manner which places the *E. faecalis* protein coding region downstream from the IPTG-inducible promoter and in-frame with an initiating AUG and the six histidine codons.

The ligation mixture was transformed into competent *E. coli* cells using
15 standard procedures such as those described by Sambrook et al., *supra*. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), was used in carrying out the illustrative example described herein. This strain, which was only one of many that are suitable for expressing a *E. faecalis* polypeptide, is available commercially
20 (QIAGEN, Inc., *supra*). Transformants were identified by their ability to grow on LB agar plates in the presence of ampicillin and kanamycin. Plasmid DNA was isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs were grown overnight ("O/N") in
25 liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture was used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells were grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. Isopropyl-β-D-thiogalactopyranoside ("IPTG") was then added to a final concentration of 1 mM to induce transcription

from the lac repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently were incubated further for 3 to 4 hours. Cells then were harvested by centrifugation.

The cells were then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8.

- 5 The cell debris was removed by centrifugation, and the supernatant containing the *E. faecalis* polypeptide was loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity were purified in a simple one-step procedure (for details see: The QIAexpressionist, 1995, QIAGEN, Inc., *supra*). Briefly the
- 10 supernatant was loaded onto the column in 6 M guanidine-HCl, pH 8, the column was first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the *E. faecalis* polypeptide was eluted with 6 M guanidine-HCl, pH 5.

- The purified protein was then renatured by dialyzing it against
- 15 phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein could be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of
- 20 1.5 hours or more. After renaturation the proteins can be eluted by the addition of 250 mM imidazole. Imidazole was removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein was stored at 4°C or frozen at -80°C.

- Some of the polypeptide of the present invention were prepared using a non-
- 25 denaturing protein purification method. For these polypeptides, the cell pellet from each liter of culture was resuspended in 25 mls of Lysis Buffer A at 4°C (Lysis Buffer A = 50 mM Na-phosphate, 300 mM NaCl, 10 mM 2-mercaptoethanol, 10% Glycerol, pH 7.5 with 1 tablet of Complete EDTA-free protease inhibitor cocktail (Boehringer Mannheim #1873580) per 50 ml of buffer). Absorbance at 550 nm was

approximately 10-20 O.D./ml. The suspension was then put through three freeze/thaw cycles from -70°C (using a ethanol-dry ice bath) up to room temperature. The cells were lysed via sonication in short 10 sec bursts over 3 minutes at approximately 80W while kept on ice. The sonicated sample was then centrifuged at 15,000 RPM for 30 minutes at 4°C. The supernatant was passed through a column containing 1.0 ml of CL-4B resin to pre-clear the sample of any proteins that may bind to agarose non-specifically, and the flow-through fraction was collected.

The pre-cleared flow-through was applied to a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (Quiagen, Inc., *supra*). Proteins with a 6 X His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure. Briefly, the supernatant was loaded onto the column in Lysis Buffer A at 4°C, the column was first washed with 10 volumes of Lysis Buffer A until the A280 of the eluate returns to the baseline. Then, the column was washed with 5 volumes of 40 mM Imidazole (92% Lysis Buffer A / 8% Buffer B) (Buffer B = 50 mM Na-Phosphate, 300 mM NaCl, 10% Glycerol, 10 mM 2-mercaptoethanol, 500 mM Imidazole, pH of the final buffer should be 7.5). The protein was eluted off of the column with a series of increasing Imidazole solutions made by adjusting the ratios of Lysis Buffer A to Buffer B. Three different concentrations were used: 3 volumes of 75 mM Imidazole, 3 volumes of 150 mM Imidazole, 5 volumes of 500 mM Imidazole. The fractions containing the purified protein were analyzed using 8 %, 10 % or 14% SDS-PAGE depending on the protein size. The purified protein was then dialyzed 2X against phosphate-buffered saline (PBS) in order to place it into an easily workable buffer. The purified protein was stored at 4° C or frozen at -80°.

The following alternative method may be used to purify *E. faecalis* expressed in *E coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per

unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

5 The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

10 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *E. faecalis* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x g) to remove insoluble particles,
15 the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *E. faecalis* polypeptide solution, a previously prepared
20 tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same
25 buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *E. faecalis* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive

Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A₂₈₀ monitoring of the effluent. Fractions containing the *E. faecalis* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *E. faecalis* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 µg of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 2(b): Alternative Expression and Purification Enterococcal polypeptides in E. coli

The vector pQE10 was alternatively used to clone and express some of the polypeptides of the present invention for use in the soft tissue and systemic infection models discussed below. The difference being such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus of that polypeptide. The bacterial expression vector pQE10 (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311) was used in this example. The components of the pQE10 plasmid are arranged such that the inserted DNA sequence encoding a polypeptide of the present invention expresses the polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus.

The DNA sequences encoding the desired portions of a polypeptide of Table 1 were amplified using PCR oligonucleotide primers from genomic *E. faecalis* DNA. The PCR primers anneal to the nucleotide sequences encoding the desired amino acid

sequence of a polypeptide of the present invention. Additional nucleotides containing restriction sites to facilitate cloning in the pQE10 vector were added to the 5' and 3' primer sequences, respectively.

For cloning a polypeptide of the present invention, the 5' and 3' primers were
5 selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begins may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 5' primer was designed so the coding sequence of the 6 X His tag is aligned with the restriction site so as to maintain
10 its reading frame with that of *E. faecalis* polypeptide. The 3' was designed to include an stop codon. The amplified DNA fragment was then cloned, and the protein expressed, as described above for the pQE60 plasmid.

The DNA sequences encoding the amino acid sequences of Table 1 may also be cloned and expressed as fusion proteins by a protocol similar to that described
15 directly above, wherein the pET-32b(+) vector (Novagen, 601 Science Drive, Madison, WI 53711) is preferentially used in place of pQE10.

The above methods are not limited to the polypeptide fragments actually produced. The above method, like the methods below, can be used to produce either full length polypeptides or desired fragments thereof.

20

Example 2(c): Alternative Expression and Purification of Enterococcal polypeptides in E. coli

The bacterial expression vector pQE60 is used for bacterial expression in this example (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). However, in
25 this example, the polypeptide coding sequence is inserted such that translation of the six His codons is prevented and, therefore, the polypeptide is produced with no 6 X His tag.

The DNA sequence encoding the desired portion of the *E. faecalis* amino acid sequence is amplified from an *E. faecalis* genomic DNA prep the deposited DNA

clones using PCR oligonucleotide primers which anneal to the 5' and 3' nucleotide sequences corresponding to the desired portion of the *E. faecalis* polypeptides. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' primer sequences.

5 For cloning a *E. faecalis* polypeptides of the present invention, 5' and 3' primers are selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 3' and 5' primers
10 contain appropriate restriction sites followed by nucleotides complementary to the 5' and 3' ends of the coding sequence respectively. The 3' primer is additionally designed to include an in-frame stop codon.

 The amplified *E. faecalis* DNA fragments and the vector pQE60 are digested with restriction enzymes recognizing the sites in the primers and the digested DNAs
15 are then ligated together. Insertion of the *E. faecalis* DNA into the restricted pQE60 vector places the *E. faecalis* protein coding region including its associated stop codon downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

20 The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for
25 expressing *E. faecalis* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-b-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the *lac* repressor sensitive promoter, by inactivating the *lacI* repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

To purify the *E. faecalis* polypeptide, the cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the *E. faecalis* polypeptide is dialyzed against 50 mM Na-acetate buffer pH 6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH 7.4, containing protease inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *E. faecalis* polypeptide. The purified protein is stored at 4°C or frozen at -80°C.

The following alternative method may be used to purify *E. faecalis* polypeptides expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells were then lysed by passing the solution through a microfluidizer

(Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

5 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *E. faecalis* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x g) to remove insoluble particles,
10 the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *E. faecalis* polypeptide solution, a previously prepared
15 tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same
20 buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *E. faecalis* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive
25 Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5.

Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the *E. faecalis* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *E. faecalis* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

10 *Example 2(d): Cloning and Expression of E. faecalis in Other Bacteria*

E. faecalis polypeptides can also be produced in: *E. faecalis* using the methods of S. Skinner et al., (1988) Mol. Microbiol. 2:289-297 or J. I. Moreno (1996) Protein Expr. Purif. 8(3):332-340; *Lactobacillus* using the methods of C. Rush et al., 1997 Appl. Microbiol. Biotechnol. 47(5):537-542; or in *Bacillus subtilis* using the methods
15 Chang et al., U.S. Patent No. 4,952,508.

Example 3: Cloning and Expression in COS Cells

A *E. faecalis* expression plasmid is made by cloning a portion of the DNA encoding a *E. faecalis* polypeptide into the expression vector pDNAI/Amp or
20 pDNAIII (which can be obtained from Invitrogen, Inc.). The expression vector pDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several
25 codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a DNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived

from the influenza hemagglutinin protein described by Wilson et al. 1984 Cell 37:767. The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pDNAIII contains, in addition, the selectable neomycin marker.

5 A DNA fragment encoding a *E. faecalis* polypeptide is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The DNA from a *E. faecalis* genomic DNA prep is amplified using primers that contain convenient restriction sites, much as described above for construction of vectors for expression of
10 *E. faecalis* in *E. coli*. The 5' primer contains a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *E. faecalis* polypeptide. The 3' primer, contains nucleotides complementary to the 3' coding sequence of the *E. faecalis* DNA, a stop codon, and a convenient restriction site.

 The PCR amplified DNA fragment and the vector, pDNAI/Amp, are digested
15 with appropriate restriction enzymes and then ligated. The ligation mixture is transformed into an appropriate *E. coli* strain such as SURE™ (Stratagene Cloning Systems, La Jolla, CA 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis
20 or other means for the presence of the fragment encoding the *E. faecalis* polypeptide

 For expression of a recombinant *E. faecalis* polypeptide, COS cells are transfected with an expression vector, as described above, using DEAE-dextran, as described, for instance, by Sambrook et al. (*supra*). Cells are incubated under conditions for expression of *E. faecalis* by the vector.

25 Expression of the *E. faecalis*-HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow et al., *supra*.. To this end, two days after transfection, the cells are labeled by incubation in media containing ³⁵S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM

NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson et al. (*supra*). Proteins are precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression
5 product of the expected size is seen in the cell lysate, which is not seen in negative controls.

Example 4: Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of *E. faecalis* polypeptide in this
10 example. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Accession No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early promoter. Chinese hamster ovary cells or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies) supplemented with the
15 chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented. *See, e.g.,* Alt et al., 1978, J. Biol. Chem. 253:1357-1370; Hamlin et al., 1990, Biochem. et Biophys. Acta, 1097:107-143; Page et al., 1991, Biotechnology 9:64-68. Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target
20 enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated into one
25 or more chromosome(s) of the host cell.

Plasmid pC4 contains the strong promoter of the long terminal repeat (LTR) of the Rouse Sarcoma Virus, for expressing a polypeptide of interest, Cullen, et al. (1985) Mol. Cell. Biol. 5:438-447; plus a fragment isolated from the enhancer of the immediate early gene of human cytomegalovirus (CMV), Boshart, et al., 1985, Cell

41:521-530. Downstream of the promoter are the following single restriction enzyme cleavage sites that allow the integration of the genes: *Bam* HI, *Xba* I, and *Asp* 718.

Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the
5 expression, e.g., the human β -actin promoter, the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLV. Clontech's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the *E. faecalis* polypeptide in a regulated way in mammalian cells (Gossen et al., 1992, Proc. Natl. Acad. Sci. USA 89:5547-5551. For the polyadenylation of the mRNA
10 other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the chromosomes can also be selected upon co-transfection with a selectable marker such as gpt, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

15 The plasmid pC4 is digested with the restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel. The DNA sequence encoding the *E. faecalis* polypeptide is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the desired portion of the gene. A 5' primer containing a
20 restriction site, a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *E. faecalis* polypeptide is synthesized and used. A 3' primer, containing a restriction site, stop codon, and nucleotides complementary to the 3' coding sequence of the *E. faecalis* polypeptides is synthesized and used. The amplified fragment is digested with the restriction endonucleases and then purified
25 again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for

transfection. Five μg of the expression plasmid pC4 is cotransfected with 0.5 μg of the plasmid pSVneo using a lipid-mediated transfection agent such as Lipofectin™ or LipofectAMINE™ (LifeTechnologies Gaithersburg, MD). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme
5 that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well
10 petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μM , 2 μM , 5 μM , 10 μM , 20 μM). The same procedure is repeated until clones are obtained which grow at a concentration of
15 100-200 μM . Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 5: Quantitative Murine Soft Tissue Infection Model for E. faecalis

Compositions of the present invention, including polypeptides and peptides,
20 are assayed for their ability to function as vaccines or to enhance/stimulate an immune response to a bacterial species (e.g., *E. faecalis*) using the following quantitative murine soft tissue infection model. Mice (e.g., NIH Swiss female mice, approximately 7 weeks old) are first treated with a biologically protective effective amount, or immune enhancing/stimulating effective amount of a composition of the present
25 invention using methods known in the art, such as those discussed above. See, e.g., Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988). An example of an appropriate starting dose is 20ug per animal.

The desired bacterial species used to challenge the mice, such as *E. faecalis*, is grown as an overnight culture. The culture is diluted to a concentration of 5×10^8 cfu/ml, in an appropriate media, mixed well, serially diluted, and titered. The desired doses are further diluted 1:2 with sterilized Cytodex 3 microcarrier beads preswollen in sterile PBS (3g/100ml). Mice are anesthetized briefly until docile, but still mobile and injected with 0.2 ml of the Cytodex 3 bead/bacterial mixture into each animal subcutaneously in the inguinal region. After four days, counting the day of injection as day one, mice are sacrificed and the contents of the abscess is excised and placed in a 15 ml conical tube containing 1.0ml of sterile PBS. The contents of the abscess is then enzymatically treated and plated as follows.

The abscess is first disrupted by vortexing with sterilized glass beads placed in the tubes. 3.0mls of prepared enzyme mixture (1.0ml Collagenase D (4.0 mg/ml), 1.0ml Trypsin (6.0 mg/ml) and 8.0 mls PBS) is then added to each tube followed by a 20 min. incubation at 37C. The solution is then centrifuged and the supernatant drawn off. 0.5 ml dH2O is then added and the tubes are vortexed and then incubated for 10 min. at room temperature. 0.5 ml media is then added and samples are serially diluted and plated onto agar plates, and grown overnight at 37C. Plates with distinct and separate colonies are then counted, compared to positive and negative control samples, and quantified. The method can be used to identify composition and determine appropriate and effective doses for humans and other animals by comparing the effective doses of compositions of the present invention with compositions known in the art to be effective in both mice and humans. Doses for the effective treatment of humans and other animals, using compositions of the present invention, are extrapolated using the data from the above experiments of mice. It is appreciated that further studies in humans and other animals may be needed to determine the most effective doses using methods of clinical practice known in the art.

Example 6: Murine Systemic Neutropenic Model for E. faecalis Infection

Compositions of the present invention, including polypeptides and peptides, are assayed for their ability to function as vaccines or to enhance/stimulate an immune response to a bacterial species (e.g., *E. faecalis*) using the following qualitative murine systemic neutropenic model. Mice (e.g., NIH Swiss female mice, approximately 7
5 weeks old) are first treated with a biologically protective effective amount, or immune enhancing/stimulating effective amount of a composition of the present invention using methods known in the art, such as those discussed above. *See, e.g.*, Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988). An example of an appropriate starting dose is 20ug per animal.
10 Mice are then injected with 250 - 300 mg/kg cyclophosphamide intraperitoneally. Counting the day of C.P. injection as day one, the mice are left untreated for 5 days to begin recovery of PMNL'S.

The desired bacterial species used to challenge the mice, such as *E. faecalis*, is grown as an overnight culture. The culture is diluted to a concentration of 5×10^8
15 cfu/ml, in an appropriate media, mixed well, serially diluted, and titered. The desired doses are further diluted 1:2 in 4% Brewer's yeast in media.

Mice are injected with the bacteria/brewer's yeast challenge intraperitoneally. The Brewer's yeast solution alone is used as a control. The mice are then monitored twice daily for the first week following challenge, and once a day for the next week to
20 ascertain morbidity and mortality. Mice remaining at the end of the experiment are sacrificed. The method can be used to identify compositions and determine appropriate and effective doses for humans and other animals by comparing the effective doses of compositions of the present invention with compositions known in the art to be effective in both mice and humans. Doses for the effective treatment of
25 humans and other animals, using compositions of the present invention, are extrapolated using the data from the above experiments of mice. It is appreciated that further studies in humans and other animals may be needed to determine the most effective doses using methods of clinical practice known in the art.

The disclosure of all publications (including patents, patent applications, journal articles, laboratory manuals, books, or other documents) cited herein are hereby incorporated by reference in their entireties.

The present invention is not to be limited in scope by the specific
5 embodiments described herein, which are intended as single illustrations of individual aspects of the invention. Functionally equivalent methods and components are within the scope of the invention, in addition to those shown and described herein and will become apparant to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of
10 the appended claims.

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF001-1 (SEQ ID NO:1)

TGAAAGAATA TTGCCAGAAC GTGGCGAGCA AATTGTTTTTA TAAATTTTTTT TAAGGGAGAG
 AAAAAAATGA AGTTCAAAAC TCTAGCAACA ACAGTGTTAG CAACCGCAGC TATTTTCGCA
 TTGGGGGGCTT GTGGTAACGG TAATGGGGCC AAAGAATCAA ACGATATTGT GAAAGAAGTG
 AAGGAAGATA CGACAATCAC TTCTGGCAT GCAATGAATG GGGTTCAAGA AGAAGCGTTA
 AAAAAATTAA CGAAAGACTT CATGAAAGAA AATCCAAAAA TTAAAGTGGA ATTACAAAAT
 CAATCTGCTT ACCCTGATTT ACAAGCCAAA ATCAATTCTGA CTTTAACTTC ACCAAAAGAT
 TTACCAACAA TTACGCAAGC GTACCCAGGC TGGTTATGGA ATGCTGCACA AGATGAAATG
 TTAGTGGAAT TAAAACCATA TATGGATGAT GACACAATCG GCTGGAAAGA TGCAGAGCCA
 ATTCGTGAAG TATTGTTAGA CGGCGCCAAA ATCGACGGCA AACAATACGG CATTCCATTT
 AATAAATCGA CAGAAATGTT ATTCTATAAT GCTGATTGTG TGAAAGAATA TGGTGTGTA
 GTACCGAAAA CATTAGAGGA ATTAAGAGAA GCTTCTAAAA CAATTTACGA AAAATCCAAC
 AAAGAAGTCG TTGGTGCTGG TTTTGACTCG TTAAATAACT ATTACGCAAT TGAATGAAA
 AACAAAGGCG TTGATTTTAA TAAAGACTTA GATTTAACAA GCAAAGATTTC ACAAGAAGTC
 GTGGACTATT ACCGTGATGG TATCGAAGCA GGTACTTCC GCACAGCTGG TTCAGATAAA
 TATTTATCTG GCCCATTGTC AAACAAAAAG GTAGCAATGT TTGTCGGTAG TATTGCTGGT
 GCTGGTTTTG TTCAAAAAGA TGCTGAAGCT GGTGGCTATG AATACGGTGT TGCACCACGT
 CCTGAAAAAA TCAACTTACA ACAAGGAACA GATATTTATA TGTTTCGATAG TGCTACGCCA
 GAACAACGGA CAGCGGCATT TGAATTCATG AAATTCTTAG CTACTCCTGA TTCACAATTG
 TACTGGGCAC AACAAACAGG TTATATGCCA ATTTTAGAAT CTGTTTTACA CAGTGATGAG
 TACAAAAATT CTAAGACAAC CAAAGTACCT GCACAACCTG AAAACGCAGT AAAAGATTTA
 TTCGCTATCC CAGTAGAAGA AAATGCTGAT TCAGCCTATA ATGAAATGCG GACAATTATG
 GAAAGTATTT TTGCTTCATC AAATAAAGAC ACGAGAAAAT TATTGAAAGA TGCAACATCA
 CAATTTGAAC AAGCATGGAA CCAATAA

EF001-2 (SEQ ID NO:2)

MKFKTLATT VLATAAIFAL GACGNGNGAK ESNDIVKEVK
 EDTTITFWHA MNGVQEEALT KLTGDFMKEN PKIKVELQNG SAYPDLQAKI NSTLTSPKDL
 PTITQAYPGW LWNAAQDEML VDLKPYMDDD TIGWKDAEPI REVLLDGAKI DGKQYGIPFN
 KSTEMLFYNA DLLKEYGVEV PKTLEELKEA SKTIYEKSNK EVVGAGFDSL NNYAIGMKN
 KGVDFNKDL LSKDSQEVV DYYRDGIEAG YFRTAGSDKY LSGPFANKKV AMFVGSIAA
 GFVQKDAEAG GYEYGVAPRP EKINLQQGTD IYMFDSATPE QRTAAFEFMK FLATPDSQLY
 WAQQTGYMPI LESVLHSDEY KNSKTTKVPA QLENVAVKDLF AIPVEENADS AYNEMRTIME
 SIFASSNKDT RKLLKDATSQ FEQAWNQ

EF001-3 (SEQ ID NO:3)

TT GTGGTAACGG TAATGGGGCC AAAGAATCAA ACGATATTGT GAAAGAAGTG
 AAGGAAGATA CGACAATCAC TTCTGGCAT GCAATGAATG GGGTTCAAGA AGAAGCGTTA
 AAAAAATTAA CGAAAGACTT CATGAAAGAA AATCCAAAAA TTAAAGTGGA ATTACAAAAT
 CAATCTGCTT ACCCTGATTT ACAAGCCAAA ATCAATTCTGA CTTTAACTTC ACCAAAAGAT
 TTACCAACAA TTACGCAAGC GTACCCAGGC TGGTTATGGA ATGCTGCACA AGATGAAATG
 TTAGTGGAAT TAAAACCATA TATGGATGAT GACACAATCG GCTGGAAAGA TGCAGAGCCA
 ATTCGTGAAG TATTGTTAGA CGGCGCCAAA ATCGACGGCA AACAATACGG CATTCCATTT
 AATAAATCGA CAGAAATGTT ATTCTATAAT GCTGATTGTG TGAAAGAATA TGGTGTGTA
 GTACCGAAAA CATTAGAGGA ATTAAGAGAA GCTTCTAAAA CAATTTACGA AAAATCCAAC
 AAAGAAGTCG TTGGTGCTGG TTTTGACTCG TTAAATAACT ATTACGCAAT TGAATGAAA
 AACAAAGGCG TTGATTTTAA TAAAGACTTA GATTTAACAA GCAAAGATTTC ACAAGAAGTC
 GTGGACTATT ACCGTGATGG TATCGAAGCA GGTACTTCC GCACAGCTGG TTCAGATAAA
 TATTTATCTG GCCCATTGTC AAACAAAAAG GTAGCAATGT TTGTCGGTAG TATTGCTGGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCTGGTTTTG TTCAAAAAGA TGCTGAAGCT GGTGGCTATG AATACGGTGT TGCACCACGT
 CCTGAAAAAA TCAACTTACA ACAAGGAACA GATATTTATA TGTTGATAG TGCTACGCCA
 GAACAACGGA CAGCGGCATT TGAATTCATG AAATTCCTTAG CTACTCCTGA TTCACAATTG
 TACTGGGCAC AACAAACAGG TTATATGCCA ATTTTAGAAT CTGTTTTACA CAGTGATGAG
 TACAAAAATT CTAAGACAAC CAAAGTACCT GCACAACCTG AAAACGCAGT AAAAGATTTA
 TTCGCTATCC CAGTAGAAGA AAATGCTGAT TCAGCCTATA ATGAAATGCG GACAATTATG
 GAAAGTATTT TTGCTTCATC AAATAAGAC ACGAGAAAAT TATTGAAAGA TGCAACATCA
 CAATTTGAAC AAGCATGGAA CCAA

EF001-4 (SEQ ID NO:4)

CGNGNGAK ESNDIVKEVK
 EDTTITFWHA MNGVQEEALT KLTKDFMKEN PKIKVELQNO SAYPDLQAKI NSTLTSPKDL
 PTITQAYPGW LWNAAQDEML VDLKPYMDDD TIGWKDAEPI REVLLDGAKI DGKQYGIPFN
 KSTEMLFYNA DLLKEYGVEV PKTLEELKEA SKTIYEKSNK EVVGAGFDSL NNYYAIGMKN
 KGVDFNKDL LTKSDSQEVV DYYRDGIEAG YFRTAGSDKY LSGPFANKKV AMFVGSIIAGA
 GFVQKDAEAG GYEEGVAPRP EKINLQQGTD IYMFDSATPE QRTAAFEFMK FLATPDSQLY
 WAQQTGYMPI LESVLHSEY KNSKTTKVPA QLENAVKDLF AIPVEENADS AYNEMRTIME
 SIFASSNKDT RKLLKDATSQ FEQAWNQ

EF002-1 (SEQ ID NO:5)

TAAATAGCGG AGGTAGTACA AATGAAATTT TGGAAAAAG GCTTAACAGC GGCAGCGCTG
 TTAGCAGTGG CGGCAGTAAC TTAAACAGCA TGTGGTGGTT CAAGTGAAAA GAAAGCAACT
 GAAAAGAGTG AAGATGGCAA AACAAAATTA ACAGTAACTA CTGGAATTA TGACACGACC
 CCAGAATTG AGAAATTATT CAGAGCTTTT GAAGCGGAAA ATCCTGATAT CACTATTGAA
 CCGGTGGACA TTGCTTCAGA TGATTATGAC ACAAAGTAA CAACGATGCT TTCATCAGGA
 GATACGACGG ATATTTTAAC CATGAAAAAC TTACTTTTCAT ATTCTAATTA CGCGCTACGC
 AATCAATTGG TGGATTTAAC CGATCACGTT AAAGATTTAG ATATCGAACC TGCCAAAGCA
 AGTTACGAGA TGTATGAAAT CGATGGTAAA ACCTATGCTC AGCCTTACCG TACAGATTTT
 TGGGTATTGT ATTACAATAA AAAAATGTTT GATGAAGCCG GAATTGCCTA TCCCGATAAC
 TTAACCTGGG ATGAATATGA AGCGTTAGCG AAAAAATTAT CTAAACCAGA AGAACAAGTA
 TATGGTGCCT ATCAACATAC TTGGCGCTCA ACCGTTCAAG CGATTGCTGC TGCTCAAAAC
 AATGCCAATT TGATTGAACC AAAATACAAT TATATGGAAC CTTATTATGA TCGCGCATTG
 AGAATGCAAA AAGATCAATC ACAAATGGAT TTTGGAACAG CAAAATCAAC AAAAGTAACG
 TATCAATCAC AATTGAAAA TTCAAAAGCG GCGATGATGT ACATGGGTAG CTGGTACATG
 GGGACTTTAT TAACAAACAT TGATGATGGC AAAACAAATG TCGAATGGGG GATTGCCGAA
 ATACCACAAC AAGAAAAAGG CAAAGCAACT ACCTTTGGCT CACCGACAAG TTTTGCAATT
 AATAAAAAACA GTAAAAACA AAAAGCTGCT CAAAAATTCT TAGACTTTGC TTCAGGTAAA
 GAAGGTGCAA AACTTTTAGC AGAAGTAGGG GTGGTTCTCT CTTATAAAAC AGATGAAATT
 GATAAAATCT ACTTTGCAAG AAAAGGAATG CCTTCAGACG AGTCTCACA AAAGCCTTTA
 ACCCAGATAC AATTAATTTA G

EF002-2 (SEQ ID NO:6)

MKFW KKGLTAAALL AVAAVTLTAC GGSSEKKATE KSEDGKTKLT VTTWNYDTTP
 EFEKLFRAFE AENPDITIEP VDIASDDYDT KVTTMLSSGD TTDILTMKNL LSYSNYALRN
 QLVDLTDHVK DLDIEPAKAS YEMYEIDGKT YAQPYRTDFW VLYNKKMFD EAGIAYPDNL
 TWDEYEALAK KLSKPEEQVY GAYQHTWRST VQAIAAAQNN ANLIEPKYNY METYYDRALR
 MQKDQSQMDF GTAKSTKVTY QSQFENSKAA MMYMGSWYMG TLLTNIDDGK TNVEWGIAEI
 PQQEKGKATT FGSPTSFAIN KNSKKQKAAQ KFLDFASGKE GAKLLAEVGV VPSYKTDEID

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

KIYFARKGMP SDESHKKPLT QIQLI

EF002-3 (SEQ ID NO:7)

A TGTGGTGGTT CAAGTGAAAA GAAAGCAACT
 GAAAAGAGTG AAGATGGCAA AACAAAATTA ACAGTAACTA CTGGAATTA TGACACGACC
 CCAGAATTTG AGAAATTATT CAGAGCTTTT GAAGCGGAAA ATCCTGATAT CACTATTGAA
 CCGGTGGACA TTGCTTCAGA TGATTATGAC ACAAAAGTAA CAACGATGCT TTCATCAGGA
 GATACGACGG ATATTTTAAC CATGAAAAAC TTACTTTCAT ATTCTAATTA CGCGCTACGC
 AATCAATTGG TGGATTTAAC CGATCACGTT AAAGATTTAG ATATCGAACC TGCCAAAGCA
 AGTTACGAGA TGTATGAAAT CGATGGTAAA ACCTATGCTC AGCCTTACCG TACAGATTTT
 TGGGTATTGT ATTACAATAA AAAAATGTTT GATGAAGCCG GAATTGCCTA TCCCGATAAC
 TTAAC TTGGG ATGAATATGA AGCGTTAGCG AAAAAATTAT CTAAACCAGA AGAACAAGTA
 TATGGTGCCT ATCAACATAC TTGGCGCTCA ACCGTTCAAG CGATTGCTGC TGCTCAAAAC
 AATGCCAATT TGATTGAACC AAAATACAAT TATATGGAAT CTTATTATGA TCGCGCATTG
 AGAATGCAAA AAGATCAATC ACAAATGGAT TTTGGAACAG CAAAATCAAC AAAAGTAACG
 TATCAATCAC AATTTGAAAA TTCAAAAGCG GCGATGATGT ACATGGGTAG CTGGTACATG
 GGGACTTTAT TAACAAACAT TGATGATGGC AAAACAAATG TCGAATGGGG GATTGCCGAA
 ATACCACAAC AAGAAAAAGG CAAAGCAACT ACCTTTGGCT CACCGACAAG TTTTGCAATT
 AATAAAAACA GTAAAAACA AAAAGCTGCT CAAAAATTCT TAGACTTTGC TTCAGGTAAA
 GAAGGTGCAA AACTTTTAGC AGAAGTAGGG GTGGTTCCTT CTTATAAAC AGATGAAATT
 GATAAATCT ACTTTGCAAG AAAAGGAATG CCTTCAGACG AGTCTCACA AAAGCCTTTA
 ACCCAGATAC AATTAATT

EF002-4 (SEQ ID NO:8)

C GGSSEKKATE KSEDGKTKLT VTIWNYDTTP
 EFEKLFRAFE AENPDITIEP VDIASDDYDT KVTTMLSSGD TTDILTMKNL LSYSNYALRN
 QLVDLTDHVK DLDIEPAKAS YEMYEIDGKT YAQPYRTDFW VLYYNKKMFD EAGIAYPDNL
 TWDEYEALAK KLSKPEEQVY GAYQHTWRST VQAIAAAQNN ANLIEPKYNY METYYDRALR
 MQKDQSQMDF GTAKSTKVTV QSQFENSKAA MMYMGSWYMG TLLTNIDDGK TNVEWGIAEI
 PQQEKGKATT FGSPTSFAIN KNSKKQKAAQ KFLDFASGKE GAKLLAEVGV VPSYKTDEID
 KIYFARKGMP SDESHKKPLT QIQLI

EF003-1 (SEQ ID NO:9)

TAGGAGGACA AAAGAATGAA GAAGTTTTAT TTAGCNACAT TCGCTGTTAT TGCAACAGTT
 ATTTTAGCTG CCTGTGGGGG AAATAAACAA GCAGACCAGA AAGAAGACAA GGAGATTACC
 GTTGCCGTGC AATTGGAATC TTCAAAAGAT ATCTTGGAGA TTGCCAAGAA AGAAGCTGAG
 AAAAAAGGGT ACAAATTAA CATTATGGAA GTGAGCGACA ATGTTGCCTA CAACGATGCC
 GTGCAACATG ACGAAGCGGA TGCTAATTTT GCGCAACATC AACCCTTCAT GGAAATGTTT
 AACAAAGAGA AAAAAGCTGA TTTAGTGGCT GTGCAACCGA TTTATTATTT TGCTGGTGGT
 TTCTATTCAA AAGAATACCA AGATGCGAAA GATTTACCTG AAAATGCCAA AGTGGGGATT
 CCTAGCGATC CAACCAATGA AGGTGCTGCT TTAGCAATTT TAAATGCAAA CGGCGTGATT
 AAATTAAGG AAGGTGTCCG CTTTAACGGC ACGGTGGCAG ATGTCGTGGA AAATCCTAAA
 AACATCACTT TTGAAAGCAT TGATTTACTG AATTTAGCTA AAGCCTATGA TGAAAAAGAC
 ATCGCTATGG TGTCTGCTA CCCAGCCTAC TTAGAACCCTG CTGGTTTAAC AACGAAAGAT
 GCGATCTTGT TAGAAGATAA AGAAGCAAGT AAACATTACG CATTGCAAGT TGTGACACGC
 AAAGGCGAAA AAGATAGCGA AAAAATCAAG GTTTTAAAG AAGCGATGAC AACAAAAGAA
 GTTGCTGAAT ACATCAAGAA AAATTCTAAA GCGGCCAATA TTCCTGCGTT TTAA

EF003-2 (SEQ ID NO:10)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

MKKFYLA ATFVIAITVI LAACGGNKQA DQKEDKEITV AVQLESSKDI LEIAKKEAEK
 KGYKINIMEV SDNVAYNDAV QHDEADANFA QHQPFFMEMFN KEKKADLVAV QPIYYFAGGF
 YSKEYQDAKD LPENAKVGIP SDPTNEGRAL AILNANGVIK LKEGVGFNGT VADVVENPKN
 ITFESIDLLN LAKAYDEKDI AMVFCYPAYL EPAGLTTKDA ILLEDKEASK HYALQVVTRK
 GEKDSEKIKV LKEAMTTKEV AEYIKKNSKG ANIPAF

EF003-3 (SEQ ID NO:11)

CTGTGGGGG AAATAAACAA GCAGACCAGA AAGAAGACAA GGAGATTACC
 GTTGCCGTC AATTGGAATC TTCAAAGAT ATCTTGGAGA TTGCCAAGAA AGAAGCTGAG
 AAAAAAGGT ACAAATTA CATTATGGAA GTGAGCGACA ATGTTGCCA CAACGATGCC
 GTGCAACATG ACGAAGCGGA TGCTAATTTT GCGCAACATC AACCTTCAT GGAAATGTTT
 AACAAAGAGA AAAAAGCTGA TTTAGTGGCT GTGCAACCGA TTTATTATTT TGCTGGTGGT
 TTCTATTCAA AAGAATACCA AGATGCGAAA GATTACCTG AAAATGCCAA AGTGGGGATT
 CCTAGCGATC CAACCAATGA AGGTCGTGCT TTAGCAATTT TAAATGCAAA CGGCGTGATT
 AAATTAAAG AAGGTGTCGG CTTTAACGGC ACGGTGGCAG ATGTCGTGGA AAATCCTAAA
 AACATCACCTT TTGAAAGCAT TGATTTACTG AATTTAGCTA AAGCCTATGA TGAAAAAGAC
 ATCGCTATGG TGTTCTGCTA CCCAGCCTAC TTAGAACCCTG CTGGTTTAAAC AACGAAAGAT
 GCGATCTTGT TAGAAGATAA AGAAGCAAGT AAACATTACG CATTGCAAGT TGTGACACGC
 AAAGGCGAAA AAGATAGCGA AAAAATCAAG GTTTTAAAG AAGCGATGAC AACAAAAGAA
 GTTGCTGAAT ACATCAAGAA AAATTCATAA GCGCCAATA TTCCTGCGTT T

EF003-4 (SEQ ID NO:12)

CGGNKQA DQKEDKEITV AVQLESSKDI LEIAKKEAEK
 KGYKINIMEV SDNVAYNDAV QHDEADANFA QHQPFFMEMFN KEKKADLVAV QPIYYFAGGF
 YSKEYQDAKD LPENAKVGIP SDPTNEGRAL AILNANGVIK LKEGVGFNGT VADVVENPKN
 ITFESIDLLN LAKAYDEKDI AMVFCYPAYL EPAGLTTKDA ILLEDKEASK HYALQVVTRK
 GEKDSEKIKV LKEAMTTKEV AEYIKKNSKG ANIPAF

EF004-1 (SEQ ID NO:13)

TAAATCGAAA GAAGGATGAT AGAAATGAAA AAAATGATTA AATTTGCAGG CATTGCTCTT
 ATTTTTGCAG CTCTTCTCTC TGCCTGTAGC AACGCAAAA ATAATACACA AAAGAAAGCC
 GAAACTGCTG CCCAGTCAAG CACTATTGAA GCTTCAGACA GTAACGAAAA CGAGCCTAAT
 ACAGAAAACA TAACCCAAGC AGTTAAACAG TTAGAAGAAA AATTTAACTC TGACGAGAAA
 TTAGTAAAAA TAGATGTTAA AAATAATGTT AAAGATGACA CATCAGATAA CCCTCACGCT
 GTCATTACGG TTAAGGTAAT TAATGATGAA GCAAAAAAAA ATATGGAAGA AATGCAGACT
 GCGATAGATT CCAACTCAGG TACAGAGGCA CAAAAGACTG CCATATACGG AATTCAATTA
 AATGTTGAAG AAGTAGCCAA AACATTAGAA AATGATAACG ATGTTATTTT TTTTCATCACA
 CCTTACACGA ATGGGAACGA CAGAACCATA GCAAAATCAA CTA AAAATGA AAATATTATT
 CCGTTAGTAA AATAA

EF004-2 (SEQ ID NO:14)

MKK MIKFIAGIALI FAALLSACSN AKNNTQKKAE TAAQSSTIEA SDSNENEPNT
 ENITQAVKQL EEKFNSEKL VKIDVKNVVK DDTSDNPHAV ITVKVINDEA KKNMEEMQTA
 IDSNSGTEAQ KTAIYGIQLN VEEVAKTLEN DNDVISFITP YTNGNDRTIA KSTKNENIIP
 LVK

EF004-3 (SEQ ID NO:15)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CTGTAGC AACGCAAAAA ATAATACACA AAAGAAAGCC
 GAAACTGCTG CCCAGTCAAG CACTATTGAA GCTTCAGACA GTAACGAAAA CGAGCCTAAT
 ACAGAAAACA TAACCCAAGC AGTTAAACAG TTAGAAGAAA AATTTAACTC TGACGAGAAA
 TTAGTAAAAA TAGATGTTAA AAATAATGTT AAAGATGACA CATCAGATAA CCCTCACGCT
 GTCATTACGG TTAAGGTAAT TAATGATGAA GCAAAAAAAA ATATGGAAGA AATGCAGACT
 GCGATAGATT CCAACTCAGG TACAGAGGCA CAAAAGACTG CCATATACGG AATTCAATTA
 AATGTTGAAG AAGTAGCCAA AACATTAGAA AATGATAACG ATGTTATTTC TTTCATCACA
 CCTTACACGA ATGGGAACGA CAGAACCATA GCAAAATCAA CTAAAAATGA AAATATTATT
 CCGTTAGTAA AA

EF004-4 (SEQ ID NO:16)

CSN AKNNTQKKAE TAAQSSTIEA SDSNENEPNT
 ENITQAVKQL EEKFNSEKL VKIDVKNNVK DDTSDNPHAV ITVKVINDEA KKNMEEMQTA
 IDSNSGTEAQ KTAIYGIQLN VEEVAKTLEN DNDVISFITP YTNGNDRTIA KSTKNENIIP
 LVK

EF005-1 (SEQ ID NO:17)

TAAAAAATGA AAAAACGATT GACGATTGTG GGGATGCTTT TTCTGGCCAT TTTAGTAATG
 GTTGGTTGTG GTAAAAATCA GCAAGCAACG ACAAAGAAA AAGAGACAAA ACCTGAAGAA
 CTAACCTCTT ACATTGTGCG CCACGGAAAA ACCATGTTAA ATACGACGGA CCGCGTACAA
 GGATGGTCAG ATGCGGTCTT AACACCAGAA GGTGAAAAAG TTGTGACAGC AACTGGGATT
 GGACTGAAAG ATGTTGCCTT TCAAAATGCA TATAGTAGTG ATAGTGGCCG CGCCTTGCAA
 ACTGCTCAAC TTATTTTAGA TCAAAATAAA GCAGGCAAAG ACCTTGAAGT CGTGCGTGAC
 CCAGATTTAC GTGAATTTAA TTTTGGTAGC TATGAAGGGG ATTTAAATAA GACAATGTGG
 CAGGATATTG CTGATGATCA AGGTGTTTCC TTAGAAGAAT TTATGAAAAA CATGACTCCT
 GAATCCTTTG CCAATAGTGT AGCTAACTG GATCAACAGC GCGAGGAAAG CAAGAATAAC
 TGGCCTGCAG AAGACTATGC TACAATTACT AAACGTTTGA AAAAAGGCTT AGATAAAATT
 GTTGCCACAG AATCAGCCAA TTCTGGGAAT GGCAATGTTT TAGTGGTCTC TCATGGCTTG
 AGTATTTTCA CTTGTGTAGC AACTTTATTT GATGATTTTA AAGTCCCAGA AGCGGGTTTG
 AAGAATGCTA GTGTCACAAC AATTCATTAC AAAAATGGCG AATATACTTT GGATAAAGTC
 AATGATGTCA GCTACTTAGA AGCAGGCGAA AAAGAATCAA AATAA

EF005-2 (SEQ ID NO:18)

MKKRLTIVG MLFLAILVMV GCGKNQQT KEKETKPEEL TLYIVRHGKT MLNNTDRVQG
 WSDAVLTPEG EKVVTTATGIG LKDVAFQNAV SSDSGRALQT AQLILDQNK A GKDLEVVRDP
 DLREFNFGSY EGDLNKTMWQ DIADDQGVSL EEFMKNMTP SFANSVAKLD QQREESKNNW
 PAEDYATITK RLKKGDKIV ATEANSNGN NVLVVSHGLS ISALLATLFD DFKVPEGGLK
 NASVTTHYK NGEYTLDKVN DVSYLEAGEK ESK

EF005-3 (SEQ ID NO:19)

TTGTG GTAAAAATCA GCAAGCAACG ACAAAGAAA AAGAGACAAA ACCTGAAGAA
 CTAACCTCTT ACATTGTGCG CCACGGAAAA ACCATGTTAA ATACGACGGA CCGCGTACAA
 GGATGGTCAG ATGCGGTCTT AACACCAGAA GGTGAAAAAG TTGTGACAGC AACTGGGATT
 GGACTGAAAG ATGTTGCCTT TCAAAATGCA TATAGTAGTG ATAGTGGCCG CGCCTTGCAA
 ACTGCTCAAC TTATTTTAGA TCAAAATAAA GCAGGCAAAG ACCTTGAAGT CGTGCGTGAC
 CCAGATTTAC GTGAATTTAA TTTTGGTAGC TATGAAGGGG ATTTAAATAA GACAATGTGG
 CAGGATATTG CTGATGATCA AGGTGTTTCC TTAGAAGAAT TTATGAAAAA CATGACTCCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAATCCTTTG CCAATAGTGT AGCTAAACTG GATCAACAGC GCGAGGAAAG CAAGAATAAC
 TGGCCTGCAG AAGACTATGC TACAATTACT AAACGTTTGA AAAAAGGCTT AGATAAAATT
 GTTGCCACAG AATCAGCCAA TTCTGGGAAT GGCAATGTTT TAGTGGTCTC TCATGGCTTG
 AGTATTTTCA CTTGTTAGC AACTTTATTT GATGATTTTA AAGTCCCAGA AGGCGGTTTG
 AAGAATGCTA GTGTCACAAC AATTCATTAC AAAAATGGCG AATATACTTT GGATAAAGTC
 AATGATGTCA GCTACTTAGA AGCAGGCGAA AAAGAATCAA AA

EF005-4 (SEQ ID NO:20)

CGKNQQATT KEKETKPEEL TLYIVRHGKT MLNTTDRVQG
 WSDAVLTPEG EKVVTTATGIG LKDVAFQNAV SSDSGRALQT AQLILDQNK A GKDLEVVRDP
 DLREFNFGSY EGDNLKTMWQ DIADDQGVSL EEFMKNMTPE SFANSVAKLD QQREESKNNW
 PAEDYATITK RLKKGLDKIV ATEANSNGNG NVLVVSHGLS ISALLATLFD DFKVPEGGLK
 NASVTTHYK NGEYTLDKVN DVSYLEAGEK ESK

EF006-1 (SEQ ID NO:21)

TAAACGATAA ATGGAGGGAA TAAGATGAAA AAACGTACAT TATGGTCAGT AATTACTGTA
 GCAGTAGCTG TCTTAGTTTT AGGGGCTTGC GGCAATAAAA AGAGTGATGA CTCGGTCTTG
 AAAGTTGGAG CTTCAACAGT TCCACATGCA GAGATTTTAG AACATGTAAA ACCTTTATTA
 GAAAAAGAAG GCGTAAAATT AGAAGTGACG ACTTATACAG ATTACGTGCT ACCTAACAAG
 GCGTTGGAAA GTGGCGATAT CGATGCCAAC TATTTC AACAT ATGTGCCGTT CTTTAATGAA
 GCGGTTAAAG AAAATGATTA TGACTTTGTG AATGCAGGTG CGATTCATTT AGAACCAGTT
 GGGCTTTACT CGAAAAAATA CAAATCGTTA CAAGAAATTC CTGATGGTTC AACGATTTAC
 GTTAGCTCTT CCGTTTCAGA TTGGCCACGC GTATTAACTA TCTTAGAAGA TGCTGGTTTA
 ATCAGCGTGA AAGAAGGGGT AGACCGGACA ACTGCTACTT TCGATGATAT TGATAAAAAT
 ACTAAAAAGT TGAATTTCAA TCATGAAAGT GATCCAGCAA TCATGACCAC TCTTTATGAC
 AATGAAGAAG GGGCTGCGGT TTTAATTAAC TCAAACCTTG CCGTGGATCA AGGATTAAAT
 CCGAAAAAAG ATGCGATTGC CTTAGAAAAA GAAAGTTCAC CTTATGCCAA TATTATTGCG
 GTTCGTAAAG AAGACGAAAA CAACGAAAAAT GTAAAAAAT TAGTCAAAGT GTTACGTAGC
 AAAGAAGTCC AAGATTGGAT TACGAAAAAA TGAACGGCG CTATTGTTCC AGTCAATGAA
 TAA

EF006-2 (SEQ ID NO:22)

MKK RTLWSVITVA VAVLVLGACG NKSDDSVLK VGASPVPHAE ILEHVKPLLE
 KEGVKLEVTT YTDYVLPNKA LESGDIDANY FQHVPPFFNEA VKENDYDFVN AGAIHLEPVG
 LYSKKYKSLQ EIPDGSTIYV SSSVSDWPRV LTILEDAGLI TLKEGVDRTT ATFDDIDKNT
 KKLKFNHESD PAIMTTLYDN EEGAAVLINS NFAVDQGLNP KKDAIALEKE SSPYANIIAV
 RKEDENNENV KKLKVLRSK EVQDWITKKW NGAIVPVNE

EF006-3 (SEQ ID NO:23)

TTGC GGCAATAAAA AGAGTGATGA CTCGGTCTTG
 AAAGTTGGAG CTTCAACAGT TCCACATGCA GAGATTTTAG AACATGTAAA ACCTTTATTA
 GAAAAAGAAG GCGTAAAATT AGAAGTGACG ACTTATACAG ATTACGTGCT ACCTAACAAG
 GCGTTGGAAA GTGGCGATAT CGATGCCAAC TATTTC AACAT ATGTGCCGTT CTTTAATGAA
 GCGGTTAAAG AAAATGATTA TGACTTTGTG AATGCAGGTG CGATTCATTT AGAACCAGTT
 GGGCTTTACT CGAAAAAATA CAAATCGTTA CAAGAAATTC CTGATGGTTC AACGATTTAC
 GTTAGCTCTT CCGTTTCAGA TTGGCCACGC GTATTAACTA TCTTAGAAGA TGCTGGTTTA
 ATCAGCGTGA AAGAAGGGGT AGACCGGACA ACTGCTACTT TCGATGATAT TGATAAAAAT
 ACTAAAAAGT TGAATTTCAA TCATGAAAGT GATCCAGCAA TCATGACCAC TCTTTATGAC
 AATGAAGAAG GGGCTGCGGT TTTAATTAAC TCAAACCTTG CCGTGGATCA AGGATTAAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCGAAAAAAG ATGCGATTGC CTTAGAAAAA GAAAGTTCAC CTTATGCCAA TATTATTGCG
 GTTCGTAAAG AAGACGAAAA CAACGAAAAT GTAAAAAAT TAGTCAAAGT GTTACGTAGC
 AAAGAAGTCC AAGATTGGAT TACGAAAAAA TGAACGGCG CTATTGTTCC AGTCAATGAA

EF006-4 (SEQ ID NO:24)

CG NKKSDSVLK VGASVPVPHAE ILEHVKPLLE
 KEGVKLEVTT YTDYVLPNKA LESGDIDANY FQHVPPFNEA VKENDYDFVN AGAIHLEPVG
 LYSKKYKSLQ EIPDGSTIYV SSSVSDWPRV LTILEDAGLI TLKEGVDRIT ATFDIDKNT
 KKLKFNHESD PAIMTTLYDN EEGAALINS NFAVDQGLNP KKDAIALEKE SSPYANIIIV
 RKEDENNENV KKLKVLRSK EVQDWITKKW NGAIVPVNE

EF008-1 (SEQ ID NO:25)

TAAACCGTGA GAAAGAAATG GAGGAATCAA CGAATGAAAA AATTTAGTTT ATTTTTTTTA
 AACTTTTTAG CAGGGTTAAC GTTAGCTGCT TCGGGGAATC AAGCCGCTGA AAAGAAAGAA
 AAATTAGCAA TTGTGACAAC GAACTCGATC CTATCTGATT TAGTGAAAAA TGTTGGGCAA
 GACAAAATTG AGCTGCATAG TATTGTGCCA ATTGGGACAG ACCCTCACGA ATATGAACCG
 TTACCAGAAG ACATTGCGAA AGCTTCTGAA GCGGACATTT TATTCTTTAA CGGCTTGAAC
 TTAGAAACAG GCGGAAATGG CTGGTTTAAC AAATTAATGA AAACGGCCAA AAAAGTTGAG
 AATAAGATT ACTTTTCTAC AAGCAAAAAT GTTACGCCAC AATATTTAAC AAGTGCCGGT
 CAAGAACAAA CAGAAGATCC ACATGCTTGG TTAGACATTG AAAATGGCAT TAAATATGTA
 GAAAACATTC GTGACGTGTT AGTAGAAAAA GATCCAAAAA ATAAAGATTT CTATACAGAA
 AACGCGAAAA ATTATACCGA AAAACTTAGC AAATACATG AGGAAGCCAA AGCTAAATTT
 GCTGATATTC CTGATGATAA AAAATTATTA GTTACAAGTG AAGGTGCCTT TAAATATTTT
 TCCAAAGCTT ATGATTTAAA TGCCGCTTAT ATTTGGGAAA TTAACACAGA AAGTCAAGGN
 ACACCTGAAC AAATGACCAC GATTATTGAT ACCATTAAGA AATCAAAAGC ACCTGTGTTA
 TTTGTTGAAA CCAGTGTCGA TAAACGTAGT ATGGAACGGG TCTCAAAAGA AGTGAAACGA
 CCAATTTACG ATACACTTTT CACAGACTCT CTTGCCAAAG AAGGAACAGA AGGCGATACG
 TACTACAGCA TGATGAACTG GAATTTAACA AAAATCCATG ATGGCTTAAT GAGTAAATAA

EF008-2 (SEQ ID NO:26)

MKKFSLFFLT LLAGLTLAAC GNQAAEKKEK LAIVTTNSIL SDLVKNVGQD
 KIELHSIVPI GTDPHEYEPL PEDIAKASEA DILFFNGLNL ETGGNGWFNK LMKTAKKVEN
 KDYFSTSKNV TPQYLTSAGQ EQTEDPHAWL DIENGIKYVE NIRDVLVEKD PKNKDFYTEN
 AKNYTEKLSK LHEEAKAKFA DIPDDKLLV TSEGAFKYFS KAYDLNAAI WEINTESQGT
 PEQMTTIIDT IKKSKAPVLF VETSVDKRSM ERVSKEVKRP IYDTLFTDSL AKEGTEGDTY
 YSMNNWNLTK IHDGLMSK

EF008-3 (SEQ ID NO:27)

T TCGGGGAATC AAGCCGCTGA AAAGAAAGAA
 AAATTAGCAA TTGTGACAAC GAACTCGATC CTATCTGATT TAGTGAAAAA TGTTGGGCAA
 GACAAAATTG AGCTGCATAG TATTGTGCCA ATTGGGACAG ACCCTCACGA ATATGAACCG
 TTACCAGAAG ACATTGCGAA AGCTTCTGAA GCGGACATTT TATTCTTTAA CGGCTTGAAC
 TTAGAAACAG GCGGAAATGG CTGGTTTAAC AAATTAATGA AAACGGCCAA AAAAGTTGAG
 AATAAGATT ACTTTTCTAC AAGCAAAAAT GTTACGCCAC AATATTTAAC AAGTGCCGGT
 CAAGAACAAA CAGAAGATCC ACATGCTTGG TTAGACATTG AAAATGGCAT TAAATATGTA
 GAAAACATTC GTGACGTGTT AGTAGAAAAA GATCCAAAAA ATAAAGATTT CTATACAGAA
 AACGCGAAAA ATTATACCGA AAAACTTAGC AAATACATG AGGAAGCCAA AGCTAAATTT
 GCTGATATTC CTGATGATAA AAAATTATTA GTTACAAGTG AAGGTGCCTT TAAATATTTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCCAAAGCTT ATGATTTAAA TGCCGCTTAT ATTTGGGAAA TTAACACAGA AAGTCAAGGN
 ACACCTGAAC AAATGACCAC GATTATTGAT ACCATTAAGA AATCAAAAGC ACCTGTGTTA
 TTTGTTGAAA CCAGTGTCGA TAAACGTAGT ATGGAACGGG TCTCAAAAGA AGTGAAACGA
 CCAATTTACG ATACACTTTT CACAGACTCT CTTGCCAAAG AAGGAACAGA AGGCGATACG
 TACTACAGCA TGATGAACTG GAATTTAACA AAAATCCATG ATGGCTTAAT GAGTAAA

EF008-4 (SEQ ID NO:28)

C GNQAAEKKEK LAIVTTNSIL SDLVKNVGQD
 KIELHSIVPI GTDPHEYEP L PEDIAKASEA DILFFNGLNL ETGGNGWFNK LMK TAKKVEN
 KDYFSTSKNV TPQYLTSAGQ EQTEDPHAWL DIENGIKYVE NIRDVLVEKD PKNKDFYTEN
 AKNYTEKLSK LHEEAKAKFA DIPDDKLLV TSEGAFKYFS KAYDLNAAI WEINTESQGT
 PEQMTTIIDT IKKSKAPVLF VETSVDKRS M ERVSKEVKRP IYDTLFTDSL AKEGTEGDTY
 YSMNWNLT K IH DGLMSK

EF009-1 (SEQ ID NO:29)

TGACAAATGA AAAAATTTAG TAAATTAATT GGACTTATTG GGGTATTAGC TTTTACGATT
 GCAGGTTGTG CATCGGGGTC TGTGAAGGAT ACTAAGACAG AAACCGTTAA ACTAGGGGTT
 GTAGGAACAA AAAATGATGA ATGGGAATCG GTCAAAGACC GTTTGAAAAA GAAAAATATT
 GATTTACAAT TGGTAGAATT TACAGACTAT ACGCAACCAA ACGCAGCATT AGCAGAAAAA
 GAAATTGATT TAAATGCCTT TCAGCATCAA ATCTTTTTAG ACAATTACAA TAAAGAGCAT
 GGAACGAAAT TAGTATCAAT TGGCAATACA GTCAATGCAC CATTGGGAAT TTACGCTAAT
 AAATTGAAAG ATATCACGAA AATTAAAGAC GGCGGAGAAA TTGCTATTCC TAATGACCCA
 ACGAATGGCG GGCGGGCGTT AATTTTATTA CAAACTGCAG GACTGATAAA AGTAGATCCT
 GCGAAACAGC AACTACCGAC TGTCAGTGAT ATTACTGAAA ATAAACGCCA ATTGAAAATA
 ACTGAATTAG ATGCTACGCA AACAGCGCGC GCTTTACAAG ATGTCGATGC TTCAGTGATT
 AATAGCGGCA TGGCTGTCTGA TGCTGGGTAT ACACCAGATA AAGATGCTAT TTTCTTAGAA
 CCTGTAAACG AAAAAGCGAA ACCTTATGTG AACATTGTGC TGGCCCGAGA AGAAGATCAA
 GAGAATAAAC TTTATCAAAA AGTTGTAGAA GAATATCAAC AAGAAGAAAC GAAAAAGGTC
 ATTGCAGAAA CATCAAAAGG CGCCAATGTT CCAGCCTGGG AAACATTTGG TAAAAAATAA

EF009-2 (SEQ ID NO:30)

MKKFSKLIG LIGVLAFTIA GCASGSVKDT KTETVKLG VV GTKNDEWESV KDRLKKKNID
 LQLVEFTDYT QPNAALAEKE IDLNAFQHQI FLDNYNKEHG TKLVSIGNTV NAPLGIYANK
 LKDITKIKDG GEIAIPNDPT NGGRALILLQ TAGLIKVDPA KQQLPTVSDI TENKRQLKIT
 ELDATQTARA LQDVDAVIN SGMAVDAGYT PDKDAIFLEP VNEKAKPYVN IVVAREEDQE
 NKLYQKVVEE YQQEETKKVI AETSKGANVP AWETFGKK

EF009-3 (SEQ ID NO:31)

TTGTG CATCGGGGTC TGTGAAGGAT ACTAAGACAG AAACCGTTAA ACTAGGGGTT
 GTAGGAACAA AAAATGATGA ATGGGAATCG GTCAAAGACC GTTTGAAAAA GAAAAATATT
 GATTTACAAT TGGTAGAATT TACAGACTAT ACGCAACCAA ACGCAGCATT AGCAGAAAAA
 GAAATTGATT TAAATGCCTT TCAGCATCAA ATCTTTTTAG ACAATTACAA TAAAGAGCAT
 GGAACGAAAT TAGTATCAAT TGGCAATACA GTCAATGCAC CATTGGGAAT TTACGCTAAT
 AAATTGAAAG ATATCACGAA AATTAAAGAC GGCGGAGAAA TTGCTATTCC TAATGACCCA
 ACGAATGGCG GGCGGGCGTT AATTTTATTA CAAACTGCAG GACTGATAAA AGTAGATCCT
 GCGAAACAGC AACTACCGAC TGTCAGTGAT ATTACTGAAA ATAAACGCCA ATTGAAAATA
 ACTGAATTAG ATGCTACGCA AACAGCGCGC GCTTTACAAG ATGTCGATGC TTCAGTGATT
 AATAGCGGCA TGGCTGTCTGA TGCTGGGTAT ACACCAGATA AAGATGCTAT TTTCTTAGAA
 CCTGTAAACG AAAAAGCGAA ACCTTATGTG AACATTGTGC TGGCCCGAGA AGAAGATCAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAGAATAAAC TTTATCAAAA AGTTGTAGAA GAATATCAAC AAGAAGAAAC GAAAAAGGTC
 ATTGCAGAAA CATCAAAAGG CGCCAATGTT CCAGCCTGGG AAACATTTGG TAAAAAA

EF009-4 (SEQ ID NO:32)

CASGSVKDT KTETVKLGVV GTKNDEWESV KDRLKKKNID
 LQLVEFTDYT QPNAALAEKE IDLNAFQHQI FLDNYNKEHG TKLVSIGNTV NAPLGIYANK
 LKDITKIKDG GEIAIPNDPT NGGRALILLQ TAGLIKVDPA KQQLPTVSDI TENKRQLKIT
 ELDATQTARA LQDVDAVIN SGMAVDAGYT PDKDAIFLEP VNEKAKPYVN IVVAREEDQE
 NKLYQKVVEE YQQEETKKVI AETSKGANVP AWETFGKK

EF010-1 (SEQ ID NO:33)

TGAAAGAATA AAATTGTACA GGAGGAAATA AGGAATGAAA AAATGGCAAA AAGGATTAGC
 CGTAGCTGGC GCACAGCTTT AGCTGTAGGA CTAAGCGCGT GCGGTAAATC TTCAAAAGAT
 GCAGCGTCAA AAGGTGATGA TAGTACACCA ACGTTATTAA TGTATCGTGT TGGGGACAAA
 CCAGATAATT ATGACCAATT AATCGATAAT GCGAATAAAA TTATCGAGAA AAAAATTGGG
 GCAAAATTAA AAATGGAATT TGTGTTGGG GCGGATTGGG ACCAAAAAAT GTCAACAATC
 GTTGCTTCTG GTGAAAGCTA TGATATTTCA TTAGCACAAA ATTATGCAAC GAATGCACAA
 AAAGGCGCCT ATGCTGATTT AACTGATTTA GCACCTAAAT ATGCCAAAGA AGCCTATGAT
 CAATTGCCAG ATAACCTATAT TAAAGGAAAT ACGATTAAAT GAAAACCTGT TCGCTTCCCA
 ATTTTAGGTA ACTCTTACGG TCAACAAGTT TTAACCTTTA ATAAAGAATA TGTCGATAAA
 TACAATTTAG ATATTAGTAA AGTCGATGGT AGTTATGAAA GTGCAACGGA AGTTCTAAAA
 GAATTCNTA AAAANGANCC AAATATTGCT GCTTTTGCTA TCGGCCAAC ATTCTTTGCA
 ACAGGTAATT ATGACTTCCC TATTGGTAAC CAATATCCAT TTGCAGTAAA AACAACGTAT
 ACTGGCTCAC CAAAAATTAT TAACCAATAT GCCGACAAAG ACATGATTAA TAACTTAAAA
 GTCTTGCTAC AATGGTATAA AGATGGCTTG ATTCCAACAG ATGCTGCTAC AAGTACAACA
 CCATATGACT TAAATACCAA TACTTGGTTT ATGCGTCAAG AAACACAAGG ACCTATGGAT
 TATGGTGATA CAATCTTAAC ACAAGCTGCT GGCAAACCAC TTGTTTCTCG TCCACTAACA
 GAACCATTA AAACAACAGC TCAAGCGCAA ATGGCTAACT ATGTTGTTGC AAACACGTCT
 AAAAACAAAG AAAAATCTGT TGAATTGTTA GGTTTATTAA ACAGCAATCC AGAATTGTTA
 AACGGACTTG TTTATGGTGA AGAAGGCAAA CAATATGAAA AAGTTGGCGA TGATCGTGTG
 AAATTGTTGA AAGATTACAC ACCAACAACCT CATTTGAGTG CTTGGAACAC AGGAAACAAC
 TTAATCATTT GGCCAGAAGA ATCTGTCACT GAAGAAATGG TTAAAGAAGC TGATAAGAGC
 ATCGAAGAAG CAAAAGATTC ACCAATTCTT GGTTTTACTT TTGTAAATGA TAAAGTGAAA
 ACTGAAATCA CTAACGTTGC TACAGTTATG AACC GTTACG CAGCAAGCTT AAATACAGGA
 ACTGTTGATC CAGAAGAAAC ACTTCCAAAA TTAATGGATG ACCTAAAAAC AGCTGGCTGG
 GATAAAGTTC AAAAAGAAAT GCAAACACAA TTAGACGAAT ATATCCAATC TCAAAAATAA

EF010-2 (SEQ ID NO:34)

MAKRISR SWRTALAVGL SACGKSSKDA ASKGDDSTPT LLMYRVGDKP
 DNYDQLIDNA NKIEKKIGA KLKMEFVGWG DWDQKMSTIV ASGESYDISL AQNYATNAQK
 GAYADLTDLA PKYAKEAYDQ LPDNYIKGNT INGKLYAFPI LGNSYQQVL TFNKEYVDKY
 NLDISKVDGS YESATEVLKE FXKXXPNIAA FAIGQTFEAT GNYDFPIGNQ YPFAVKTTDT
 GSPKIINQYA DKDMINNLKV LHQWYKDGLI PTDAATSTTP YDLNNTWFM RQETQGPM DY
 GDTILTQAAG KPLVSRPLTE PLKTTAQAQM ANYVVANTSK NKEKSVELLG LLNSNPELLN
 GLVYGEEGKQ YEKVGDDRVK LLKDYTPPTH LSAWNTGNL IIWPEESVTE EMVKERDKSI
 EEAKDSPILG FTFVNDKVK EITNVATVMN RYAASLNTGT VDPEETLPKL MDDLKTAGWD
 KVQKEMQTQL DEYIQSQK

EF010-3 (SEQ ID NO:35)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GT GCGGTAAATC TTCAAAAGAT
 GCAGCGTCAA AAGGTGATGA TAGTACACCA ACGTTATTAA TGTATCGTGT TGGGGACAAA
 CCAGATAATT ATGACCAATT AATCGATAAT GCGAATAAAA TTATCGAGAA AAAAAATGGG
 GCAAAATTAA AAATGGAATT TGTTGGTTGG GGCGATTGGG ACCAAAAAAT GTCAACAATC
 GTTGCTTCTG GTGAAAGCTA TGATATTTCA TTAGCACAAA ATTATGCAAC GAATGCACAA
 AAAGGCGCCT ATGCTGATTT AACTGATTTA GCACCTAAAT ATGCCAAAAGA AGCCTATGAT
 CAATTGCCAG ATAACATATAT TAAAGGAAAT ACGATTAAATG GAAACTGTA TGCCTTCCCA
 ATTTTAGGTA ACTCTTACGG TCAACAAGTT TTAACTTTTA ATAAAGAATA TGTGATAAAA
 TACAATTTAG ATATTAGTAA AGTCGATGGT AGTTATGAAA GTGCAACGGA AGTTCTAAAA
 GAATTCNTA AAAANGANCC AAATATTGCT GCTTTTGCTA TCGGCCAAAC ATTCTTTGCA
 ACAGGTAATT ATGACTTCCC TATTGGTAAC CAATATCCAT TTGCAGTAAA AACAACTGAT
 ACTGGCTCAC CAAAAATTAT TAACCAATAT GCCGACAAAG ACATGATTAA TAACTTAAAA
 GTCTTGATC AATGGTATAA AGATGGCTTG ATTCCAACAG ATGCTGCTAC AAGTACAACA
 CCATATGACT TAAATACCAA TACTTGTTT ATGCGTCAAG AAACACAAGG ACCTATGGAT
 TATGGTGATA CAATCTTAAC ACAAGCTGCT GGCAAACCAC TTGTTTCTCG TCCACTAACA
 GAACCATTA AAACAACAGC TCAAGCGCAA ATGGCTAACT ATGTTGTTGC AAACACGTCT
 AAAACAAAG AAAAATCTGT TGAATTGTTA GGTTTATTAA ACAGCAATCC AGAATTGTTA
 AACGGACTTG TTTATGGTGA AGAAGGCAA CAATATGAAA AAGTTGGCGA TGATCGTGTG
 AAATTGTTGA AAGATTACAC ACCAACAACT CATTTGAGTG CTTGGAACAC AGGAAACAAC
 TTAATCATTT GGCCAGAAGA ATCTGTCACT GAAGAAATGG TTAAAGAACG TGATAAGAGC
 ATCGAAGAAG CAAAAGATTC ACCAATTCCT GGTTTTACTT TTGTAAATGA TAAAGTAAAA
 ACTGAAATCA CTAACGTTGC TACAGTTATG AACCCTTACG CAGCAAGCTT AAATACAGGA
 ACTGTTGATC CAGAAGAAAC ACTTCCAAAA TTAATGGATG ACCTAAAAAC AGCTGGCTGG
 GATAAAGTTC AAAAAGAAAT GCAAACACAA TTAGACGAAT ATATCCAATC TCAAAAA

EF010-4 (SEQ ID NO:36)

CGKSSKDA ASKGDDSTPT LLMYRVGDKP
 DNYDQLIDNA NKIIIEKKIGA KLKMEFVGWG DWDQKMSTIV ASGESYDISL AQNYATNAQK
 GAYADLTDLA PKYAKEAYDQ LPDNYIKGNT INGKLYAFPI LGNSYQQOVL TFNKEYVDKY
 NLDISKVDGS YESATEVLKE FXKXXPNIAA FAIGQTFEAT GNYDFPIGNQ YPFAVKTTDT
 GSPKIINQYA DKDMINNLKV LHQWYKGLI PTDAATSTTP YDLNNTWFM RQETQGPMDY
 GDTILTQAAG KPLVSRPLTE PLKTTAQAM ANYVVANTSK NKEKSVELLG LLNSNPPELLN
 GLVYGEQKQ YEKVGDDRVK LLKDYTPPTH LSAWNTGNL IWPPEESVTE EMVKERDKSI
 EEAKDSPILG FTFVNDKVKL EITNVATVMN RYAASLNTGT VDPEETLPKL MDDLKTAGWD
 KVQKEMQTQL DEYIQSQK

EF011-1 (SEQ ID NO:37)

TAACGTTTTT GGAGGAAAAG AATGAAAAAG AAATTTTTAG CAATGATGGC AGTTTCAATG
 ATGGGACTGT TAATGTTAAG TGCTTGTCAC ACAAATAAAA AAACAGCAGA TTCTGCAACA
 ACAGAAACAA CAGCTAAAAC GGAAGTCACA GTCAAAGACA CCAATGGTCA ATTAACCGTT
 CCCAAAAATC CTAAGAAAGT CGTTGTTTTT GATAATGGTT CCTTGATAC AATGGATGCA
 CTAGGTGTCG GTGACCGCGT GGTAGGTGCG CCAACTAAAA ATATCCCTGC GTATTTGAAA
 AAATACCAAA AAGTTGAATC AGCAGGCGGC ATTAAGAAGC CAGATTTAGA AAAAAATCAAT
 CAACTAAAAC CAGACTTAAT TATTATTTCT GGTCGTCAAC AAGATTATCA AGAACAATTA
 AAAGCCATTG CGCCAACCAT TTACTTAGCT GTAGATGCCA AAAATCCTTG GGCATCAACG
 AAACAAAATA TCGAAACGTT AGGCACTATT TTTGATAAAG AAGAGGTAGC TAAAGAAAAA
 ATAACCTGGCT TAGAAAAAGA AATTGCTGAC GTGAAAAAAC AAGCAGAAGC TAGCGCGAAT
 AATGCGCTTG TTGTGTTAGT TAACGAAGGA CAACTTTCCG CTTACGAAA AGGCTCTCGT
 TTCGGTTTAA TTCATGATAC ATTTGGCTTC AAAGCAGCAG ACGATAAGAT TGAAGCTTCC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACTCATGGGC AAAGTGTTTC TTACGAATAT GTTTTAGAAA AAAATCCTGG GATTCTCTTT
 GTGGTAGATC GCACCAAAGC AATTGGTGGC GACGATTCAA AAGATAACGT CGCTGCAAAC
 GAATTGATTC AAAAAACCGA TGCTGGTAAA AATGATAAAG TCATTATGCT TCAACCAGAT
 GTTTGGTATC TAAGCGGTGG TGGATTAGAA TCAATGCATT TGATGATAGA AGATGTTAAA
 AAAGGATTAG AGTAA

EF011-2 (SEQ ID NO:38)

MKKK FLAMMAVSM GLLMLSACQT NKKTADSATT ETTAKTEVTV KDTNGQLTVP
 KNPKKVVVFD NGLDITMDAL GVGDRVVGAP TKNIPAYLKK YQKVESAGGI KEPDLEKINQ
 LKPDLIISG RQQDYQEQLK AIAPTIYLAV DAKNPWASTK QNIETLGTIF DKEEVAKKI
 TGLEKEIADV KKQAEASANN ALVVLVNEGQ LSAYGKGSRF GLIHDTFGFK AADDKIEAST
 HGQSVSYEYV LEKNPGILFV VDRTKAIGGD DSKDNVAANE LIQKTDAGKN DKVIMLQPDV
 WYLSGGGLES MHLMIEDVKK GLE

EF011-3 (SEQ ID NO:39)

TTGTCAA ACAAATAAAA AACAGCAGA TTCTGCAACA
 ACAGAAACAA CAGCTAAAC GGAAGTCACA GTCAAAGACA CCAATGGTCA ATTAACCGTT
 CCCAAAAATC CTAAGAAAGT CGTTGTTTTT GATAATGGTT CCTTGGATAC AATGGATGCA
 CTAGGTGTGCG GTGACCGCGT GGTAGGTGCG CCAACTAAAA ATATCCCTGC GTATTTGAAA
 AAATACCAAA AAGTTGAATC AGCAGGCGGC ATTAAAGAAC CAGATTTAGA AAAATCAAT
 CAACTAAAAC CAGACTTAAT TATTATTTCT GGTCGTCAAC AAGATTATCA AGAACAATTA
 AAAGCCATTG CGCCAACCAT TACTTAGCT GTAGATGCCA AAAATCCTTG GGCATCAACG
 AAACAAAATA TCGAAACGTT AGGCACTATT TTTGATAAAG AAGAGGTAGC TAAAGAAAAA
 ATAAGTGGCT TAGAAAAAGA AATTGCTGAC GTGAAAAAAC AAGCAGAAGC TAGCGCGAAT
 AATGCGCTTG TTGTGTTAGT TAACGAAGGA CAACTTTCCG CTTACGGAAA AGGCTCTCGT
 TTCGGTTTAA TTCATGATAC ATTTGGCTTC AAAGCAGCAG ACGATAAGAT TGAAGCTTCC
 ACTCATGGGC AAAGTGTTTC TTACGAATAT GTTTTAGAAA AAAATCCTGG GATTCTCTTT
 GTGGTAGATC GCACCAAAGC AATTGGTGGC GACGATTCAA AAGATAACGT CGCTGCAAAC
 GAATTGATTC AAAAAACCGA TGCTGGTAAA AATGATAAAG TCATTATGCT TCAACCAGAT
 GTTTGGTATC TAAGCGGTGG TGGATTAGAA TCAATGCATT TGATGATAGA AGATGTTAAA
 AAAGGATTAG AG

EF011-4 (SEQ ID NO:40)

CQT NKKTADSATT ETTAKTEVTV KDTNGQLTVP
 KNPKKVVVFD NGLDITMDAL GVGDRVVGAP TKNIPAYLKK YQKVESAGGI KEPDLEKINQ
 LKPDLIISG RQQDYQEQLK AIAPTIYLAV DAKNPWASTK QNIETLGTIF DKEEVAKKI
 TGLEKEIADV KKQAEASANN ALVVLVNEGQ LSAYGKGSRF GLIHDTFGFK AADDKIEAST
 HGQSVSYEYV LEKNPGILFV VDRTKAIGGD DSKDNVAANE LIQKTDAGKN DKVIMLQPDV
 WYLSGGGLES MHLMIEDVKK GLE

EF012-1 (SEQ ID NO:41)

TGAGGGGGCA ACAACATGAA ATTGGGGAAA AAAGTAGTAG GTTTGATTGC AACAGGGTTT
 CTTTGTAGCCG CATGTGGCGG AACCAAAGAA GCGGCAGAGA AAGTAGATTG GGGAAATTTA
 GCAGCTGAAC AAAAAATCAG TATTAGTTCA CCTGCACCAA TCTCAACATT GGATACAACA
 CAAACAACAG ATAAAAATAC CTTTACAATG GCACAACATT TATTTGAAGG CCTTTATCGG
 TTTGATGATG ATAGTGCCAC GGTGCCAGCT CTAGCTAAAG ATGTCAAGAT TAGTGACGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GGGCGCAAGT ACCACTTTTAC CTTGCGGGAG GGGATTAAAGT GGAGCAACGG CGAGCCAATC
 ACGGCCCAAG ATTTTGTTTA TTCTTGGAAG AAAGTGGTGA CACCAGCGAC GATTGGACCG
 AATGCCTATT TACTAGACAG TGTAAAAAAT AGTTTGTGAAA TACGCAACGG TGAAGAGTCA
 GTCGATGAAT TAGGGATTTC AGCCCCGAAT GACAAAGAAT TCATTGTTGA ATTAAACAG
 GCCCAACCTT CCTTCTTAGC AGTCGTTTCG ATTGCTTGGT TAGCGCCACA AAATCAAAAA
 TTTGTGGAAG CGCAAGGCAA AGATTACGCC TTGGATAGTG AACATTTACT TTATAGCGGG
 CCATTTACGC TAGCCAATTG GGATGCGACT TCAGATACTT GGACATTGAA AAAAAATCCA
 GAATACTATG ATGCGGATCA AGTGAAACTG GAAGAAGTTG CGGTTAGCAC AATCAAAGAA
 GATAAATCTG GGATTAACCT ATATCAAGTG AATGAAGTAG ACTTAGTTCG CATTAAACGGA
 CAATATGTTT AACAATATCA AGATGATCCA GGCTATGTCA GTCATCCAGA TGTGGCCAAC
 TACTTCTTAG ATTTCAACAA AAAAGAAGGA ACGCCATTAG CGAATGTTCA TTTACGAAAA
 GCGATTGGCC AAGCAATTGA TAAAGAAGCC TTAACACAAA GTGTCCTTAA CGATGGGTCA
 AAACCCCTTA ACGGATTGAT TCCAAGTAAA CTTTATGCGA ATCCAGAAAC GGATGAAGAT
 TTCCGAGCTT ACAGTGGCGA ATATTGTGAAA AATGACGTCA AAAAAAGCTCA AGCTGAATGG
 ACGAAAGCCC AAGCGGATGT CGGTAAAAAA GTGAAACTTT CATTGCTGGC GGCAGACACA
 GATCAAGGAA AACGAATTGC TGAATATGTT CAAAGTCAGT TGCAAGAAAA TCTGCCAGGT
 TTAGAAATTA CCAATTCATC GCAACCAAGT AATAATGTGA ACCAATCGCG ACGTGAAAAA
 AATTATGAGT TGCTCTCTTC AGGATGGATT GCCGGCAGTA GTGAATTAGA CTCTTACTTT
 AACTTATATG CAGGAGAATC AAGTTACAAT TACGGCAATT ATCATAATGC CAAATACGAC
 CAATTGGTAG AAGAGGCACG AACGATTAAT GCCAATAATC CAGAGAAACA GTTTGCAGAA
 TACAAAGAAG CGGAAGACAT CTTGTTGAAC CAAGATGCTG CCCAAGTACC GCTGTATCAA
 AGTGCCTCAA ATTATCTAAT CAATCCTAAA TTGAAAGGCA TTAGTTATCA CTGTATGGG
 GATTATTTCC ACTTGCGCAA TGCCTATTTA ACAGAATGA

EF012-2 (SEQ ID NO:42)

MKLGKK VVGLIATGFL LAACGGTKEA AEKVDGSLA AEQKISISSP APISTLDTTQ
 TTDKNFTMA QHLFEGLYRF DDDSATVPAL AKDVKISDDG RKYHFTLREG IKWSNGEPIT
 AQDFVYSWKK LVTPTATGPN AYLLDSVKNS FEIRNGEKSV DELGISAPND KEFIVELKQA
 QPSFLAVVSI AWLAPQNQKF VEAQGDYAL DSEHLLYSGP FTLANWDATS DTWTLKKNPE
 YYDADQVKLE EVAVSTIKED NTGINLYQVN ELDLVRINGQ YVQYQDDPG YVSHPDVANY
 FLDFNKKEGT PLANVHLRKA IGQAIDKEAL TQSVLNDGSK PLNGLIPSKL YANPETDEDF
 RAYSGEYLKN DVKKAQAEWT KAQADVGGKV KLSLLAADTD QGKRIAQYVQ SQLQENLPGL
 EITISSQPSN NVNQSRREKN YELSLSGWIA GSSELDYFN LYAGESSYNY GNYHNAKYDQ
 LVEEARTINA NNPEKQFAEY KEAEDILLNQ DAAQVPLYQS ASNYLINPKL KGISYHLYGD
 YFHLRNAYLT E

EF012-3 (SEQ ID NO:43)

ATGTGGCGG AACCAAAGAA GCGGCAGAGA AAGTAGATTC GGGAAATTTA
 GCAGCTGAAC AAAAAATCAG TATTAGTTCA CCTGCACCAA TCTCAACATT GGATACAACA
 CAAACAACAG ATAAAAATAC CTTTACAATG GCACAACATT TATTGTAAGG CCTTTATCGG
 TTTGATGATG ATAGTGCCAC GGTGCCAGCT CTAGCTAAAG ATGTCAAGAT TAGTGACGAT
 GGGCGCAAGT ACCACTTTTAC CTTGCGGGAG GGGATTAAAGT GGAGCAACGG CGAGCCAATC
 ACGGCCCAAG ATTTTGTTTA TTCTTGGAAG AAAGTGGTGA CACCAGCGAC GATTGGACCG
 AATGCCTATT TACTAGACAG TGTAAAAAAT AGTTTGTGAAA TACGCAACGG TGAAGAGTCA
 GTCGATGAAT TAGGGATTTC AGCCCCGAAT GACAAAGAAT TCATTGTTGA ATTAAACAG
 GCCCAACCTT CCTTCTTAGC AGTCGTTTCG ATTGCTTGGT TAGCGCCACA AAATCAAAAA
 TTTGTGGAAG CGCAAGGCAA AGATTACGCC TTGGATAGTG AACATTTACT TTATAGCGGG
 CCATTTACGC TAGCCAATTG GGATGCGACT TCAGATACTT GGACATTGAA AAAAAATCCA
 GAATACTATG ATGCGGATCA AGTGAAACTG GAAGAAGTTG CGGTTAGCAC AATCAAAGAA
 GATAAATCTG GGATTAACCT ATATCAAGTG AATGAAGTAG ACTTAGTTCG CATTAAACGGA
 CAATATGTTT AACAATATCA AGATGATCCA GGCTATGTCA GTCATCCAGA TGTGGCCAAC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TACTTCTTAG ATTTCAACAA AAAAGAAGGA ACGCCATTAG CGAATGTTCA TTTACGAAAA
 GCGATTGGCC AAGCAATTGA TAAAGAAGCC TTAACACAAA GTGTCTTAAA CGATGGGTCA
 AAACCCCTTA ACGGATTGAT TCCAAGTAAA CTTTATGCGA ATCCAGAAAC GGATGAAGAT
 TTCCGAGCTT ACAGTGGCGA ATATTTGAAA AATGACGTCA AAAAAGCTCA AGCTGAATGG
 ACGAAAGCCC AAGCGGATGT CGGTAAAAAA GTGAAACTTT CATTGCTGGC GGCAGACACA
 GATCAAGGAA AACGAATTGC TGAATATGTT CAAAGTCAGT TGCAAGAAAA TCTGCCAGGT
 TTAGAAATTA CCATTTTCATC GCAACCAAGT AATAATGTGA ACCAATCGCG ACGTGAAAAA
 AATTATGAGT TGTCTCTTTC AGGATGGATT GCCGGCAGTA GTGAATTAGA CTCTTACTTT
 AACTTATATG CAGGAGAATC AAGTTACAAT TACGGCAATT ATCATAATGC CAAATACGAC
 CAATTGGTAG AAGAGGCACG AACGATTAAT GCCAATAATC CAGAGAAACA GTTTGCAGAA
 TACAAAGAAG CGGAAGACAT CTTGTTGAAC CAAGATGCTG CCCAAGTACC GCTGTATCAA
 AGTGCCTCAA ATTTACTAAT CAATCCTAAA TTGAAAGGCA TTAGTTATCA CTTGTATGGG
 GATTATTTCC ACTTGCGCAA TGCCTATTTA ACAGAA

EF012-4 (SEQ ID NO:44)

CGGTKEA AEKVDSGNLA AEQKISISSP APISTLDTTQ
 TTDKNTFTMA QHLEGLYRF DDDSATVPAL AKDVKISDDG RKYHFTLREG IKWSNGEPIT
 AQDFVYSWKK LVTPATIGPN AYLLDSVKNS FEIRNGEKS DELGISAPND KEFIVELKQA
 QPSFLAVVSI AWLAPQNQKF VEAQCKDYAL DSEHLLYSGP FTLANWDATS DTWLKKNPE
 YYDAQVKLE EVAVSTIKED NTGINLYQVN ELDLVRINGQ YVQQYQDDPG YVSHPDVANY
 FLDPNKKEGT PLANVHLRKA IGQAIDKEAL TQSVLNDGSK PLNGLIPSKL YANPETDEDF
 RAYSGEYLKN DVKKAQAEWT KAQADVKKV KLSLLAADTD QGKRIAERYVQ SQLQENLPGL
 EITISSQPSN NVNQSRREKN YELSLSGWIA GSSELDSEYFN LYAGESSYNY GNYHNAKYDQ
 LVEEARTINA NNPEKQFAEY KEAEDILLNQ DAAQVPLYQS ASNYLINPKL KGISYHLYGD
 YFHLRNAYLT E

EF013-1 (SEQ ID NO:45)

TAACGAAAAA TGAAAAAAT TGCTTTGTTC AGTATGTTAA CGTTCAGTGT ATTGTCTTTA
 AGTCTAGCAG GATGTGGAAA CAAAAAACA GCAAGCACAA ATGATTCCTAA GCCAAAGCAA
 GAAACAAAGA AAGCCACGCA GAAATCCTCT AGCCAACAAG AAATGAAAAG TAGTCATTCTG
 TCTGTACGCG GTCAAAATTC TAATGTGACA GGGGAAAATC CGTCAGAAAA TGCCACGCAG
 CCTTCTGCAG GAACTGATGA AACGAATGAA GTCCCTCAA ACCAAGCACC TGATACAAAC
 ATTACAATTA CCAATGTTGT TTTCAATCCT GAAAGAAATG AAATTAATGG TACTACATTA
 CCTAATGCAA CCATTACAGC AACGGTAGTC GGTGATGCTT CTGCACAAGC AGGTGTTTTT
 TATGCGGATG CCAATGGCAA TTTTACAGTA ATTAGTCCCA GAGCGGGAGC GACTACTCAA
 TTAATCGCAA CCGTTGATCA ACGGAATAGT GCACCTGTCC AAATTGATAT TCCAAGTTCA
 GGACAAGAAG CAGCGCTTTC TTTTAGCAAT ATTACGATTG ATCCGAAACA AGGGACAATT
 TCTGGTAAAA CAGCACCGAA TGCAACTATT TTAGTGTAC GTGCAGATGA TGCGCGGGTG
 ATTTTAGCAA GTTTTACTGC GGATGCCCAA GGAATTTCA CAGCCAGTAA TTTAGTTCCC
 GGCACAAAAA ATCGCTTAGA TGTACGTTA AATGAGAAA TAGGGACACC TTACTTGTTT
 GATTTACCAA ATTAA

EF013-2 (SEQ ID NO:46)

MKKIALFS MLTFSVLSLS LAGCGNKKTA STNDSKPKQE TKKATQKSSS QQEMKSSHSS
 VTGQNSNVTG ENPSENATQP SAGTDETNV PQNQAPDTNI TITNVFNPE RNEINGTTLF
 NATITATVVG DASAQGVFY ADANGNFTVI SPRAGATTQL IATVDQRNSA PVQIDIPSSG
 QEALSFNSI TIDPKQGTIS GKTAPNATIL VSRADDARVI LASFTADAQG NFTASNLVPG
 TKNRLDVTLN GEIGTPYLED LPN

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF013-3 (SEQ ID NO:47)

ATGTGGAAA CAAAAAACA GCAAGCACAA ATGATTCTAA GCCAAAGCAA
 GAAACAAAGA AAGCCACGCA GAAATCCTCT AGCCAACAAG AAATGAAAAG TAGTCATTTCG
 TCTGTCACGG GTCAAAATTC TAATGTGACA GGGGAAAATC CGTCAGAAAA TGCCACGCAG
 CCTTCTGCAG GAACTGATGA AACGAATGAA GTCCCTCAAA ACCAAGCACC TGATACAAAC
 ATTACAATTA CCAATGTTGT TTTCAATCCT GAAAGAAATG AAATTAATGG TACTACATTA
 CCTAATGCAA CCATTACAGC AACGGTAGTC GGTGATGCTT CTGCACAAGC AGGTGTTTTTT
 TATGCGGATG CCAATGGCAA TTTTACAGTA ATTAGTCCCA GAGCGGGAGC GACTACTCAA
 TTAATCGCAA CCGTTGATCA ACGGAATAGT GCACCTGTCC AAATTGATAT TCCAAGTTCA
 GGACAAGAAG CAGCGCTTTC TTTTAGCAAT ATTACGATTG ATCCGAAACA AGGGACAATT
 TCTGGTAAAA CAGCACCGAA TGCAACTATT TTAGTGTCAC GTGCAGATGA TGCGCGGGTG
 ATTTTAGCAA GTTTTACTGC GGATGCCCAA GGGAAATTCA CAGCCAGTAA TTTAGTTCCC
 GGCACAAAAA ATCGCTTAGA TGTTACGTTA AATGGAGAAA TAGGGACACC TTACTTGTTC
 GATTTACCAA AT

EF013-4 (SEQ ID NO:48)

CGNKKTA STNDSKPKQE TKKATQKSSS QQEMKSSHSS
 VTGQNSNVTG ENPSENATQP SAGTDETNEV PQNQAPDTNI TITNVVFNP RNEINGTTL P
 NATITATVVG DASAQAGVFY ADANGNFTVI SPRAGATTQL IATVDQRNSA PVQIDIPSSG
 QEALSFNSI TIDPKQGTIS GKTAPNATIL VSRADDARVI LASFTADAQG NPTASNLVPG
 TKNRLDVTLN GEIGTPYLFDP LPN

EF014-1 (SEQ ID NO:49)

TGATGGTGGA GACTTTTTTAA GAGAGAGGAA GTACAGCCAA TGAGTAGGAA GCGAAAAATC
 AGCTTAATTA GTTTAGTCAT CATTTTGGTT TTTGTCACAG TCGGCTCAGC ATACTTTGCT
 GTAGCGGGTA GCTATTTTAA GAAAACAATT GATAAAGGCT ATGTTCCCAT AAAAAATGAT
 TATAATGAAG CGCAAAATAA AGATAGTCAA TCGTTTTTGA TTATGGGGCT AGACAATACA
 ATTGAACGGA AATTAGGCAC AACTAGGACT GATGCTATGA TGGTGATTAC CGTGAATAAC
 AAGACGAAGA AAATAACCTA TTTAAGTTTG CCACGGGATA GTTTTGTTCA AATTGATGCG
 AAAAAATTACC AAGGGATGCA GCGAATTGAA GCCGCCTATA CCTACGATGG ACCAACAGCT
 TCTGTTAACA CAGTTGAGAA ATTATTGAAT ATTCCAATCA ATCATTACGT TGTGTTTAAAC
 TTTTATCTTT TTATTAAGTT AATTGATGCG GTTGGCGGCA TAGATGTCAA TGTCAAGCAG
 GCGTTTGATG GTGTCACCAA AGACGGGCCA GGATCCATTC ATTTTGATGC AGGGAAACAG
 CATTTAGATG GTACGAAAGC TTTATCTTAT GCCCGTGAAA GACATAGCGA TAACGATATT
 ATGCGTGGAT TCCGACAACA AGAAATTATT CAAGCAGTTG AAGACAAGTT GAAATCTGGT
 CAATCAATCA TGAATAAAT GGACATTATT GATTTCGTTA ATGGAACAT TCAAACATGAT
 GTGGATTCCA ATGAATTGAC TCATTTAGTC AAAGAAGGTT TGACTTGGAC CAATTATGAT
 AAACAACAGC TTTCTTTTGA CTGGCGCACT TTTAGTAATG AAGGGCGCAG TATGGTTGAA
 CTATACCCAG ATAGTATTGA AAATGTCCGT CATCAATTAC GTGTGTCTTT AAATTTAGAA
 AAGCCAGATG AACGAGATCA AGACGGCTAT GTCTTCCATA CGAACGGTGA ATTTTATAT
 CAAAGTGATT ATACCGTTCA AGATGAAGCA GCTGAGGAAA ACGAAATGAC TTCCATCAAC
 GGCAATACGT ATATTGGTGT TCCTGGTAAT ACACAGACCG GCCCGTTGCC ATCAGTTAAA
 ACGGAAAATG GCTTTATAAA ATAA

EF014-2 (SEQ ID NO:50)

MSRRRKIS LISLVIIIVF VTVGSAYFAV AGSYLKKTID KGYVPIKNDY
 NEAQNKDSQS FLIMGLDNTI ERKLGTTTRTD AMMVITVNNK TKKITYLSLP RDSFVQIDAK
 NYQMQRIEA AYTVDGPTAS VNTVEKLLNI PINHYVVFNF LSFILIDAV GGIDVNVKQA
 FDGVTKDGP SIHFDAKQH LDGTKALSYA RERHSDNDIM RGFRQQEIIQ AVEKDKLSGQ
 SIMKIMDIID SLNGNIQTDV DSNELTHLVK EGLTWTNYDK QQLSFDWRTF SNEGRSMVEL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

YPDSIENVRH QLRVSLNLEK PDERDQDGYV FHTNGEFLYQ SDYTVQDEAA EENEMTSING
NTYIGVPGNT QTGPLPSVKT ENGFIK

EF014-3 (SEQ ID NO:51)

TGCT

GTAGCGGGTA GCTATTTTAAA GAAAACAATT GATAAAGGCT ATGTTCCCAT AAAAAATGAT
TATAATGAAG CGCAAAATAA AGATAGTCAA TCGTTTTTGA TTATGGGGCT AGACAATACA
ATTGAACGGA AATTAGGCAC AACTAGGACT GATGCTATGA TGGTGATTAC CGTGAATAAC
AAGACGAAGA AAATAACCTA TTTAAGTTTG CCACGGGATA GTTTTGTTCA AATTGATGCG
AAAAATTACC AAGGGATGCA GCGAATTGAA GCCGCCTATA CCTACGATGG ACCAACAGCT
TCTGTTAACA CAGTTGAGAA ATTATTGAAT ATTCCAATCA ATCATTACGT TGTGTTTAAAC
TTTTTATCTT TTATTAAGTT AATTGATGCG GTTGGCGGCA TAGATGTCAA TGTCAGCAG
GCGTTTGATG GTGTCACCAA AGACGGGCCA GGATCCATTC ATTTTGATGC AGGGAAACAG
CATTTAGATG GTACGAAAGC TTTATCTTAT GCCCGTGAAA GACATAGCGA TAACGATATT
ATGCGTGGAT TCCGACAACA AGAAATTATT CAAGCAGTTG AAGACAAGTT GAAATCTGGT
CAATCAATCA TGAAAAAAT GGACATTATT GATTCTGTAA ATGGAAACAT TCAAACATGAT
GTGGATTCCA ATGAATTGAC TCATTTAGTC AAAGAAGGTT TGACTTGGAC CAATTATGAT
AAACAACAGC TTTCTTTTGA CTGGCGCACT TTTAGTAATG AAGGGCGCAG TATGGTTGAA
CTATACCCAG ATAGTATTGA AAATGTCCGT CATCAATTAC GTGTGTCTTT AAATTTAGAA
AAGCCAGATG AACGAGATCA AGACGGCTAT GTCTTCATA CGAACGGTGA ATTTTATAT
CAAAGTGATT ATACCGTTCA AGATGAAGCA GCTGAGGAAA ACGAAATGAC TTCCATCAAC
GGCAATACGT ATATTGGTGT TCCTGGTAAT ACACAGACCG GCCCGTTGCC ATCAGTTAAA
ACGGAAAATG GCTTTATAAA A

EF014-4 (SEQ ID NO:52)

AV AGSYLKKTID KGYVPIKNDY

NEAQNKDSQS FLIMGLDNTI ERKLGTTTRTD AMMVITVNNK TTKITYLSLP RDSFVQIDAK
NYQGMQRIEA AYTYDGPTAS VNTVEKLLNI PINHYVVFNF LSFIKLIDAV GGIDVNVKQA
FDGVTKDGP SIHFDAGQKH LDGKALSYA RERHSDNDIM RGFRQOEIIQ AVEDKLKSGQ
SIMKIMDIID SLNGNIQTDV DSNELTHLVK EGLTWTNYDK QQLSFDWRTF SNEGRSMVEL
YPDSIENVRH QLRVSLNLEK PDERDQDGYV FHTNGEFLYQ SDYTVQDEAA EENEMTSING
NTYIGVPGNT QTGPLPSVKT ENGFIK

EF015-1 (SEQ ID NO:53)

TAATTAAAAA TGTGTAAAAA GGGTCTGATG AAAAAAGGAG ACATAATAGT TATTATCTTT
TTAATAGCTA TCTCTTTTTC TCCATATTTT ATTTTITTTTC ACAATAATCC ATTTAACTCC
AAAAGTTTTC ACGACACTAA ATATGCTGTG GTCAAGATAG ATGGGAAAGA GATTGAGCGT
ATAAATTTAG ATGATTCAAA AGAATTTATC AAAACATATT ATCCATCAAA AGGGCAATAT
AATACTATAG AAGTTAAAAA TGGGCACGTT CGTGTAATAA AAGATAATAG TCCAGATCAA
ATTGCGGTGA AAACAGGATG GATATCAGAA CCAGGGCNAA CTAGTATCTG TATTCTCAC
AGATTCATTT TAGAAATTGT TCAACAATAT TCTAAGGATT ATTATATTTA CTAA

EF015-2 (SEQ ID NO:54)

MK KGDIIVIIFL IAISFSPYFI FFHNNPFNSK SFDDTKYAVV KIDGKEIERI
NLDDSKEFIK TTYPSKGQYN TIEVKNGHVR VKKDNSPDQI AVKTGWISEP GXTSICIPHR
FILEIVQQYS KDYYIY

EF015-3 (SEQ ID NO:55)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAATAATCC ATTTAACTCC

AAAAGTTTTG ACGACACTAA ATATGCTGTG GTCAAGATAG ATGGGAAAGA GATTGAGCGT
 ATAAATTTAG ATGATTCAAA AGAATTTATC AAAACATATT ATCCATCAAA AGGGCAATAT
 AATACTATAG AAGTTAAAAA TGGGCACGTT CGTGTAAGAA AAGATAATAG TCCAGATCAA
 ATTGCGGTGA AAACAGGATG GATATCAGAA CCAGGGCNAA CTAGTATCTG TATTCCTCAC
 AGATTCAATTT TAGAAATTGT TCAACAATAT TCTAAGGATT ATTATATTTA C

EF015-4 (SEQ ID NO:56)

NNPFNSK SFDDTKYAVV KIDGKEIERI

NLDDSKFIK TYYPKSGQYN TIEVKNGHVR VKKDNSPDQI AVKTGWISEP GXTSICIPHR
 FILEIVQQYS KDYYIY

EF016-1 (SEQ ID NO:57)

TGACGGTTGC CCCCCTCCAA TAGAAAGGAG TTTATGATGA AAAAGAAATA TTCTTTAGCC
 TTGCTGGTTA TCTGTTGTAG TTTACTCCTA TTTGCAGGTT GTGGTAAAAG AAAAAGCAAC
 GAAGATCAAT GGACACGGAT TAACGAAGAA AAACGGATTA TTATTGGCTT AGATGACTCC
 TTTGTGCCCA TGGGTTTTCA AGATAAATCA GGCAAAATTG TCGGCTTTGA TGTCGACTTA
 GCCAAAGCGG TTTTTAAACT TTATGGCATT TCCGTTGACT TCCAACCGAT TGATTGGTCT
 ATGAAAGAAA CAGAATTACA AAATCAAACC ATTGATCTTA TTTGGAACGG CTACACTAAA
 ACGAGCGAGC GGGCCGAAAA AGTTCAATTC ACACAACCTT ACATGACGAA CGACCAAGTA
 CTGTGTTCTT TAAAAGAAAA AAACATTGCA ACAGCGAGCG ACATGCAAGG CAAAATTTTA
 GGGGTTCAAA ACGGCTCTTC TGGCTATGAT GGCTTCGAAA GTCAGCCTGA CGTTTTGAAA
 AAATTTGTTA AAGACCAAAC ACCTATTTTA TATGACGGCT TTAATGAAGC TTTCTTAGAT
 TTAATAATCTG GTCGAATTGA CGGACTCCTA ATCGATCGCG TTTACGCCAA CTACTATCTT
 TCCCACGAAG ATAATTTAAA AAACATACTT ATTTCTCATG TAGGCTATGA CAATGAAGAT
 TTTGCTGTGG GCGTCCGCAA ATCAGACAAT CAATTAGTCC AAAAAATCAA TACTGCCTTT
 GAAACGTTAC GAAAAGATGG CACCCTTAGT AAAATTCTC AAAAAATGGT TGGAGAGGAC
 GTTACAAATA ACACAAAAAT AAACATA

EF016-2 (SEQ ID NO:58)

MMKKKYLAL LVICCSLLLF AGCGKRKSNE DQWTRINEEK RIIIGLDDSF
 VPMGFQDKSG KIVGFDVLA KAVFKLYGIS VDFQPIDWSM KETELQNTI DLIWNGYTKT
 SERAEKVQFT QPYMTNDQVL VSLKEKNIAT ASDMQKILG VQNGSSGYDG FESQPDVLKK
 FVKDQTPILY DGFNEAFLDL KSGRIDGLLI DRVYANYLS HEDNLKNYTI SHVGYDNEDF
 AVGVKSDNQ LVQKINTAFE TLRKDGTLSK ISQKWFGEDV TNNTKIN

EF016-3 (SEQ ID NO:59)

AAGCAAC

GAAGATCAAT GGACACGGAT TAACGAAGAA AAACGGATTA TTATTGGCTT AGATGACTCC
 TTTGTGCCCA TGGGTTTTCA AGATAAATCA GGCAAAATTG TCGGCTTTGA TGTCGACTTA
 GCCAAAGCGG TTTTTAAACT TTATGGCATT TCCGTTGACT TCCAACCGAT TGATTGGTCT
 ATGAAAGAAA CAGAATTACA AAATCAAACC ATTGATCTTA TTTGGAACGG CTACACTAAA
 ACGAGCGAGC GGGCCGAAAA AGTTCAATTC ACACAACCTT ACATGACGAA CGACCAAGTA
 CTGTGTTCTT TAAAAGAAAA AAACATTGCA ACAGCGAGCG ACATGCAAGG CAAAATTTTA
 GGGGTTCAAA ACGGCTCTTC TGGCTATGAT GGCTTCGAAA GTCAGCCTGA CGTTTTGAAA
 AAATTTGTTA AAGACCAAAC ACCTATTTTA TATGACGGCT TTAATGAAGC TTTCTTAGAT
 TTAATAATCTG GTCGAATTGA CGGACTCCTA ATCGATCGCG TTTACGCCAA CTACTATCTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCCCACGAAG ATAATTTAAA AACTATACT ATTTCTCATG TAGGCTATGA CAATGAAGAT
 TTTGCTGTGG GCGTCCGCAA ATCAGACAAAT CAATTAGTCC AAAAAATCAA TACTGCCTTT
 GAAACGTTAC GAAAAGATGG CACCCTTAGT AAAATTTCTC AAAAAATGGT TGGAGAGGAC
 GTTACAAATA ACACAAAAAT AAAC

EF016-4 (SEQ ID NO:60)

SNE DQWTRINEEK RIIIGLDDSF

VPMGFQDKSG KIVGFDVDLA KAVFKLYGIS VDFQPIDWSM KETELQNQTI DLIWNGYTKT
 SERAEKVQFT QPYMTNDQVL VSLKEKNIAT ASDMQGKILG VQNGSSGYDG FESQPDVLKK
 FVKDQTPILY DGFNEAFLDL KSGRIDGLLI DRVYANYYLS HEDNLKNYTI SHVGYDNEFD
 AVGVKSDNQ LVQKINTAFE TLRKDGTLK ISQKWFGEVDV TNNTKIN

EF017-1 (SEQ ID NO:61)

TGAGGTGTTT TTATGAAAAG GGCAACAAAG CAAAGGCTGT CTTTGGCAGC AATCATGGTT
 CTACTTCTCT CGGGCTGTGG AAGTGTGGG AAAGAAACCA AAAAGCAAGA ACAACAGGTA
 TTACGGGTCG GGATTGATTC GGAATTATCA ACGGCAGACG TGTCGTTGGC AATGGATAAT
 ACCGCAGCAG ATGTAATGAG CCAAGTAGGG GAGGGACTTT TCTCCTTTGA CGAAAAAGGA
 GAAGCGAAAC CAGCATTGGC AACTGAAAAA GTACAGCCCT CCAATGATGG TTTAAGCTAT
 ACTTTTACGA TTCGAAAAGA TGCAAAATGG AGTAACGGCG AGCCAATCAC AGCAAATGAT
 TTTGAATACT CTTGGAAGCG CACAGTGGAC CAAAAACAG CTTCCCGCA AGCGTATTAC
 TTTGAAGGGT TAAAAAATTA TCGTGCTATT GTTGACGGTA GCAAATCTAA AGAAGAGTTA
 GGGGTAACAG CCATTGATGA CCATACCTTG GAAGTAGAGC TAAGCTATCC TATGAGTTAT
 TTTCAACAAT TATTGGCGGT ACCAGCTTTT TATCCTTTAA ATGAAGCATT TGTCGAAAAA
 ACGGGCAAAA ACTATGGTAC ATCAGCTGAG TCAACACTTT ACAATGGCGC CTTACATTA
 GAAGGTGGG ATGGCACGAA TAATACTTGG TCCTATGTGA AGAATAAAAA TTATTGGGAT
 CAAGCGAATG TTTGCTAGA TAAGGTGGAT GTCCAAGTAG TTAAAGAAGT CAATACTGGG
 AAAAATCTTT TCGAAGGGAA AGAATTAGAT GTTGTAAGAA TTTCTGGAGA AATTGTTGCA
 CAAGAACAAG GCAATGCAGC TTTGAAAATT CGTGAAATTC CTGGAACGTA TTATATCCAA
 TTAAATACGC AAAAAGATCT TTTGGCAAAT AAGAATGCAC GTCGAGCAAT AGCATTATCA
 TTGAATTCTG AGCGTTTAGC TAAAAATGTT TTAAATGATG GCTCAAAAAA AGCACTTGGC
 TTCGTGCCAA CAGGTTTCAC TAATCAAGAA ACGCAAAAAG ATTTTGCAGA GGAATTAGGA
 GATTTAAATC CTAGTGAACC AGAAAAAGCG AAAGAGTTAT GGCAACGGC TAAAAAGAA
 TTAGGAATTG AAAAAGCGGA GCTAACGATT TTAAGTTCGG ATACAGAAAA TGCTAAAAAA
 ATCAGTAGT ATGTTCAAGG AGCTTTAGCA GATAATTTAG AAAATTTAAC AGTCAATGTT
 TCACCAAGTC CTTTTAATAA TCGTTTAGAA AAAAGTCGCA GCGGAGATTT CGACATTGTG
 GTTGGTGGCT GGACGACAGT ATATGCTGAT CCAATCGATT TCTTAAACTT ACTGCAATCA
 AAAAATTCCA ATAATTTTGG TAAATGGTCT AATAAGACCT TTGATCAGTT GCTTCAAGAA
 GCAAACGTAA CTTATGCAAA TAAATATGAA GAACGTTGGA AAACATTACA AAAAGCGGAT
 CAATTGGTTG CGGAAGAAGC CCCCTAGTT CCTCTTTATC AATTAACAGA AGCACGCTTA
 GTGGCCGATT CTGTCCAAAA TTAGTCTAT GGTCCATTAG GTTCAGGCTA TTACAAATCA
 GTCTCTATCG GCGACAAGTA A

EF017-2 (SEQ ID NO:62)

MKRATKQ RLSLAAIMVL LLSGCGSVGK ETKKQEQVL RVGIDSELST ADVSLAMDNT

AADVMSQVGE GLFSFDEKGE AKPALATEKV QPSNDGLSYT FTIRKDAKWS NGEPIITANDF
 EYSWKRTVPD KTASPOAYYF EGLKNYRAIV DGSKSKEELG VTAIDDHTLE VELSYPMYSYF
 QQLLAVPAFY PLNEAFVEKT GKNYGTSAES TLYNGAFTLE GWDGTNNTWS YVKNKNYWDQ
 ANVSLDKVDV QVVKEVNTGK NLFEGKELDV VKISGEIVAQ EQGNAALKIR EIPGTYIIQL
 NTQKDLLANK NARRAIALSL NSERLAKNVL NDGSKKALGF VPTGFTNQET QKDFAEELGD

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LNPSEPEKAK ELWQTAKKEL GIEKAELTIL SSDTENAKKI SEYVQALAD NLENLTVNVS
 PVPFNNRLEK SRSGDFDIVV GGWTPVYADP IDFLNLLQSK NSNNFGKWSN KTFDQLLQEA
 NVTYANKYEE RWKTLQKADQ LVAEEAPLVP LYQLTEARLV ADSVQNLVYG PLGSGYYKSV
 SIGDK

EF017-3 (SEQ ID NO:63)

CTGTGG AAGTGTGGG AAAGAAACCA AAAAGCAAGA ACAACAGGTA
 TTACGGGTGCG GGATTGATTC GGAATTATCA ACGGCAGACG TGTCGTTGGC AATGGATAAT
 ACCGCAGCAG ATGTAATGAG CCAAGTAGGG GAGGGACTTT TCTCCTTTGA CGAAAAAGGA
 GAAGCGAAAC CAGCATTGGC AACTGAAAAA GTACAGCCCT CCAATGATGG TTTAAGCTAT
 ACTTTTACGA TTCGAAAAGA TGCAAAATGG AGTAACGGCG AGCCAATCAC AGCAAATGAT
 TTTGAATACT CTTGGAAGCG CACAGTGGAC CCAAAAACAG CTTCCCCGCA AGCGTATTAC
 TTTGAAGGGT TAAAAAATTA TCGTGCTATT GTTGACGGTA GCAAATCTAA AGAAGAGTTA
 GGGGTAACAG CCATTGATGA CCATACCTTG GAAGTAGAGC TAAGCTATCC TATGAGTTAT
 TTTCAACAAT TATTGGCGGT ACCAGCTTTT TATCCTTTAA ATGAAGCATT TGTCGAAAAA
 ACGGGCAAAA ACTATGGTAC ATCAGCTGAG TCAACACTTT ACAATGGCGC CTTACACATTA
 GAAGGTTGGG ATGGCACGAA TAATACTTGG TCCTATGTGA AGAATAAAAA TTATTGGGAT
 CAAGCGAATG TTTGCTAGA TAAGGTGGAT GTCCAAGTAG TTAAAGAAGT CAATACTGGG
 AAAAATCTTT TCGAAGGGAA AGAATTAGAT GTTGTAAGAA TTTCTGGAGA AATTGTTGCA
 CAAGAACAAG GCAATGCAGC TTTGAAAATT CGTGAAATTC CTGGAACGTA TTATATCCAA
 TTAAATACGC AAAAAGATCT TTTGGCAAAAT AAGAATGCAC GTCGAGCAAT AGCATTATCA
 TTGAATTCTG AGCGTTTTCAG TAAAAATGTT TTAAATGATG GCTCAAAAAA AGCACTTGGC
 TTCGTGCCAA CAGGTTTCAC TAATCAAGAA ACGCAAAAAG ATTTTGCAGA GGAATTAGGA
 GATTTAAATC CTAGTGAACC AGAAAAAGCG AAAGAGTTAT GGCAACGGC TAAAAAGAA
 TTAGGAATTG AAAAAGCGGA GCTAACGATT TTAAGTTCGG ATACAGAAAA TGCTAAAAAA
 ATCAGTGAGT ATGTTCAAGG AGCTTTAGCA GATAATTTAG AAAATTTAAC AGTCAATGTT
 TCACCAGTTC CTTTTAATAA TCGTTTAGAA AAAAGTCGCA GCGGAGATTT CGACATTGTG
 GTTGGTGGCT GGACGCCAGT ATATGCTGAT CCAATCGATT TCTTAACTT ACTGCAATCA
 AAAAATTCCA ATAATTTTGG TAAATGGTCT AATAAGACCT TTGATCAGTT GCTTCAAGAA
 GCAAACGTAA CTTATGCAAA TAAATATGAA GAACGTTGGA AAACATTACA AAAAGCGGAT
 CAATTGGTTG CGGAAGAAGC CCCCTAGTT CCTCTTTATC AATTAAACAGA AGCAGCCTTA
 GTGGCCGATT CTGTCCAAAA TTTAGTCTAT GGTCCATTAG GTTCAGGCTA TTACAAATCA
 GTCTCTATCG GCGACAAG

EF017-4 (SEQ ID NO:64)

CGSVGK ETKKQEQVL RVGIDSELST ADVSLAMDNT
 AADVMSQVGE GLFSFDEKGE AKPALATEKV QPSNDGLSYT FTIRKDAKWS NGEPIITANDF
 EYSWKRTVDP KTASPQAYYF EGLKNYRAIV DGSKSKEELG VTAIDDHTLE VELSYPMYSYF
 QQLLAVPAFY PLNEAFVEKT GKNYGTSAES TLYNGAFTLE GWDGTNNTWS YVKNKNYWDQ
 ANVSLDKVDV QVVKEVNTGK NLFEGKELDV VKISGEIVAQ EQGNAALKIR EIPGTYYIQL
 NTQKDLLANK NARRAIALSL NSERLAKNVL NDGSKKALGF VPTGFTNQET QKDFAEELGD
 LNPSEPEKAK ELWQTAKKEL GIEKAELTIL SSDTENAKKI SEYVQALAD NLENLTVNVS
 PVPFNNRLEK SRSGDFDIVV GGWTPVYADP IDFLNLLQSK NSNNFGKWSN KTFDQLLQEA
 NVTYANKYEE RWKTLQKADQ LVAEEAPLVP LYQLTEARLV ADSVQNLVYG PLGSGYYKSV
 SIGDK

EF018-1 (SEQ ID NO:65)

TGTCATTACA ACGATACCAA TTTTAATCAT TTATCCATTA CTACAAAAAC ACTTTATCGG
 CCGTATGATG GCCGGTGCAG TAAAAGAATA AAGAAAGTAG GGAACAATAT GAAAAAAGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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TTAGCGGGTT TATTGGTGGC AACGGCGGTC GTTAGTTTAG CGGCCTGTAG CGGTGGGGAA
AAGAAAGCTA GCTCAGATGT CTCAATTAAG GATCGGTATG AATTAGATGA AAAGACGCCT
GCTTGGAAGT TAGATAAGAA GAAAGAACCG ACCAAGATTA AATGGTATAT TAACTCAGAT
TGGACGGCGC TGCCTTTTGG AAAAGACGTG ACCACTGCGC AGATTAAAAA AGACTTAAAT
GTGGATATTG AATTTATTTT CGGCGATGAT TCAAAATTAA ATGCCATGAT TTCAAGTGGA
GATATGCCTG ATATCGTGAC ATTAACTGAA AAAACTGGAC AAGCAGCATT GAAAGCAGAT
TCTTGGGCCT ATTCTTTAAA CGATTTAGCT AAAAAATATG ACCCCTATTT AATGAAAGTT
GTTAACCAAG ATACGTTTAA ATGGTATGCC TTAGAGGATG GAAAAACATA TGGTTACCCT
AATTACTCTA ATACAAAAGC GGATTATGAA AGTGGAATA TCCAGTAAA TGATAATTTT
GTTATTCGTG AAGATGTCTA TAATGCATTA GGCAAGCCAG ACGTTTCAAC ACCAGAAAAT
TTTGAAAAAG TCATGCAACA GATTAAAGAA AAATATCCTG AGATGACCCC AATGGGCTTC
ACCACAGTGG GCGATGGTGC AGGACCATTT TTAGACAAAT TACAAGACTT CTTAGGTGTT
CCTTTAGAGG ATAAAAATGG TAAATACTAT GATCGAAATT TAGATAAAGA ATATTTAGAA
TGGTTAAAAA CATTTAATGA TGTTTACCGA GCAGGCAATA TTAGTGATGA TAGCTTCACA
GATGATGGGG CAACGTTTGA TGA AAAAGTG AAACAAGGAA ATTATGCAAC CATGCTCGTT
GCTGGAACCA GTGGTCAAGG TGGGAACCTT ACAGAATTTA TGAAAAAATC TGGCACACGT
TATATAGCCA TTGATGGACC AAGTAGCACT TCTGCGCGAA AACCAACATT AAATCAAACC
GGCATTTCAG GTTGGTTAAG TAATTACATT ACGAAAGATG CGAAAGATCC AGCAAAAGTC
ACTCAACTGT TCACATATTT AATTGATGAA CCGGGACAAA TTTTAAACAA ATATGGCGTT
GAAGGAGTTA CTTATGCGTA CAATGATCAA GGAAAAATTG ATTATTTACC AGAAGTGAAA
AAATTAGAAC AAACAGACAA TGATGCCTAC AACAAAAAAT ATGGCATTAG TCGTTTCCTA
TACTTTAACA ACGACCGTGT CAATAAACTA AAAGTACCAA TGGAAAGTGC TTTAACGCAA
ATGCAAGAAT GGGGCAAGG AAAATTAGTC CCACATTTTC TAATTGAAAA TATTAATCCA
GATGCAGGAA CGCCGGAAGC TCGTGCGAAT GAAGCGATTG AAACCAAACCT AAATACAACC
GTTATTTCAA TGATTCGTGC GAAAGATGAT AAAGCCTTTG ACAAATCTTT AGAAGACTAC
AAAGCATTCT TAAATGCAAA TAAATGGGAT GCAATTGAAA AAATAAAATC TGAGAAAATG
GCGGAAAACA GAGACAAACT TAAGTAA

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EF018-2 (SEQ ID NO:66)

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MKKV LGGLLVATAV VSLAACSGGE
KKASSDVS IK DRYELDEKTP AWKLDKKKEP TKIKWYINSD WTALPFGKDV TTAQIKKDLN
VDIEFISGDD SKLNAMEISSG DMPDIVTLTE KTGQAALKAD SWAYSINLDA KKYDPYLMKV
VNQDTFKWYA LEDGKTYGYP NYSNTKADYE SGNIPVNDNF VIREDVYNAL GKPVDSTPEN
FEKVMQOIKE KYPEMTPMGF TTVGDGAGPF LDKLQDFLG V PLEDKNGKYY DRNLDKLEYLE
WLKTFNDVYR AGNISDDSFY DDGATFDEKV KQGNATMLV AGTSGQGGNF TEFMKKSGTR
YIAIDGPSST SGRKPTLNQT GISGWLSNYI TKDAKDPKV TQLFTYLIDE PGQILTKYGV
EGVTYAYNDQ GKIDYLPEVK KLEQTDNDAY NKKYGISRFL YFNNDRVNKL KVPMESALTQ
MQEWGKGLV PHFVIENINP DAGTPEARAN EAIETKLNTT VISMIRAKDD KAFDKSLEDY
KAFKLSNKWD AIEKIKSEKM AENRDKLK

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EF018-3 (SEQ ID NO:67)

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CTGTAG CGGTGGGGAA
AAGAAAGCTA GCTCAGATGT CTCAATTAAG GATCGGTATG AATTAGATGA AAAGACGCCT
GCTTGGAAGT TAGATAAGAA GAAAGAACCG ACCAAGATTA AATGGTATAT TAACTCAGAT
TGGACGGCGC TGCCTTTTGG AAAAGACGTG ACCACTGCGC AGATTAAAAA AGACTTAAAT
GTGGATATTG AATTTATTTT CGGCGATGAT TCAAAATTAA ATGCCATGAT TTCAAGTGGA
GATATGCCTG ATATCGTGAC ATTAACTGAA AAAACTGGAC AAGCAGCATT GAAAGCAGAT
TCTTGGGCCT ATTCTTTAAA CGATTTAGCT AAAAAATATG ACCCCTATTT AATGAAAGTT
GTTAACCAAG ATACGTTTAA ATGGTATGCC TTAGAGGATG GAAAAACATA TGGTTACCCT
AATTACTCTA ATACAAAAGC GGATTATGAA AGTGGAATA TCCAGTAAA TGATAATTTT
GTTATTCGTG AAGATGTCTA TAATGCATTA GGCAAGCCAG ACGTTTCAAC ACCAGAAAAT
TTTGAAAAAG TCATGCAACA GATTAAAGAA AAATATCCTG AGATGACCCC AATGGGCTTC

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACCACAGTGG GCGATGGTGC AGGACCATTT TTAGACAAAT TACAAGACTT CTTAGGTGTT
 CCTTTAGAGG ATAAAAATGG TAAATACTAT GATCGAAATT TAGATAAAGA ATATTTAGAA
 TGGTTAAAAA CATTTAATGA TGTTTACCGA GCAGGCAATA TTAGTGATGA TAGCTTCACA
 GATGATGGGG CAACGTTTGA TGAAAAAGTG AAACAAGGAA ATTATGCAAC CATGCTCGTT
 GCTGGAACCA TTGGTCAAGG TGGGAACCTC ACAGAATTTA TGAAAAATC TGGCACACGT
 TATATAGCCA TTGATGGACC AAGTAGCACT TCTGGCCGAA AACCAACATT AAATCAAACC
 GGCATTTTCA GTTGGTTAAG TAATTACATT ACGAAAGATG CGAAAGATCC AGCAAAAGTC
 ACTCAACTGT TCACATATTT AATTGATGAA CCGGGACAAA TTTTAACAAA ATATGGCGTT
 GAAGGAGTTA CTTATGCGTA CAATGATCAA GGAAAAATTG ATTATTTACC AGAAGTGAAA
 AAATTAGAAC AAACAGACAA TGATGCCTAC AACAAAAAAT ATGGCATTAG TCGTTTCCTA
 TACTTTAACA ACGACCGTGT CAATAAATA AAAGTACCAA TGGAAAGTGC TTTAACGCAA
 ATGCAAGAAT GGGGCAAAAG AAAATTAGTC CCACATTTTCG TAATTGAAAA TATTAATCCA
 GATGCAGGAA CGCCGGAAGC TCGTGCGAAT GAAGCGATTG AAACCAAAC AAATACAACC
 GTTATTTCAA TGATTCGTGC GAAAGATGAT AAAGCCTTTG ACAAATCTTT AGAAGACTAC
 AAAGCATTCT TAAAATCAAA TAAATGGGAT GCAATTGAAA AAATAAAATC TGAGAAAATG
 GCGGAAAACA GAGACAAACT TAAG

EF018-4 (SEQ ID NO:68)

CSGGE

KKASSDVSIK DRYELDEKTP AWKLDKKKEP TKIKWYNSD WTALPFGKDV TTAQIKKDLN
 VDIEFISGDD SKLNAMESSG DMPDIVTLTE KTGQAALKAD SWAYSLNDLA KKYDPYLMKV
 VNQDTFKWYA LEDGKTYGYP NYSNTKADYE SGNIPVNDNF VIREDVYNAL GKPDVSTPEN
 FEKVMQIQKE KYPEMTPMGF TTVGDGAGPF LDKLQDFLGV PLEDKNGKYY DRNLDKEYLE
 WLKTFNDVYR AGNISDDSTF DDGATFDEKV KQGNATMLV AGTSGQGGNF TEFMKKSGTR
 YIAIDGPSST SGRKPTLNQT GISGWSNYI TKDAKDPKV TQLFTYLIDE PGQILTKYGV
 EGVTYAYNDQ GKIDYLEPVK KLEQTDNDAY NKKYGISRFL YFNNDRVNKL KVPMEALSTQ
 MQEWGKGKLV PHFVIENINP DAGTPEARAN EAIETKLNTT VISMIRAKDD KAFDKSLEDY
 KAFLKSNKWD AIEKIKSEKM AENRDKLK

EF019-1 (SEQ ID NO:69)

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 CTTGGTTCAT TCTTACTCGC AGCTTGTTGGT AATACGAATA AAGAAGCCAA CAACGCTGAC
 AAAACACATG AAGTACAGA TACCTTAGGC AATAAAGTAA CCGTCCCCGC GAAACCCAAA
 CGGATTATTG CGAGTTATTT AGAAGATTAT CTAGTTGCAT TAGGAGAAAA ACCAGTGCCA
 CAATGGACAG TTGGACAAGG CAGCATTCAA GATTATTTAG CGAAAGAATT GAAAGATGTC
 CCCACTATTT CCTATGACTT GCCATATGAA GCGGTTCTAA AATTTGAACC TGACTTATTA
 TTAATCAGTT CATCTGCTCT AGTTGAAGGC GGTAATACA AAGAATACAG TAAATTTGCG
 CCAACTTATG TAGTCAAAAA CGGCGAAAAT GTCACCTGGC GTGATCAATT GGAAGATATT
 GCCACTGTTT TAGATAAAAA AGAACAAGCG AAAAAAGTGT TAGAAGATTA TGATACCTTA
 ACCAAAGGCG TCCAAGAATA TCTTGCCAAA AAAGATGCTG GCAAATCTGC GGCAGTCTTA
 TGGGTAACCA ACAACCAAGT CTTTATGGTT AGCGATAATC GCTCAAGCGG AACCCTGCTC
 TATCAGGACT TAGGCCTCCA AGTTCCAAAA TTAGTGGAAG AAATTTCTAA AAACGCTACT
 GCGGATTGGA ATCAAGTTTC TTTAGAAAAA TTAGCTGAGC TTGACGCAGA CCACATTTTC
 CTTGTAAACA GCGATGAATC AGCACCTCTT TTCCAAGAAC CAATTTGGAA GAACTTACCT
 GCTGTGAAAA ATAACCAAGT TCATACCTAT GATAAAAAAA GTAGTTGGTT ATACAACGGA
 CCTATTGCGA ATACTCAAAT TGTTGAAGAT GTAAAAAAG CGCTCTTAAA TTAA

EF019-2 ((SEQ ID NO:70)

MKLLKK TVLIGTTLLL GSFLAACGN TNKEANNADK THEVTDTLGN KVTVPKPKR
 IIASYLELYL VALGEKPVAQ WTVGQGSIQD YLAKELKDVP TISYDLPYEA VLKFEPLDLLL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ISSSALVEGG KYKEYSKIAP TYVVKNGENV TWRDQLEDIA TVLDKKEQAK KVLEDYDTLT
 KGVQEYLGKK DAGKSAAVLW VTNNQVFMVS DNRSSGTVLY QDLGLQVPKL VEEISKNATA
 DWNQVSLEKL AELDADHIFL VNSDESAPLF QEAIWKNLPA VKNNQVHTYD KKSSWLYNGP
 IANTQIVEDV KKALLN

EF019-3 (SEQ ID NO:71)

TTGTGGT AATACGAATA AAGAAGCCAA CAACGCTGAC
 AAAACACATG AAGTAACAGA TACCTTAGGC AATAAAGTAA CCGTCCCCGC GAAACCCAAA
 CGGATTATTG CGAGTTATTT AGAAGATTAT CTAGTTGCAT TAGGAGAAAA ACCAGTGGCA
 CAATGGACAG TTGGACAAGG CAGCATTCAA GATTATTTAG CGAAAGAATT GAAAGATGTC
 CCCACTATTT CCTATGACTT GCCATATGAA GCGGTTCTAA AATTTGAACC TGAATTATTA
 TTAATCAGTT CATCTGCTCT AGTTGAAGGC GGTAAATACA AAGAATACAG TAAAATTGCG
 CCAACTTATG TAGTCAAAAA CGGCGAAAAAT GTCACCTGGC GTGATCAATT GGAAGATATT
 GCCACTGTTT TAGATAAAAA AGAACAAGCG AAAAAAGTGT TAGAAGATTA TGATACCTTA
 ACCAAAGGCG TCCAAGAATA TCTTGGCAAA AAAGATGCTG GCAAATCTGC GGCAGTCTTA
 TGGGTAACCA ACAACCAAGT CTTTATGGTT AGCGATAATC GCTCAAGCGG AACCGTGCTC
 TATCAGGACT TAGGCCTCCA AGTTCCAAAA TTAGTGGAAG AAATTTCTAA AAACGCTACT
 GCGGATTGGA ATCAAGTTTC TTTAGAAAAA TTAGCTGAGC TTGACGCAGA CCACATTTTC
 CTTGTAAACA GCGATGAATC AGCACCTCTT TTCCAAGAAG CAATTTGGAA GAACTTACCT
 GCTGTGAAAA ATAACCAAGT TCATACCTAT GATAAAAAAA GTAGTTGGTT ATACAACGGA
 CCTATTGCGA AACTCAAAAT TGTGAAGAT GTAAAAAAG CGCTCTTAAA T

EF019-4 (SEQ ID NO:72)

CGN TNKEANNADK THEVTDLGN KVTVPKPKR
 IIASYLEDYL VALGEKPVAQ WTVGQSIQD YLAKELKDVP TISYDLPYEA VLKFEPDLLL
 ISSSALVEGG KYKEYSKIAP TYVVKNGENV TWRDQLEDIA TVLDKKEQAK KVLEDYDTLT
 KGVQEYLGKK DAGKSAAVLW VTNNQVFMVS DNRSSGTVLY QDLGLQVPKL VEEISKNATA
 DWNQVSLEKL AELDADHIFL VNSDESAPLF QEAIWKNLPA VKNNQVHTYD KKSSWLYNGP
 IANTQIVEDV KKALLN

EF020-1 (SEQ ID NO:73)

TGAGGAGATG AGAAAAATGAA AAAGGTAGTT TCAATTTTGT TGATGGTTGT TGCAGTCTTC
 ACATTAACTG CATGTAATGG TTCTAAATTA GATAAAACAG GTGAAGAATT TAAAAATTCT
 ATAATGAAAG ATTCTTCATA TGGTGATGAA TATTCAGAAG ATGGTTTTAG TTTTTAATA
 TATAAAGATA AAGACACTAA TCGTTATTTG GCTGATGTTT GGGTTCCTGT TAAAGATGAA
 ACTAGCGCAT TGGAGTATTT TTATTATTAT GATGAAGATA AGCGATTAGA TAGTACTAAA
 AGTAAAGTAA CCTTTGATGA TATGAAAGCT AGTGAAACT ATGAAGTAGT GTATAAATCA
 GGGAAATTTA AATAA

EF020-2 (SEQ ID NO:74)

MKKVVS ILLMVAVFT LTACNGSKLD KTGEFEKNSI MKDSSYGDEY SEDGFSFLIY
 KDKDTNRYLA DVWVPVKDET SALEYFYFYD EDKRLDSTKS KVTFDMMKAS GNYEVVYKSG
 KFK

EF020-3 (SEQ ID NO:75)

ATGTAATGG TTCTAAATTA GATAAAACAG GTGAAGAATT TAAAAATTCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATAATGAAAG ATTCTTCATA TGGTGATGAA TATTCAGAAG ATGGTTTTAG TTTTTTAATA
 TATAAAGATA AAGACACTAA TCGTTATTTG GCTGATGTTT GGGTTCCTGT TAAAGATGAA
 ACTAGCGCAT TGGAGTATTT TTATTATTAT GATGAAGATA AGCGATTAGA TAGTACTAAA
 AGTAAAGTAA CCTTTGATGA TATGAAAGCT AGTGGAAACT ATGAAGTAGT GTATAAATCA
 GGGAAATTTA AA

EF020-4 (SEQ ID NO:76)

CNGSKLD KTGEFFKNSI MKDSSYGDEY SEDGFSFLIY
 KDKDTRNYLA DVWVPVKDET SALEYFYYYD EDKRLDSTKS KVTFFDDMKAS GNYEVVYKSG
 KFK

EF021-1 (SEQ ID NO:77)

TAGTIGTTTA AATACATTAA ACTATTTTTA GGAGGCTTTA CAGAAATGAA AAAAGCAAAA
 TTATTCGGTT TTAGTTTGAT TGCATTAGGT TTATCAGTTT CACTTGCAGC ATGTGGTGGT
 GGCAAAGGCA AAACCGCTGA AAGCGGCGGT GGCAAAGGGG ATGCAGCGCA TAGTGCTGTA
 ATCATTACAG ATACAGGCGG CGTGGATGAC AAGTCGTTCA ACCAATCTTC TTGGGAAGGA
 TTGCAAGCTT GGGGTAAAGA ACATGATTTA CCAGAAGGTT CAAAAGGGTA TGCATATATT
 CAATCGAATG ATGCAGCTGA CTATACAACC AATATTGACC AAGCGGTATC AAGTAAATTC
 AACACAATCT TTGGTATTGG CTACTTGCTA AAAGATGCAA TTTCTTCTGC AGCAGATGCC
 AACCCGTGATA CAAACTTTGT TTTAATCGAT GATCAAATCG ATGGCAAAA GAATGTCGTT
 TCTGCAACAT TTAGAGATAA TGAAGCAGT TACTTAGCCG GTGTTGCTGC TGCAAATGAA
 ACAAAAACGA ACAAGTCGG TTTTGTGGT GGTGAAGAAG GGGTCGTAAT TGACCGTTTC
 CAAGCTGGTT TTGAAAAAGG TGTGGCTGAT GCTGCGAAAG AATTAGGTAA AGAAATTACT
 GTTGATACGA AATATGCGGC TTCATTTGCT GATCCTGCCA AAGGGAAAGC TTTAGCTGCT
 GCAATGTACC AAAACGGCGT TGATATCATC TTCCATGCTT CTGGTGCAC TGGACAAGGG
 GTCTTCCAAG AAGCAAAAGA CTTGAATGAA TCAGGTTCTG GCGACAAAGT TTGGGTAATC
 GCGGTTGACC GCGATCAAGA TGCTGATGGC AAGTACAAA CAAAAGACGG CAAAGAAGAC
 AACTTCACGT TAACTTCAAC GCTTAAAGGT GTCGGCACAG CGGTTCAAGA TATTGCCAAC
 CGTGCGTTAG AAGACAAATT CCCTGGTGGC GAACATTTAG TTTATGGATT AAAAGATGGT
 GCGGTTGACT TAACAGACGG CTATTTAAAC GACAAAACAA AAGAAGCTGT TAAAACAGCA
 AAAGATAAAG TAATCTCAGG TGACGTAAAA GTCCAGAAA AACCAGAATA A

EF021-2 (SEQ ID NO:78)

MKKAKL FGFSLIALGL SVSLAACGGG KGKTAESGGG KGDAHSAVI
 ITDTGGVDDK SFNQSSWEGL QAWGKEHDL ESKGYAYIQ SNDAADYTTN IDQAVSSKFN
 TIFGIGYLLK DAISSAADAN PDTNFVLIDD QIDGKKNVVS ATFRDNEAAY LAGVAAANET
 KTNKVGFVGG EEGVVIDRFQ AGFEKGVADA AKELGKEITV DTKYAASFAD PAKGKALAAA
 MYQNGVDIIF HASGATGQGV FQEAADLNE GSGDKVWVIG VDRDQDADGK YKTKDGKEDN
 FTLTSTLKG VGTAVQDIANR ALEDKFPGGE HLVYGLKDGG VDLTDGYLND KTKEAVKTAK
 DKVISGDVKV PEKPE

EF021-3 (SEQ ID NO:79)

ATGTGGTGGT
 GGCAAAGGCA AAACCGCTGA AAGCGGCGGT GGCAAAGGGG ATGCAGCGCA TAGTGCTGTA
 ATCATTACAG ATACAGGCGG CGTGGATGAC AAGTCGTTCA ACCAATCTTC TTGGGAAGGA
 TTGCAAGCTT GGGGTAAAGA ACATGATTTA CCAGAAGGTT CAAAAGGGTA TGCATATATT
 CAATCGAATG ATGCAGCTGA CTATACAACC AATATTGACC AAGCGGTATC AAGTAAATTC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AACACAATCT TTGGTATTGG CTAATTGCTA AAAGATGCAA TTTCTTCTGC AGCAGATGCC
AACCTGATA CAACTTTGT TTTAATCGAT GATCAAATCG ATGGCAAAAA GAATGTCGTT
TCTGCAACAT TTAGAGATAA TGAAGCAGCT TACTTAGCCG GTGTTGCTGC TGCAAAATGAA
ACAAAAACGA ACAAAGTCGG TTTTGTGGT GGTGAAGAAG GGGTCGTAAT TGACCGTTTC
CAAGCTGGTT TTGAAAAAGG TGTGGCTGAT GCTGCGAAAG AATTAGGTAA AGAAATTACT
GTTGATACGA AATATGCGGC TTCATTTGCT GATCCTGCCA AAGGGAAAGC TTTAGCTGCT
GCAATGTACC AAAACGGCGT TGATATCATC TTCCATGCTT CTGGTGCGAC TGGACAAGGG
GTCTTCCAAG AAGCAAAAGA CTTGAATGAA TCAGGTTCTG GCGACAAAGT TTGGGTAATC
GGCGTTGACC GCGATCAAGA TGCTGATGGC AAGTACAAAA CAAAAGACGG CAAAGAAGAC
AATTCACGT TAACCTCAAC GCTTAAAGGT GTCGGCACAG CGGTTCAAGA TATTGCCAAC
CGTGCGTTAG AAGACAAATT CCCTGGTGGC GAACATTTAG TTTATGGATT AAAAGATGGT
GGCGTTGACT TAACAGACGG CTATTTAAAC GACAAAACAA AAGAAGCTGT TAAACAGCA
AAAGATAAAG TAATCTCAGG TGACGTAAAA GTCCAGAAA AACCAGAA

EF021-4 (SEQ ID NO:80)

CGGG KGKTAESGGG KGDAHSAVI

ITDTGGVDDK SFNQSSWEGL QAWGKEHDL PEGSKGYAYIQ SNDAADYTTN IDQAVSSKFN
TIFGIGYLLK DAISSAADAN PDTNFVLIDD QIDGKKNVVS ATFRDNEAAY LAGVAAANET
KTNKVG FVGG EGVVIDRFQ AGFEKGVADA AKELGKEITV DTKYAASFAD PAKGKALAAA
MYQNGVDIIF HASGATGQGV FQEA KDLNES GSGDKVWVIG VDRDQDADGK YKTKDGKEDN
FTLTSTLKG V GTAVQDIANR ALEDKFP GGE HL VYGLKDG VDLTDGYLND KTKEAVKTAK
DKVISGDVKV PEKPE

EF022-1 (SEQ ID NO:81)

TAAGAGCATA AAAAAATGAA GAGTTATAGG AGAAAGAAGA TGAAAAAGTA TTTAAAAATC
ACAATGGTTT GTATTTTATT GGTAGGATTT TTAGCTGGGT GTACCAATAA AAATGAAAAT
AAAAAGAAAC AGAAAAATAC CAAAGAAGCC GTTCAACTGA TGTCACCCTC GGAATTAACA
ACGCTCAACA CCTCTGTATT ATTGGATTTT CCAGATGCTA TTGTCCAAAC TGCAGCGTTT
GAAGGGTTAT ATAGTTTAGA TGAACAAGAC CAATTGGTAC CAGCCGTAGC AAAAGCATTG
CCGATGATTT CAGAAGATGG AAAAACCTAC ACGATTTCTT TGAGAAAAGA AGCGGTTTGG
AGTAACGATG ATCCTGTCAC AGCACATGAT TTTGAATATG CTTGGAAAAA AATGATTGAT
CCTAAAAACG GCTTTGTTTA TAGCTTCCTC ATCGTTGAAA CAATTCAAAA TGGTGCAGAA
ATCTCAGCGG GGAAATTAGC ACCCAATGAA CTAGGTGTCA CAGCTGTGGA TGATTATACA
TTAAAGGTGA CGCTCAAAGA GCCAAAACCG TACTTTACGT CCTTGTAGC TTTTCCGACA
TTTTTCCCGC AAAATCNAAA AGTAGTCGAA CAATTTGGTG CGGACTATGG AACTGCTAGT
GATAAAGTCG TCTATAATGG TCCGTTCTGT GTAAAAGATT GGCAGCAAAC AAAGATGGAC
TGGCAACTAG CAAAAAATAA TCGCTATTGG GATCACCAGA ACGTGCCTC AGACATTATC
AATTATACAG TTATCAAAGA AACATCTACC GCATTGAATC TTTTGAAGA TGGACAATTA
GATGTGGCTA CACTAAGTGG TGAAGTGGC CAACAGAATA AAAATAATAC GTTGTATCAT
TCGTATCCAA CAGCGACAAT GAATTTTG CGCTTAAATC AAAAACCGNA AGGGCAAGCN
ACGCCGCTTG CAAACGAAAA CCTGCGTAAA GCATTGGCTT TAGGAATAGA TAAAGAAAAT
CTAGTCAATA ATATTATTGC AGATGGTTCT AAAGCGTAC ATGGTGGGAT TACGGAAGGC
TTTGTGGCGA ATCCACAAC GGGTCTCGAT TTTCTCAAG AAGCAGGTAA TTTAATGGTT
TATAACAAAG AAAAAGCGCA AAGTTATTGG AAAAAGCAC AAGCAGAATT AGGAGAAAAG
GTTAACGTTG AATTGATGGT AACAGATGAT GGTTCCTTACA AAAAAATTGG TGAAAGTTTG
CAAGGCTCGC TACAAGAATT GTTCTCTGGT TTGACAATAG AGCTAACCGC ATTGCCGACT
GAAGCTGCAT TGAACCTTGG GCGAGAAAGT GACTATGATT TATTCTTAAT TTACTGGACA
CCAGACTATC AAGACCTTAT TTCTACCCTG ATGACTTTAT ACAAGGGCAA TGATCGCAAT
TATCAGAAC CTGTCTATGA CAAATTATTA GATGAAGCAG CCACAACCTA TGCCTTAGAG
CCAGAAAAAA GATGGGCGAC ACTGATTGCA GCTGAAAAAG AAGTGATTGA AACGACTGCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GGCATGATTC CACTTAGCCA AAATGAACAA ACAGTCCTGC AAAATGATAA AGTCAAAGGC
TTGAATTTTC ATACCTTTGG CGCTCCATTA ACGTTAAAAA ATGTTTATAA GGAAAAATAA

EF022-2 (SEQ ID NO:82)

MKKYLKIT MVCILLVGFL AGCTNKNENK KKQKNTKEAV QLMSPSELTT
LNTSVLLDFP DAIVQTAAFE GLYSLDEQDQ LVPAAKALP MISEDGKTYT ISLRKEAVWS
NDDPVTAHDF EYAWKKMIDP KNGFVYSFLI VETIQNGAEI SAGKLAPNEL GVTAVDDYTL
KVTLEKPKPY FTSLLAFPTF FPQNKKVVEQ FGADYGTASD KVVYNGPFV KDWQQTMDW
QLAKNNRYWD HQNVRSIIN YTVIKETSTA LNLFEQDGLD VATLSGELAQ QNKNNTLYHS
YPTATMNYLR LNQKRXGQAT PLANENLRKA LALGIDKENL VNNIADGSK ALHGAITEGF
VANPTTGLDF RQEAGNLMVY NKEKAQSYWK KAQAELGEKV NVELMVTDDG SYKKIGESLQ
GSLQELFPGL TIELTALPTE AALNFGRESY YDLFLIYWTP DYQDPISLTM TLYKGNDRNY
QNPVYDKLLD EAATTYALEP EKRWATLIAA EKEVIETTAG MIPLSQNEQT VLQNDKVKGL
NFHTFGAPLT LKNVYKEK

EF022-3 (SEQ ID NO:83)

GT GTACCAATAA AAATGAAAAT
AAAAAGAAAC AGAAAAATAC CAAAGAAGCC GTTCAACTGA TGTCACCCTC GGAATTAACA
ACGCTCAACA CCTCTGTATT ATTGGATTTT CCAGATGCTA TTGTCCAAAC TGCAGCGTTT
GAAGGGTTAT ATAGTTTATA TGAACAAGAC CAATTGGTAC CAGCCGTAGC AAAAGCAITG
CCGATGATTT CAGAAGATGG AAAAACCTAC ACGATTTCCT TGAGAAAAGA AGCGGTTTGG
AGTAACGATG ATCCTGTCTAC AGCACATGAT TTGAATATG CTGGAAGAAA AATGATTGAT
CCTAAAAACG GCTTTGTTTA TAGCTTCCTC ATCGTTGAAA CAATTCAAAA TGGTGCAGAA
ATCTCAGCGG GGAAATTAGC ACCCAATGAA CTAGGTGTCA CAGCTGTGGA TGATTATACA
TTAAAGGTGA CGCTCAAAGA GCCAAAACCG TACTTTACGT CCTGTGTAGC TTTTCCGACA
TTTTTCCCGC AAAATCNAAA AGTAGTCGAA CAATTTGGTG CGGACTATGG AACTGCTAGT
GATAAAGTCG TCTATAATGG TCCGTTCTGT GTAAAAGATT GGCAGCAAAC AAAGATGGAC
TGGCAACTAG CAAAAAATAA TCGCTATTGG GATCACCAGA ACGTGCCTC AGACATTATC
AATTATACAG TTATCAAAGA AACATCTACC GCATTGAATC TTTTGAAGA TGGACAATTA
GATGTGGCTA CACTAAGTGG TGAAGTGGC CAACAGAATA AAAATAATAC GTTGTATCAT
TCGTATCCAA CAGCGACAAT GAATATTG CGCTTAAATC AAAACCGNA AGGGCAAGCN
ACGCGCTTG CAAACGAAAA CCTGCGTAA GCATTGGCTT TAGGAATAGA TAAAGAAAAT
CTAGTCAATA ATATTATGC AGATGGTTCT AAAGCGCTAC ATGGTGCGAT TACGGAAGGC
TTTGTGGCGA ATCCCAACAAC GGGTCTCGAT TTTCGTCAAG AAGCAGGTAA TTTAATGGTT
TATAACAAAG AAAAAGCGCA AAGTTATTGG AAAAAAGCAC AAGCAGAATT AGGAGAAAAG
GTAAACGTTG AATTGATGGT AACAGATGAT GGTCTTACA AAAAAATTGG TGAAAGTTTG
CAAGGCTCGC TACAAGAATT GTTCTCTGGT TTGACAATAG AGCTAACCAG ATTGCCGACT
GAAGCTGCAT TGAACCTTGG GCGAGAAAGT GACTATGATT TATTCTTAAT TACTGGACA
CCAGACTATC AAGACCCTAT TTCTACCCTG ATGACTTTAT ACAAGGGCAA TGATCGCAAT
TATCAGAACC CTGTCTATGA CAAATTATTA GATGAAGCAG CCACAACCTA TGCCTTAGAG
CCAGAAAAAA GATGGGCGAC ACTGATTGCA GCTGAAAAAG AAGTGATTGA AACGACTGCT
GGCATGATTC CACTTAGCCA AAATGAACAA ACAGTCCTGC AAAATGATAA AGTCAAAGGC
TTGAATTTTC ATACCTTTGG CGCTCCATTA ACGTTAAAAA ATGTTTATAA GGAAAA

EF022-4 (SEQ ID NO:84)

CTNKNENK KKQKNTKEAV QLMSPSELTT
LNTSVLLDFP DAIVQTAAFE GLYSLDEQDQ LVPAAKALP MISEDGKTYT ISLRKEAVWS
NDDPVTAHDF EYAWKKMIDP KNGFVYSFLI VETIQNGAEI SAGKLAPNEL GVTAVDDYTL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

KVTLKEPKPY FTSLLAFPTF FPQNXKVVEQ FGADYGTASD KVVYNGPFVW KDWQQTMDW
 QLAKNNRYWD HQNVRSDIIN YTVIKETSTA LNFLFEDGQLD VATLSGELAQ QNKNNTLYHS
 YPTATMNYLR LNQKRXGQAT PLANENLRKA LALGIDKENL VNNIADGSK ALHGAITEGF
 VANPTTGLDF RQEAGNLMVY NKEKAQSYWK KAQAELGEKV NVELMVTDDG SYKKIGESLQ
 GSLQELFPGL TIELTALPTE AALNFGRES DYLFLIYWTP DYQDPITSLM TLYKGNDRNY
 QNPVYDKLLD EAATTYALEP EKRWATLIAA EKEVIETTAG MIPLSQNEQT VLQNDKVKGL
 NFHTFGAPLT LKNVYKEK

EF023-1 (SEQ ID NO:85)

TAAAAATGGAG GGATCGGTAT GAAGAAATTA AAAATGTTAG GATGCGTCGG GTTGCTTTTA
 GCTTTAACGG CTTGTACAGC GGAACCGGA AACTCGGCTG ATAGTAACAA AGCAGCGGAA
 CAAAAAATTG CAATTAGTTC TGAAGCGGCT ATTTTCGACAA TGGAACCACA CACAGCGGGG
 GATACGACCT CGACTTTAGT CATGAATCAA GTTTATGAAG GACTCTATGT TTTAGGTAAA
 GAAGATGAAT TAGAGTTGGG GGTGCTGCC GAAGAACCAG CGATTTCTGA AGATGAAACC
 GTTTATACAT TTAAGATTAG AGAAGATGCC AAATGGTCCA ATGATGATCC AGTAACAGCA
 AACGACTTTG TTTATGCATG GCAACAAGTT GCTTCCCCTA AATCAGGATC GATTCATCAA
 GCTTTATTTT TTGATGTCAT TAAAAATGCT AAGGAAATTG CTTTAGAAGG CGCAGATGTG
 AATACTCTTG GGGTTAAGGC GCTAGATGAT AAAACGTTAG AAATAACTTT AGAACGGCCC
 ACCCCTTATT TGAAATCATT ACTTTCGTTT CCTGTTTTGT TTCCACAAA TGAAAAATAT
 ATCAAAGAAC AAGGGGATAA ATATGCTACT GATGCAGAAC ATTTGATTTA TAATGGTCCT
 TTTAAATTGA AAGAATGGGA TAATGCCTCT TCTGATGACT GGACCTACGA AAAAAATGAT
 ACGTATTGGG ATGCTGAAAA AGTTAAATTA ACAGAAGCGA AAGTTTCAGT AATTAAGAGC
 CCAACGACAG CCGTGAATTT GTTTGACTCG AATGAATTGG ATGTAGTGAA TAAGCTAAGT
 GGTGAATTTA TTCCTGGTTA TGTGATAAT CCAGCCTTTC TTTCAATTCC TCAATTCTGC
 ACATACTTTT TAAAAATGAA CAGCGTTCTG GATGGAAG AAAATCCGGC TTTAGCGAAC
 AACAATTTT GTAAAGCGTT GGCACAAGCT TTTGATAAAG AAAGTTTTGT AAAAGAAGTC
 TTGCAAGATC AATCAACGGC TACAGATCAA GTAATTCCGC CGGGACAAAC GATTGCGCCA
 GATGGAACAG ATTTACACAA ACTAGCTGCT AAGAAAAATA ACTACTTAAC CTACGATACA
 GCGAAAGCAA AAGAATTCCT GGAAGGAGG AAAAAAGAA TTGGGCTGGA TAAATCAAA
 TTAGAATTTT TAACAGATGA TACAGACAGC GCCAAAAAG CTGCTGAGTT TTTCCAATTT
 CAATTGGAAG AAAATCTAGA TGGATTAGAA GTGAATGTTA CTCAAGTTCC TTTTACTATT
 CGTGTGATC GTGATCAAAC GAGAGACTAT GATTTAGAAT TATCTGGTTG GGGAACCGAT
 TATCGTGATC CATTAACAGT TATGCGCATC TTTACTTCGG ATAGTACCTT GGGCGGCGTA
 ACGTTCAAGA GTGATACGTA TGATCAATTA ATTCAGAAA CTAGAACAAC ACATGCGGCT
 GATCAAGAGG CTCGTTTAAA TGACTTTGCT CAAGCACAAG ATATTTTGGT GAATCAGGAA
 ACGGTTTTAG CACCAATCTA CAATCGAAGC ATTTCTGTAT TAGCTAATCA AAAAAATCAAG
 GATCTGTATT GGCATTCAAT TGGACCCAGC TACAGTTTAA AATGGGCTTA TGTTAACATA

EF023-2 (SEQ ID NO:86)

MKKLK MLGCVGLLLA LTACQAGTGN SADSINKAAEQ KIAISSEAAI STMEPHTAGD
 TTSTLVMNQV YEGLYVLGKE DELELGVAEE EPAISEDET VTFKIREDAK WSNDDPVTAN
 DFPVYAWQQA SPKSGSIHQAL LFFDVIKNAK EIALEGADV TLGVKALDDK TLEITLERPT
 PYLKSLLSFP VLFPQNEKYI KEQGDKYATD AEHLIYNGPF KLKEWDNASS DDWYKENDT
 YWDAEKVKLT EAKVSVIKSP TTAVNLFDSN ELDVNVKLSG EFIPGYVDNP AFLSIPQFVT
 YFLKMNSVRD GKENPALANN NIRKALAQAF DKESFVKEVL QDQSTATDQV IPPGQTIAPD
 GTDFTKLAAL KNNYLYTDTA KAKEFWKKGK KEIGLDKIKL EFLTDDTDSA KKAEEFFQFQ
 LEENLDGLEV NVTQVPFTIR VDRDQTRDYD LELSGWGTDY RDPLTVMRIF TSDSTLGGVT
 FKSDTYDQLI QETRTTHAAD QEARLNDAFQ AQDILVNQET VLAPIYNRSI SVLANQKIKD
 LYWHSFGPTY SLKWAYVN

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF023-3 (SEQ ID NO:87)

GGGAACGGGA AACTCGGCTG ATAGTAACAA AGCAGCGGAA
 CAAAAAATTG CAATTAGTTC TGAAGCGGCT ATTTTCGACAA TGAACCACA CACAGCGGGG
 GATACGACCT CGACTTTAGT CATGAATCAA GTTTATGAAG GACTCTATGT TTTAGGTAAA
 GAAGATGAAT TAGAGTTGGG GGTCGCTGCC GAAGAACCAG CGATTTCTGA AGATGAAACC
 GTTTATACAT TTAAGATTAG AGAAGATGCC AAATGGTCTGA ATGATGATCC AGTAACAGCA
 AACGACTTTG TTTATGCATG GCAACAAGTT GCTTCCCTTA AATCAGGATC GATTCATCAA
 GCTTTATTTT TTGATGTCAT TAAAAATGCT AAGGAAATTG CTTTAGAAGG CGCAGATGTG
 AATACTCTTG GGGTTAAGGC GCTAGATGAT AAAACGTTAG AAATAACTTT AGAACGGCCC
 ACCCCTTATT TGAAATCATT ACTTTCGTTT CCTGTTTTGT TTCCACAAA TGAAAAATAT
 ATCAAAGAAC AAGGGGATAA ATATGCTACT GATGCAGAAC ATTTGATTTA TAATGGTCCT
 TTTAAATTGA AAGAATGGGA TAATGCCTCT TCTGATGACT GGACCTACGA AAAAAATGAT
 ACGTATTGGG ATGCTGAAAA AGTTAAATTA ACAGAAGCGA AAGTTTCAGT AATTAAGAGC
 CCAACGACAG CCGTGAATTT GTTTGACTCG AATGAATTGG ATGTAGTGAA TAAGCTAAGT
 GGTAATTTA TTCCTGGTTA TGTGATAAT CCAGCCTTTC TTTCAATTCC TCAATTGCTC
 ACATACTTTT TAAAAATGAA CAGCGTTCTG GATGAAAAAG AAAATCCGGC TTTAGCGAAC
 AACAAATATC GTAAAGCGTT GGCACAAGCT TTTGATAAAG AAAGTTTTGT AAAAGAAGTC
 TTGCAAGATC AATCAACGGC TACAGATCAA GTAATTCCGC CGGGACAAAC GATTGCGCCA
 GATGGAACAG ATTTACACAA ACTAGCTGCT AAGAAAAATA ACTACTTAAC CTACGATACA
 GCGAAAGCAA AAGAATCTCG GGAAAAAGG AAAAAAGAAA TTGGGCTGGA TAAATCAAAA
 TTAGAATTTT TAACAGATGA TACAGACAGC GCCAAAAAAG CTGCTGAGTT TTTCCAATTT
 CAATTGGAAG AAAATCTAGA TGGATTAGAA GTGAATGTTA CTCAAGTTCC TTTTACTATT
 CGTGTTGATC GTGATCAAA GAGAGACTAT GATTTAGAAT TATCTGGTTG GGGAACCGAT
 TATCGTGATC CATTAACAGT TATGCGCATC TTTACTTCCG ATAGTACCTT GGGCGGCGTA
 ACGTTCAAGA GTGATACGTA TGATCAATTA ATTCAAGAAA CTAGAACAAC ACATGCGGCT
 GATCAAGAGG CTCGTTTAA TGACTTTGCT CAAGCACAAG ATATTTTGGT GAATCAGGAA
 ACGGTTTTAG CACCAATCTA CAATCGAAGC ATTTCTGTAT TAGCTAATCA AAAAATCAAG
 GATCTGTATT GGCATTCATT TGGACCCACG TACAGTTTAA AATGGGCTTA TGTTAAC

EF023-4 (SEQ ID NO:88)

GTGN SADSNAEQ KIAISSEAAI STMEPHTAGD
 TTSTLVMNQV YEGLYVLGKE DELELGVAAE EPAISEDETV YTFKIREDAK WSNDPVTAN
 DFVYAWQQVA SPKSGSIHQ LFFDVIKNAK EIALEGADVN TLGVKALDDK TLEITLERPT
 PYLKSLLSFP VLFPPQNEKYI KEQGDKYATD AEHLIYNGPF KLKEWDNASS DDWTYEKNDT
 YWDAEKVKLT EAKVSVIKSP TTAVNLFDSN ELDVVNKLSE EFIPGYVDNP AFLSIPQFVT
 YFLKMNSVRD KENPALANN NIRKALAQAF DKESFVKEVL QDQSTATDQV IPPGQTIAPD
 GTDFTKLAKE KNNYLYTDTA KAKEFWEKKG KEIGLDKIKL EFLTDDTDSA KKAEEFFQFQ
 LEENLDGLEV NVTQVPFTIR VDRDQTRDYD LELSGWGTDY RDPLTVMRIF TSDSTLGGVT
 FKSDTYDQLI QETRTHAAD QEARLNDFAQ AQDILVNQET VLAPIYNRSI SVLANQKIKD
 LYWHSFGPTY SLKWAYVN

EF024-1 (SEQ ID NO:89)

TAATGGCCGT TTCGTCTACT AATAAAGAGG ATGAAGCTAC TCAAATGGCG TTGGCAATGG
 AACAAGGATC ATAAAAAAGG AGAAGTGAGC ATGAAAAAAG TACTACCTTT TATTGCCTTA
 GTCGGCTTGT TATTGTTGTC AGGTTGTGGA ACAGATATGA AAAAGATATT GACTGCCGAT
 GGTGGTAAAT GGAAAGTGGA AGAAACACGT GCAACTTACA CTTTTTTTGA TGACGGTAAA
 TTTTCAGCTA ATGACTCAGA GGATAGTGT AGTGGGACAT ACACTTATGA TGAAAAAAT
 AAAAAAATAA CCTTTGACNT TACTAGCAGN AACTCTTTCA TTATGGAAAA AGTNGANTNC
 AANGNTANCA AGATTACAGG GGAAATTGGC GAAAAACAAA GAACACTTAT AAAACAAAAA
 ACAGAATAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF024-2 (SEQ ID NO:90)

M KKVLPFIALV GLLLLSGCGT DMKKILTADG
 GKWKVEETRA TYTFFDDGKF SANDSEDSVS GTYTYDEKNK KITFDXTSXN SFIMEKVXXX
 XXKITGEIGE KQRTLKQKT E

EF024-3 (SEQ ID NO:91)

ATT GACTGCCGAT
 GGTGGTAAAT GGAAAGTGGG AGAAACACGT GCAACTTACA CTTTTTTTGA TGACGGTAAA
 TTTTCAGCTA ATGACTCAGA GGATAGTGTT AGTGGGACAT ACACTTATGA TGAAAAAAT
 AAAAAAATAA CCTTTGACNT TACTAGCAGN AACTCTTTCA TTATGGAAAA AGTNGANTNC
 AANGNTANCA AGATTACAGG GGAAATTGGC GAAAAACAAA GAACACTTAT AAAACAAAAA
 ACAGAA

EF024-4 (SEQ ID NO:92)

LTADG
 GKWKVEETRA TYTFFDDGKF SANDSEDSVS GTYTYDEKNK KITFDXTSXN SFIMEKVXXX
 XXKITGEIGE KQRTLKQKT E

EF025-1 (SEQ ID NO:93)

TGAATGAAAC ATATTAAAGG AATGTTGGTT TTTATCGGAT TATTTATTTT GGTIGGTTGT
 GCGCCAGATC AAGAGCCAAC GAAACAAACA ACAAGTGGTC CGCAAGAGAC AAAGCAAGTG
 AAGCAAGTTA CCGTCACCAA TCAAACGACT TCTGCGGTGG AAAAACAAGC GCCGACTAAA
 AATGACGAAC TGATTGCTAA TCAATTGACT TTTGATTCTC ATGAATACAC GTACGAAGTG
 GTTACAGGGG CCACACAAAC GACATTTGGA ACAACCCAC CAGCAAAATA TACACCGGAA
 GAAAAAAGA AAAAAATGTT TTGGTCCAAT CAACCGCCTT TGGGATTAAT GACGGGTAAC
 TATTATAAAA ATGAAGGTGT ATTTACTGGC GGAAATTACG GCATTGTAGA GATTATTACG
 GAACCTGAAA CGCAAAGGAT TCTGAATGTT GAGTTTACAG AGTTTGCTAG TGATCCTTAT
 TATGATACAC GCTATTCTGGG TGTCAACAAA CGCCTGTCGG ATTATCCTGA ATTTCAAGCA
 AGCAACACGC GTACAGACGA TACGTTAGTC ACCGTGTGTTA ATGGTATTAC TTATGTAGAA
 AAACAAATGC GTGACGAAAA TCGTGTTACA GGTAATTTTT ATACGGTACG CGGTTTCATCA
 ACTTCTGCGC GTGAAGGATT AATGCCTTTA GCAGCAGAGA TGGACACTTG GCTAAAAGAG
 CCATCGAAAG AAACGTATAT CGGTTACGCA GAAGATTTAG GCAATGGCCT AATCGCTCGA
 CTTCAAGTGA TAACAGAAGA GCAGAAAATA AAACATGTCA GCTATGATGA ATACTTTTCA
 GATGAACAGG AAAAAATCAC AGAAACAGCC TCGGCGCCTT TTATCGTCAA TCGAAATATT
 ATTCACCAGG ATACAATAAA CAAACCAACA ATTCTTTTAT TCATTTTGTA G

EF025-2 (SEQ ID NO:94)

MKHIKMLVF IGLFILVGCA PDQEPKQTT SGPQETKQVK QVTVTNQTTS AVEKQAPTKN
 DELIANQLTF DSHEYTYEVV TGATQTTFTG TPPAKYTPEE KKKKMFWSNQ PPLGLMTGNY
 YKNEGVFTGG NYGIVEIITE PETQRIINVE FTEFASDPY DTRYSGVNKR LSDYPEFQAS
 NTRTDDTLVT VVNGITYVEK QMRDENRVTG NFYTVRGSST SAREGLMPLA AEMDTWLKEP
 SKETYIGYAE DLGNGLIARL QVITEEQKIK HVSYDEYFSD EQEKITETAC GLFIVNRNII
 HQDTINKPTI LFLIL

EF025-3 (SEQ ID NO:95)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAC GAAACAAACA ACAAGTGGTC CGCAAGAGAC AAAGCAAGTG
 AAGCAAGTTA CCGTCACCAA TCAAACGACT TCTGCGGTGG AAAAACAAGC GCCGACTAAA
 AATGACGAAC TGATTGCTAA TCAATTGACT TTTGATTCTC ATGAATACAC GTACGAAGTG
 GTTACAGGGG CCACACAAAC GACATTTGGA ACAACCCAC CAGCAAAATA TACACCGGAA
 GAAAAAAGA AAAAAATGTT TTGGTCCAAT CAACCGCCTT TGGGATTAAT GACGGGTAAC
 TATTATAAAA ATGAAGGTGT ATTTACTGGC GGAAATTACG GCATTGTAGA GATTATTACG
 GAACCTGAAA CGCAAAGGAT TCTGAATGTT GAGTTTACAG AGTTTGCTAG TGATCCTTAT
 TATGATACAC GCTATTCGGG TGTCACAAA CGCCTGTCGG ATTATCCTGA ATTTCAAGCA
 AGCAACACGC GTACAGACGA TACGTTAGTC ACCGTGTTA ATGGTATTAC TTATGTAGAA
 AAACAAATGC GTGACGAAAA TCGTGTACA GGTAATTTTT ATACGGTACG CGGTTTCATCA
 ACTTCTGCGC GTGAAGGATT AATGCCCTTA GCAGCAGAGA TGGACACTTG GCTAAAAGAG
 CCATCGAAAG AAACGTATAT CGGTTACGCA GAAGATTTAG GCAATGGCCT AATCGCTCGA
 CTTCAAGTGA TAACAGAAGA GCAGAAAATA AAACATGTCA GCTATGATGA ATACTTTTCA
 GATGAACAGG AAAAAATCAC AGAAACAGCC TCGGCGCCTT TTATCGTCAA TCGAAATATT
 ATTACCAGG ATACAATAA CAAACCAACA ATTCTTTTAT TCATTTTG

EF025-4 (SEQ ID NO:96)

TKQTT SGPQETKQVK QVTVTNQTS AVEKQAPTKN
 DELIANQLTF DSHEYTYEVV TGATQTTFGT TPPAKYTPPE KKKMFWSNQ PPLGLMTGNY
 YKNEGVFTGG NYGIVEIITE PETQRILNVE FTEFASDPY DTRYSGVNRK LSDYPEFQAS
 NTRDDTLVT VVNGITYVEK QMRDENRVTG NFYTVRGSST SAREGLMPLA AEMDTWLKEP
 SKETYIGYAE DLGNGLIARL QVITEEQKIK HVSYDEYFSD EQEKITETAC GLFIVNRNII
 HQDTINKPTI LFLIL

EF026-1 (SEQ ID NO:97)

TGAGTGATG ATTACTCATT TCCCTTTGAA TCAGTTATGA TAAAGGAAGA AATAAATAAA
 TTTTITGGAG GGATTTTCAT GAAAATGTCT AAAGTACTCA CCACTGTTTT GACGGCAACT
 GCTGCTCTTG TGTGCTTAG TGCTGTTC A TCTGATAAAA AAACAGATAG TAGTTCTAGT
 AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTCGC AGCTACTGAC
 AATGTCACCT TTGATAAAGA GGTAAAGTGT GCTGGTACTT TCCATGATAA GGGGAAAGAT
 TCCAACGATG TCTATCGTAA ATTAGCACTT TATTTCCAAG ATGATAATAA AAAAGTAACT
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA ATAATTAA

EF026-2 (SEQ ID NO:98)

MKMSK VLTTVLATA ALVLLSACSS DKKTDSSSSS
 KETANSSTEV VSGASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKALY SQDDNKKVTA EYEITVPKLI VSSFNIVH GTVKGDIEVK ANGFTLNGTK
 VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF026-3 (SEQ ID NO:99)

AACAGATAG TAGTTCTAGT
 AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTCGC AGCTACTGAC
 AATGTCACCT TTGATAAAGA GGTAAAGTGT GCTGGTACTT TCCATGATAA GGGGAAAGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCCAACGATG TCTATCGTAA ATTAGCACTT TATTCCCAAG ATGATAATAA AAAAGTAACT
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA ATAAT

EF026-4 (SEQ ID NO:100)

TDSSSSS

KETANSSTEV VSGASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLALY SQDDNKKVTA EYEITVPKLI VSSENFNIVH GTVKGDIEVK ANGFTLNGTK
 VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF027-1 (SEQ ID NO:101)

TTTGGTATGA AACAGAAAAA GTGGTTAATC GGACTTGTTG CACTGGGCTT GGTTTTAGCA
 GCATGTGGAA GTGGCGGTTC GAAAACGACC TCAAACGAAC CAGCTACACA GAAAATTAAC
 GTCGCATCTG GTGGTGAAGT CTCGACATTA GACAGCGCTC ATTATACAGA TGTCTATAGT
 TCCGATATGA TTGGTCAAGT AGTTGAAGGC TTGTATCGAC AAGATAAAAA CGGAGATCCT
 GAGCTAGCTA TGGCGAAAGC AGAGCCACAA GTTAGTGAAG ACGGGTTAGT CTATACATTC
 AAGTTACGAG AAGCAAAATG GACAAACGGG GATCCAGTTA AAGCAGGGGA TTTTGTAGTT
 GCGTTTAGAA ACGTGGTCGA TCCAGCATAC GGTTCAAGTA GCAGTAATCA AATGGATATT
 TTTAAAAATG GCGGTGCGGT GCGGGAAGGA CAAGCCACGA TGGAAGAATT TGGTGTCAAA
 GCAATCGATG ACCAGACACT AGAACTAACA TTGGAAAAATC CAATTCCTTA TTTAGCCCAA
 GTCTTGGTTG GGACACCTTT TATGCCATAA AATGAAGCCT TTGCCAAGA AAAAGGTACT
 GCCTATGGGA CTTCTGCAGA TAATTTTGTG GGCAATGGGC CGTTTGTAAAT TTCAGGTGG
 GATGGCAATT CCGAAACTTG GAAATTGAAG AAGAATGATC ATTATTGGGA TAAAGAACAC
 GTAAAATTGA ATGAAATTGA TGTTCAAGTA GTGAAAGAAA TTGGCACAGG AGCCAATCTT
 TTTGATAATG GCGACTTAGA TTACACTGTT TTAGCAGATA CTTATGCACT TCAGTATAAA
 GAGTCAAAAC AAGCGCATTT TGTACCTAAA GCCATGGTGG GTTATTTAAG CCCCAATCAT
 CGCCGTGAAA TTACCGGCAA CGAACATGTT CGAAAAGCTT TTTTACAAGC GATTGACAAA
 GAAACTTTTG CAAAAGAAAT TTTAGGAGAT GGCTCGACAG CTTTAAATGG NTTTTGTACCA
 GCTAATTTTG CAAAAATCCA GATACAGGTG AAGATTTCAG CAAAGAAAAT GGTGATTTAT
 TGCCATATAA TATTAAAGAA GCCCAAGCTA ACTGGAACAA TT

EF027-2 (SEQ ID NO:102)

MKQKKWLI GLVALGLVLA ACGSGGSKTT SNEPATQKIN VASGGELSTL DSAHYTDVYS
 SDMIGQVVEG LYRQDKNGDP ELAMAKAEPQ VSEDGLVYTF KLREAKWTNG DPVKAGDFVV
 AFRNVDPAY GSSSSNQMDI FKNGRAVREG QATMEEFVK AIDDQTLELT LENPIPYLAQ
 VLVGTPFMPK NEAFAKEKGT AYGTSADNFV GNGPFVISGW DGNSETWKLK KNDHYWDKEH
 VKLNEIDVQV VKEIGTGANL FDNGDLDTV LADTYALQYK ESKQAHFVPK AMVGYLSPNH
 RREITGNEHV RKAFLQAIK ETFAKEILGD GSTALNGFVP ANFAKIQIQV KISAKKMIY
 CHIILKKPKL TGTI

EF027-3 (SEQ ID NO:103)

AACGACC TCAAACGAAC CAGCTACACA GAAAATTAAC
 GTCGCATCTG GTGGTGAAGT CTCGACATTA GACAGCGCTC ATTATACAGA TGTCTATAGT
 TCCGATATGA TTGGTCAAGT AGTTGAAGGC TTGTATCGAC AAGATAAAAA CGGAGATCCT
 GAGCTAGCTA TGGCGAAAGC AGAGCCACAA GTTAGTGAAG ACGGGTTAGT CTATACATTC
 AAGTTACGAG AAGCAAAATG GACAAACGGG GATCCAGTTA AAGCAGGGGA TTTTGTAGTT
 GCGTTTAGAA ACGTGGTCGA TCCAGCATAC GGTTCAAGTA GCAGTAATCA AATGGATATT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTTAAAAATG GCGGTGCGGT GCGGGAAGGA CAAGCCACGA TGGAAGAATT TGGTGTCAAA
 GCAATCGATG ACCAGACACT AGAACTAACA TTGGAAAATC CAATTCCTTA TTTAGCCCAA
 GTCTTGGTG GGACACCTTT TATGCCTAAA AATGAAGCCT TTGCCAAAAGA AAAAGGTACT
 GCCTATGGGA CTTCTGCAGA TAATTTTGTT GGCAATGGGC CGTTTGTAAT TTCAGGTTGG
 GATGGCAATT CCGAAACTTG GAAATTGAAG AAGAATGATC ATTATTGGGA TAAAGAACAC
 GTAAAATTGA ATGAAATTGA TGTTCAGTA GTGAAAGAAA TTGGCACAGG AGCCAATCTT
 TTTGATAATG GCGACTTAGA TTACACTGTT TTAGCAGATA CTTATGCACT TCAGTATAAA
 GAGTCAAAAC AAGCGCATTT TGTACCTAAA GCCATGGTGG GTTATTTAAG CCCCATCAT
 CGCCGTGAAA TTACCGGCAA CGAACATGTT CGAAAAGCTT TTTTACAAGC GATTGACAAA
 GAAACTTTTG CAAAAGAAAT TTTAGGAGAT GGCTCGACAG CTTTAAATGG NTTTGTACCA
 GCTAATTTTG CAAAAATCCA GATACAGGTG AAGATTTCCG CAAAGAAAAT GGTGATTTAT
 TGCCATATAA TATTAAAGAA GCCCAAGCTA A

EF027-4 (SEQ ID NO:104)

TT SNEPATQKIN VASGGELSTL DSAHYTDVYS
 SDMIGQVVEG LYRQDKNGDP ELAMAKAEPQ VSEDGLVYTF KLREAKWTNG DPVKAGDFVV
 AFRNVDPAY GSSSSNQMDI FKNGRAVREG QATMEEFVVK AIDDQLELT LENPIPYLAQ
 VLVGTPFMPK NEAFAKEKGT AYGTSADNFV GNGPFVISGW DGNSETWKLK KNDHYWDKEH
 VKLNEIDVQV VKEIGTGANL FDNGDLDTV LADTYALQYK ESKQAHFVPK AMVGYLSPNH
 RREITGNEHV RKAFLQAIK ETFKEILGD GSTALNGFVP ANFAKIQIQV KISAKKMIY
 CHIILKKPKL

EF028-1 (SEQ ID NO:105)

TAACAGAAGC AATACAACAA CTTAACACTT TGTTTACTTG TTATTTATCA GAAATCAACT
 AAGACTTGTT ATAGTCAATG TATGGGTAGA TATGAAGGAG GAAACAAGGA AATGAAGAAA
 AGAGCTTTGC TAGGGGTAC CTTATTAAACA TTCACAACAT TAGCGGGTTG TACAAATTTA
 TCTGAACAGA AAAGCGGCGA AAAACAAACA GAGGTTGCTG AAGCGAAGGC AACTGAATCT
 GAAAAAGCAT CAGTAAAAA TGTTATTTTT ATGATTGGAG ATGGCATGGG GAATCCGTAT
 ACAACGGGCT ATCGCTATTT CAAAGCCAAT CACTCAGACA AGCGTGTTC CCAAACAGCT
 TTTGATACCT ATTTGTCGG ACAGCAAGCC ACTTATCCAG AAGATGAAGA AGAGAAATGTC
 ACCGATTGAG CTTCCGCGAG GACAGCGATG GCTGCCGGAG TGAAAACCTA TAATAATGCT
 ATTGCACTCG ATAATGACAA GTCCAAAACA GAAACAGTGC TCGAACGTGC GAAAAAGTG
 GGGAAATCAA CGGGTCTTGT AGCAACATCT GAAATAACAC ATGCAACCCC TGCTGCATAT
 GCGGCACATA ATGTTTCACG CAAAAATATG GCAGAAATCG CCGATGACTA TTTTGATGAT
 CAAATCGACG GACAACACAA AGTCGATGTG TTACTTTGGCG GCGGCTCCGA ATTATTTGCC
 CGGAAAGATC GTGATTTAGT CAAAGAAATTT TCCCAAGCGG GTTATGGTCA TGTCACAGAC
 AAAAAGTCGT TAAATGAGAA CCAAGACGAC AAAATTTTAG GCTTGTGTTGC ACCAGGCGGG
 CTACCTAAAA TGATTGACCG AACGGAAGAA GTCCCTTCAT TAGCTGATAT GACAGAAGCG
 GCTCTTCAAC GGTTAGATAA AAATGAAAAA GGTTTCCTTT TAATGGTTGA AGGTAGTCAA
 ATTGATTGGG CCGGGCATAG CAATGATATT GTTGGCGCGA TGAGCGAAAT GCAAGACTTC
 GAAGCGCGCT TTGAAAAGGC CATCGATTTT GCCAAAAAAG ATGGTGAACA TTGGTGGTTA
 CAACTGCAGA TCATTCAACA GGGGGCTTGT CTTTAG

EF028-2 (SEQ ID NO:106)

MKKR ALLGVTLTTF TTLAGCTNLS
 EQKSGEKQTE VAEAKATESE KASVKNVIFM IGDGMGNPYT TGYRYFKANH SDKRVPQTAF
 DTYLVGQQAT YPEDEEENV DSASAATAMA AGVKTYNNAI ALDNDKSKTE TVLERAKKVG
 KSTGLVATSE ITHATPAAYG AHNVSRRNMA EIADDYFDDQ IDGQHKVDVL LGGGSELFAR
 KDRDLVKEFS QAGYGHVTDK KSLNENQDDK ILGLFAPGGL PKMIDRTEEV PSLADMTEAA
 LQRLDKNEKG FFLMVEGSQI DWAGHSNDIV GAMSEMDFE AAFEKAIDFA KKDGEHWWLQ

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LQIIQQGACL

EF028-3 (SEQ ID NO:107)

ACAGA AAAGCGGCGA AAAACAAACA GAGGTTGCTG AAGCGAAGGC AACTGAATCT
 GAAAAAGCAT CAGTAAAAAA TGTTATTTTT ATGATTGGAG ATGGCATGGG GAATCCGTAT
 ACAACGGGCT ATCGCTATTT CAAAGCCAAT CACTCAGACA AGCGTGTTC CCAAACAGCT
 TTTGATACCT ATTTGGTTCG ACAGCAAGCC ACTTATCCAG AAGATGAAGA AGAGAATGTC
 ACCGATTTCAG CTTCCGCAGC GACAGCGATG GCTGCCGGAG TGAAAACCTA TAATAATGCT
 ATTGCACTCG ATAATGACAA GTCCAAAACA GAAACAGTGC TCGAACGTGC GAAAAAAGTG
 GGGAAATCAA CGGGTCTTGT AGCAACATCT GAAATAACAC ATGCAACCCC TGCTGCATAT
 GGCGCACATA ATGTTTCACG CAAAAATATG GCAGAAATCG CCGATGACTA TTTTGATGAT
 CAAATCGACG GACAACACAA AGTCGATGTG TTAATTGGCG GCGGCTCCGA ATTATTTGCC
 CGGAAAGATC GTGATTTAGT CAAAGAATTT TCCCAAGCGG GTTATGGTCA TGTCACAGAC
 AAAAAGTCGT TAAATGAGAA CCAAGACGAC AAAATTTTAG GCTTGTTTGC ACCAGGCGGG
 CTACCTAAAA TGATTGACCG AACGGAAGAA GTCCCTTCAT TAGCTGATAT GACAGAAGCG
 GCTCTTCAAC GGTTAGATAA AAATGAAAAA GGTTCCTTTT TAATGGTTGA AGGTAGTCAA
 ATTGATTGGG CCGGGCATAG CAATGATATT GTTGGCGCGA TGAGCGAAAT GCAAGACTTC
 GAAGCGGCGT TTGAAAAGGC CATCGATTTT GCCAAAAAG ATGGTGAACA TTGGTGGTTA
 CAACTGCAGA TCATTCAACA GGGGGCTTGT CTT

EF028-4 (SEQ ID NO:108)

QKSGEKQTE VAEAKATESE KASVKNVIFM IGDGMGNPYT TGYRYFKANH SDKRVPQTAF
 DTYLVGQQAT YPEDEEENV TDSASAATAMA AGVKTYNNAI ALDNDKSKTE TVLERAKKV
 KSTGLVATSE ITHATPAAYG AHNVSRRKMA EIADDYFDDQ IDGQHKVDVL LGGGSELFAR
 KDRDLVKEFS QAGYGHVTDK KSLNENQDDK ILGLFAPGGL PKMIDRTEEV PSLADMTEAA
 LQRLDKNEK FFLMVEGSI DWAGHSNDIV GAMSEMDFE AAFEKAIDFA KKDGEHWWLQ
 LQIIQQGACL

EF029-1 (SEQ ID NO:109)

TGAAGGAGGG AGAAAATGAA AAAGTTAATC GGTAAAAAGT GGCTGCTGCT TACAGCAGTA
 GCCACTTTTT TATTATCAGG ATGCGCAAGT CTTGAACAAA AAGCACAGGA TAGTGTAATA
 GAAGTTACTG AAAATGTTAC TCAAACATAT TCAAACGATC AACGTATACC AGCTGATTTT
 GTTAGGCACG TGGATGGCGA TACCACAGTA TTAATAATTG ACGGAAAAGA AAAAAAGTT
 CGGTTTTTAT TAATTGACAC ACCCGAGACT GTGAAACCGA AAACAAAAGT TCAGCCGTTT
 GGATTGGAAG CTAGCAAACG CACAAAAGAG CTTTTGTCTA CTGCTTCAGA AATTACGTTT
 GAATATGATA AGGGCGATAA AACAGATCGT TACGGACGAG CGTTGGGCTA CATATTCGTA
 GATGGAACAT TACTACAAAA AACGCTTGTA AGTGAAGGAT TAGCTCGTGT TGCCTATGTA
 AAAGAGCCTA CAACTAAGTA TTTGGCAGAA CTAGAGCAAG CCAAGAACA GGCTAAAAAT
 GAGTCACTCG GAATCTGGAG CATAACAGGT TATGTGACAC AACGGGGGTT TAGTAAATAA

EF029-2 (SEQ ID NO:110)

MKKLIG KKWLLLTAVA TFLLSGCASL EQKAQDSVKE VTENVQTIS NDQRIPADTV
 RHVDGDTTVL KIDGKEQKVR FLLIDTPETV KPKTKVQPF LEASKRTKEL LSTASEITFE
 YDKGDKTDY GRALGYIFVD GTLLQKTLVS EGLARVAYVK EPTTKYLAEL EQAQEQAKNE
 SLGIWSIPGY VTQRGFSK

EF029-3 (SEQ ID NO:111)

AAATGTTAC TCAAACATAT TCAAACGATC AACGTATACC AGCTGATTTT
 GTTAGGCACG TGGATGGCGA TACCACAGTA TTAATAATTG ACGGAAAAGA AAAAAAGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CGGTTTTTAT TAATTGACAC ACCCGAGACT GTGAAACCGA AAACAAAAGT TCAGCCGTTT
 GGATTGGAAG CTAGCAAACG CACAAAAGAG CTTTTGTCTA CTGCTTCAGA AATTACGTTT
 GAATATGATA AGGGCGATAA AACAGATCGT TACGGACGAG CGTTGGGCTA CATATTCGTA
 GATGGAACAT TACTACAAAA AACGCTTGTA AGTGAAGGAT TAGCTCGTGT TGCCTATGTA
 AAAGAGCCTA CAACTAAGTA TTTGGCAGAA CTAGAGCAAG CCCAAGAACA GGCTAAAAAT
 GAGTCACTCG GAATCTGGAG CATACCAGGT TATGTGACAC AACGGGGGTT TAGTAAA

EF029-4 (SEQ ID NO:112)

NVTQTIS NDQRIPADFV
 RHVDGDTTVL KIDGKEQKVR FLLIDTPETV KPRTKVQPFQ LEASKRTKEL LSTASEITFE
 YDKGDKTDY GRALGYIFVD GTLLQKTLVS EGLARVAYVK EPTTKYLAEL EQAQEQAKNE
 SLGIWSIPGY VTQRGFSK

EF030-1 (SEQ ID NO:113)

TGATTGACAC ATAGGGGGAA TAGTATGAAA AAGTTAAAAA TGATGGGGAT TATGTTATTT
 GTTAGTACGG TCTTGGTAGG TTGTGGCACA ACAGCAGANA CAAAAATAGA CGAGAAAGCA
 ACTGAGAAAA CCAGTGTCTC GAAAAAAGTT TTAAATTTAA TGGAGAACTC GGAAATCGGT
 TCAATGGATT CTATTTTTAC ACAAGATGAA GCCAGTATTA ACGCACAGTC CAATGTCTTT
 GAAGGGTTAT ATCAATTGGA TGAAAAAGAT CAACTAATAC CTGCTGCTGC TAAAGAGATG
 CCAGAAATTT CTGAGGATGG CAAACGATAT ACCATTAAAC TAAGAGAAGA TGGCAAGTGG
 TCCAATGGTG ATGCTGTAAC AGCCAATGAT TTCGTTTTTG CTGGCGTAA ATTAGCGAAT
 CCCAAAAACC AAGCCAATTA CTTTTCTTG TTAGAAGGAA CGATTCTGAA CGGAACAGCT
 ATTACAAAAG AGGAAAAAGC ACCAGAGGAA TTGGGTGTCA AAGCGCTTGA TGATTATACT
 TTGGAGGTTA CTTTAGAAAA GCCTGTACCA TATTTTACGT CGTTATTGGC ATTTTCTCCA
 TTTTTCCCAC AAAACGAAGC ATTCGTGAAA GAAAAAGGAC AAGCCTATGG CACTTCTAGT
 GAAATGATTG TATCTAATGG TCCGTTTTTA ATGAAAAATT GGGATCAGTC AGCGATGTCG
 TGGGATTTTG TCGTAATCC CTACTATTAC GATAAAGAAA AAGTAAAATC AGAAACGATT
 CATTTTGAAG TTCTTAAAGA AACCAATACC GTTTATAATT TGTACGAATC AGGTGAATTA
 GATGTGGCTG TCTTAACAGG AGATTTTGCT AAACAAAATC GAGACAACCC AGACTATGAA
 GCAATCGAAC GGTCAAAAGT CTATTCCTTA CGTTTAAACC AAAAAAGAAA CGAAAAACCA
 TCCATTTTTG CAAATGAGAA TGTCCGCAA GCTTTAGCTT ATGCTTTGGA TAAAAAAGT
 TTAGTCGATA ATATTTTAGC AGATGGCTCA AAAGAAATTT ATGGGTACAT TCCAGAAAAA
 TTTGTATATA ACCCAGAAAC GAATGAAGAT TTTCTGCAAG AAGCAGGCGC TCTTGTCAAA
 ACAGACGCCA AAAAAGCCAA AGAGTATTTA GATAAAGCAA AAGCAGAGCT AAACGGAGAT
 GTAGCCATTG AACTTCTTTC AAGAGATGGT GATAGTGACC GA

EF030-2 (SEQ ID NO:114)

MKK LKMMGIMLFV STVLVCGGTT AXTKIDEKAT EKTSVSKVL NLMENSEIGS
 MDSIFTQDEA SINAQSNVFE GLYQLDEKDQ LIPAAAKEMP EISEDGKRYT IKLREDGKWS
 NGDAVTANDF VFAWRKLANP KNQANYFFLL EGTILNGTAI TKEEKAPEEL GVKALDDYTL
 EVTLEKVPY FTSLLAFSPF FPQNEAFVKE KGQAYGTSSE MIVSNGPFLM KNWDQSAMSW
 DFVRNPYYD KEKVKSETH FEVLKETNTV YNLYESGELD VAVLTGDFAK QNRDNPDYEA
 IERSKVYSLR LNQRNEKPS IFANENVKKA LAYALDKKSL VDNILADGSK EIYGYIPEKF
 VYNPETNEDF RQEAGALVKT DAKKAKEYLD KAKAELNGDV AIELLSRDGD SDR

EF030-3 (SEQ ID NO:115)

GAGAAAAGCA
 ACTGAGAAAA CCAGTGTCTC GAAAAAAGTT TTAAATTTAA TGGAGAACTC GGAAATCGGT
 TCAATGGATT CTATTTTTAC ACAAGATGAA GCCAGTATTA ACGCACAGTC CAATGTCTTT
 GAAGGGTTAT ATCAATTGGA TGAAAAAGAT CAACTAATAC CTGCTGCTGC TAAAGAGATG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGAAATTT CTGAGGATGG CAAACGATAT ACCATTAAAC TAAGAGAAGA TGGCAAGTGG
 TCCAATGGTG ATGCTGTAAC AGCCAATGAT TTCGTTTTTG CTTGGCGTAA ATTAGCGAAT
 CCCAAAAACC AAGCCAATTA CTTTTTCTTG TTAGAAGGAA CGATTCTGAA CGGAACAGCT
 ATTACAAAAG AGGAAAAAGC ACCAGAGGAA TTGGGTGTCA AAGCGCTTGA TGATTATACT
 TTGGAGGTTA CTTTAGAAAA GCCTGTACCA TATTTTACGT CGTTATTGGC ATTTTCTCCA
 TTTTCCCAC AAAACGAAGC ATTTCGTGAAA GAAAAAGGAC AAGCCTATGG CACTTCTAGT
 GAAATGATTG TATCTAATGG TCCGTTTTTA ATGAAAAATT GGGATCAGTC AGCGATGTCG
 TGGGATTTTG TGCCTAATCC CTACTATTAC GATAAAGAAA AAGTAAAAATC AGAAACGATT
 CATTTTGAAG TTCTTAAAGA AACCAATACC GTTTATAATT TGTACGAATC AGGTGAATTA
 GATGTGGCTG TCTTAACAGG AGATTTTGCT AAACAAAATC GAGACAACCC AGACTATGAA
 GCAATCGAAC GGTCAAAAGT CTATTCCTTA CGTTTAAACC AAAAAAGAAA CGAAAAACCA
 TCCATTTTTG CAAATGAGAA TGTCGCAAAA GCTTTAGCTT ATGCTTTGGA TAAAAAAGT
 TTAGTCGATA ATATTTTAGC AGATGGCTCA AAAGAAATTT ATGGGTACAT TCCAGAAAAA
 TTTGTATATA ACCCAGAAAC GAATGAAGAT TTTCGTCAAG AAGCAGGCGC TCTTGTCAAA
 ACAGACGCCA AAAAAGCCAA AGAGTATTTA GATAAAGCAA AAGCAGAGCT AAACGGAGAT
 GTAGCCATTG AACTTCTTTC AAGAGATGGT

EF030-4 (SEQ ID NO:116)

EKAT EKTSVSKKVL NLMENSEIGS

MDSIFTQDEA SINAQSNVFE GLYQLDEKQD LIPAAAKEMP EISEDGKRYT IKLREDGKWS
 NGDAVTANDF VFAWRKLANP KNQANYFFLL EGTILNGTAI TKEEKAPEEL GVKALDDYTL
 EVTLEKPVYPY FTSLLAFSPF FPQNEAFVKE KGQAYGTSSE MIVSNGPFLM KNWDQSAMSW
 DFVRNPYYD KEKVKSETH FEVLKETNTV YNLYESGELD VAVLTGDFAK QNRDNPDEYA
 IERSKVYSLR LNQRNEKPS IFANENVRKA LAYALDKKSL VDNILADGSK EIYGYIPEKF
 VYNPETNEDE RQEGALVKT DAKKAKEYLD KAKAELNGDV AIELLSRDG

EF031-1 (SEQ ID NO:117)

TGAGAAATTA GTTATTTTAG AAAAATAAAA ACCATTTTGG AGGAAGATTT AAAAATGAAA
 AAACGCGTAA TTTTAGGGAC ATTAGTCGCT GCAACGTTAT TAATGACTGC TTGTGGAAC
 AGCGAAGCAA CTACGAAAAG CGAGAGCAAA GGTGGAAGTA ATGCTTTAGT CGTTTCAACT
 TTCGGATTAA GTGAAGATAT TGTCAAAAAA GACATTATCG CTCCATTGTA AAAAGAGAAT
 GAAGCGAAAG TTACCTTAGA AGTAGGCAAT AGCGCAGACC GCTTTACGAA ATTAATAAAT
 AATCCCAATG CGGGAATTGA TGTCATTGAA TTAGCACAAG CAAATGCAGC ACAAGGTGGA
 AAAGATGGGT TATTTGAAAA AATTACAGAA AAAGAAGTAC CTAATTTAAG TCAGTTAACG
 CCGGGAGCAA AAGAGGTTTT TGAAAGTGGT GCTGGCGTAC CAATCGCTGT AAACAGTATC
 GGGATTGTTT ACAACAAAGA AAAATTAGGC AAAGAAAATTA AAAACTGGGA TGACTTATGG
 TCAGCTGATT TGAAAGGTAA AATTTCTGTT CCAGACGTTG CCACGACGGC AGGTCCTTTA
 ATGTTATACG TTGCTAGTGA ACATGCTGGT CAAGATATTA CAAAAGATAA CGGGAAGGCC
 GCTTTTGAAG CGATGAAAGA ATTAATAACCA AACGTTGTTA AAACGTATTC AAAATCGTCA
 GACTTAGCNA ATATGTTCCA ATCTGGTGAA ATTGAAGCAG CTGTGGTTGC TGATTTTGGC
 GTTGATATTA TTCAAGGCGC ACAGAAAACG TGA

EFO031-2 (SEQ ID NO:118)

MKK RVILGTLVAA TLLMTACGNS EATTKSESKG GSNALVVSTF

GLSEDIVKKD IAPFEKENE AKVTLEVGNs ADRFTKLKNN PNAGIDVIEL AQANAAQGGK
 DGLFEKITEK EVPNLSQLTP GAKEVFESGA GVPIAVNSIG IVYNKEKLGK EIKNWDDLWS
 ADLKGKISVP DVATTAGPLM LYVASEHAGQ DITKDNGKAA FEAMKELKPN VVKTYSSSD
 LANMFQSGEI EAAVVADFAV DIIQGAQKT

EF031-3 (SEQ ID NO:119)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AA CTACGAAAAG CGAGAGCAAA GGTGGAAGTA ATGCTTTAGT CGTTTCAACT
 TTCGGATTAA GTGAAGATAT TGTCAAAAA GACATTATCG CTCCATTTGA AAAAGAGAAT
 GAAGCGAAAG TTACCTTAGA AGTAGGCAAT AGCGCAGACC GCTTTACGAA ATTAAAAAAT
 AATCCCAATG CCGGAATTGA TGTCATTGAA TTAGCACAAAG CAAATGCAGC ACAAGGTGGA
 AAAGATGGGT TATTTGAAAA AATTACAGAA AAAGAAGTAC CTAATTTAAG TCAGTTAACG
 CCGGGAGCAA AAGAGGTTTT TGAAAGTGGT GCTGGCGTAC CAATCGCTGT AAACAGTATC
 GGGATTGTTT ACAACAAAGA AAAATTAGGC AAAGAAATTA AAAACTGGGA TGACTTATGG
 TCAGCTGATT TGAAAGGTAA AATTTCTGTT CCAGACGTTG CCACGACGGC AGGTCCTTTA
 ATGTTATACG TTGCTAGTGA ACATGCTGGT CAAGATATTA CAAAAGATAA CGGGAAGGCC
 GCTTTTGAAG CGATGAAAGA ATTAAAACCA AACGTTGTTA AAACGTATTC AAAATCGTCA
 GACTTAGCNA ATATGTTCCA ATCTGGTGAA ATTGAAGCAG CTGTGGTTGC TGATTTTGCG
 GTTGATATTA TTCAAGGCGC ACAGAAAA

EF031-4 (SEQ ID NO:120)

TTKSESKG GSNALVVSTF
 GLSEDIVKDD IAPFEKENE AKVTLEVGN SADRFTKLKNN PNAGIDVIEL AQANAAQGGK
 DGLFEKITEK EVPNLSQLTP GAKEVFESGA GVPIAVNSIG IVYNKEKLGK EIKNWDDLWS
 ADLKGKISVP DVATTAGPLM LYVASEHAGQ DITKDNGKAA FEAMKELKPN VVKTYSKSSD
 LANMFQSGEI EAAVVADFAV DIIQGAQK

EF032-1 (SEQ ID NO:121)

TGAATAAATT ATTTAGGAGG AATTATGATG AAAAAATTAA TTAGTTTAGG ATTGGTTTGT
 GTTTGTGGTA TTTCACTACT TACTGCTTGT NCGGGAATA ATGATAATAA AGATACTGAA
 AAGTCAACCA GTCAATCTAG CAGCACAGTT AAACAACCGA ATTCAAAAGA CTTTGTGCG
 TCAGGGGAAT ATTCAGTTGG AAAAGATATT GATCCTGGAG ATTACTATGC TGTATTAAC
 CAACTAGATG ATAAATCGAG CATAGTTCTT ATTACCGTCA AATCAGGCGG AGAAAATAGT
 AACCATGACT TATACGGAGT GGGAAACAAG AAAAAAGTAT CTCTTAAAAA GGGAGATACT
 CTCACATTCG AAACGCGG CAAAGATTTT GTTGTAGAT TTTTAAATGA AAAAGATTTT
 CAAGAATATA TGAAAAATCC AGTATCNAGT ACTGAAACTA GCAAAACANAA AACAGTAAAC
 TCTGATGTTT CTAAAAGTAG TAGCCAAGAT AATAACAAT CTGATGTATC TGAAAAAAA
 GAAGTAAGTA CTGAAGCGAA GTCTGATGTA GCTACTAATA CTTTACCGAG CGAAGATAAA
 AATACTAATG ACATTACTAA GCTAGCAGAT GAGCCAACCT TAGAACAACA AACCGTCTTA
 GATACTTTAG CTAAGCATCA ATTTAATGAT ATGTATCCTT ATAAAGGAAG CAAAATGCAT
 TCAATTATCG GCGTCATCCC AACCATGGAC GCAAAAAGAT GGTAA

EF032-2 (SEQ ID NO:122)

MK KLISLGLVCV CGISLLTACX GNNDNKDTEK STSQSSSTVK QPNSKDFVAS
 GEYSVGKDID PGDYAVLTQ LDDKSSIVLI TVKSGGENSN HDLYGVGNKK KVSLLKGDTL
 TFETADKDFV VRFLNEKDFQ EYMKNPVSS ETSKXKTVNS DVSKSSSQDN KQSDVSEKKE
 VSTEAKSDVA TNTLPSEDKN TNDITKLADE PTLEQQTVLD TLAKHQFNDM YPYKSGSKMHS
 IIGVIPTMDA KRW

EF032-3 (SEQ ID NO:123)

TA ATGATAATAA AGATACTGAA
 AAGTCAACCA GTCAATCTAG CAGCACAGTT AAACAACCGA ATTCAAAAGA CTTTGTGCG
 TCAGGGGAAT ATTCAGTTGG AAAAGATATT GATCCTGGAG ATTACTATGC TGTATTAAC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAACTAGATG ATAAATCGAG CATAGTTCCTT ATTACCGTCA AATCAGGCGG AGAAAATAGT
 AACCATGACT TATACGGAGT GGGAAACAAG AAAAAAGTAT CTCTTAAAAA GGGAGATACT
 CTCACATTCG AAAC TGCCGA CAAAGATTTT GTTGTTAGAT TTTTAAATGA AAAAGATTTT
 CAAGAATATA TGAAAAATCC AGTATCNAGT ACTGAACTA GCAAACANAA AACAGTAAAC
 TCTGATGTTT CTAAAAGTAG TAGCCAAGAT AATAACAAT CTGATGTATC TGAAAAA
 GAAGTAAGTA CTGAAGCGAA GTCTGATGTA GCTACTAATA CTTTACCGAG CGAAGATAAA
 AATACTAATG ACATTACTAA GCTAGCAGAT GAGCCAACCT TAGAACAACA AACCGTCTTA
 GATACTTTAG CTAAGCATCA ATTTAATGAT ATGTATCCTT ATAAAGGAAG CAAAATGCAT
 TCAATTATCG GCGTCATCCC AACCATGGAC GCAAAAAGAT GG

EF032-4 (SEQ ID NO:124)

NDNKDTEK STSQSSSTVK QPNSKDFVAS
 GEYSVGKID PGDYYAVLTQ LDDKSSIVLI TVKSGGENSN HDLYGVGNKK KVSLLKGDITL
 TFETADKDFV VRFLNEKDFQ EYMKNPVSST ETSKXKTVNS DVSKSSSQDN KQSDVSEKKE
 VSTEAKSDVA TNITLPSEKDN TNDITKLAD PTLEQQTIVLD TLAKHQFNMD YPYKSGSKMHS
 IIGVIPTMDA KRW

EF033-1 (SEQ ID NO:125)

TGACTGCTTT TTTTCTATTG GAGAAAAAAG TGGTTTTTTT GTATTGTTTT GACGTTGAGA
 CAAAGGAGGT TCATTTTCTA AAATTTTCCC CAAAATAAAA TAGACGAATG CGAGGATGAA
 AAAATGAAAA AATTTACTTT AACAAATGATG ACTTTAGGTT TAGTAGCAAC ACTTGGCTTA
 GCAGGATGTG GTAAACAGGA AAAGAAAGCA ACTACCTCTT CTGAAAAAAC AGAAGTAACG
 TTACCAACCA AAGACCGTAG CGGCAAAGAA ATTACTTTAC CCAAAGAAGC AACCAAAATT
 ATTTCCCTAG TGCCATCAAC AACAGAAAGTG ATTGAAGACT TAGGTAAAC CGACCAATTA
 ATCGCAGTTG ATACTCAAAG TAGTACAATG ATGACTGATT TAAAAAAATT ACCACAAATG
 GATATGATGG CTGTGCGATG CGAAAAATTG ATTGCCTTGA AACCACAAAT TGTATTATGTG
 AATGACATCA ATTTAGCTAG CTCAGAAAGT GTTTGGAAGC AAGTGAAGA TGCTGGAATT
 ACAGTCGTTA ATATCCCCAC TAGTACAAGC ATCAAAGCAA TCAAAGAAGA CGTCCAATTC
 ATCGCTGATA GCTTATCTGA ACATGAAAAA GGACAAAAGT TAATCAAAAC AATGGATCAA
 GAAATCGACG AGTAG

EF033-2 (SEQ ID NO:126)

MKKFTLTMMT LGLVATLGLA
 GCGKQEKAT TSSEKTEVTL PTKDRSGKEI TLPKEATKII SLVPSTTEVI EDLGKTDQLI
 AVDTQSSTMM TDLKKLPQMD MMAVDKELI ALKPQIVYVN DINLASSES WKQVEDAGIT
 VVNIPTSTSI KAIEDVQFI ADSLSEHEKG QKLIKMDQE IDE

EF033-3 (SEQ ID NO:127)

CTCTT CTGAAAAAAC AGAAGTAACG
 TTACCAACCA AAGACCGTAG CGGCAAAGAA ATTACTTTAC CCAAAGAAGC AACCAAAATT
 ATTTCCCTAG TGCCATCAAC AACAGAAAGTG ATTGAAGACT TAGGTAAAC CGACCAATTA
 ATCGCAGTTG ATACTCAAAG TAGTACAATG ATGACTGATT TAAAAAAATT ACCACAAATG
 GATATGATGG CTGTGCGATG CGAAAAATTG ATTGCCTTGA AACCACAAAT TGTATTATGTG
 AATGACATCA ATTTAGCTAG CTCAGAAAGT GTTTGGAAGC AAGTGAAGA TGCTGGAATT
 ACAGTCGTTA ATATCCCCAC TAGTACAAGC ATCAAAGCAA TCAAAGAAGA CGTCCAATTC
 ATCGCTGATA GCTTATCTGA ACATGAAAAA GGACAAAAGT TAATCAAAAC AATGGATCAA
 GAAATCGACG AGTAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF033-4 (SEQ ID NO:128)

SSEKTEVTI PTKDRSGKEI TLPKEATKII SLVPSTTEVI EDLGKTDQLI
 AVDTQSSTMM TDLKKLPQMD MMAVDAEKLI ALKPQIVYVN DINLASSESV WKQVEDAGIT
 VVNIPTSTSI KAIKEDVQFI ADSLSEHEKG QKLIKTMDE IDE

EF034-1 (SEQ ID NO:129)

TAGGAGGGAG TAATCATGAA AAAAATCGGG TATTTTAGTT GTATTATTTT TTTCATGTTT
 TTGGTAGGTT GTAGTAATAA CAAAAAAGAA AACGGCAATC TTTTGAATGC CAGTTCGTTT
 CCTTTAATAC TCACCACGAT TATTGAAAAA GAAGAAGACC TAACGAAAGG TTCAATTTTT
 TTCAACAAGG ATAAAACCAT GACGCTTGAA AAAGAATATT TAGTTAATCC CAATAATGAA
 GACACAAAAA AAACAAGTAG AACAGAAAAA AAGGTATATA AAAATATTAA AATACAAGAA
 AATAAAGAGA GCTATGAAAT TATAGGTCAA TTGGACAAAA AAACGAAAAA AATAGAGTTT
 AAAAAAGTTG ATGAAGGTAA ACGTATATCT GATGCAGAAG GTAATGTGTA TGGTGATTTT
 GGTGGTAAAT AG

EF034-2 (SEQ ID NO:130)

MKKIGY FSCIIFMFL VGCSNNKKEN GNLLNASSFP LILTTIIEKE EDLTKGSIFF
 NKDKTMTLEK EYLVNPNND TKKTSRTEKK VYKNIQIEN KESYEIIGQL DKKTKKIEFK
 KVDEGKRISD AEGNVYGDFG GK

EF034-3 (SEQ ID NO:131)

AGAA AACGGCAATC TTTTGAATGC CAGTTCGTTT
 CCTTTAATAC TCACCACGAT TATTGAAAAA GAAGAAGACC TAACGAAAGG TTCAATTTTT
 TTCAACAAGG ATAAAACCAT GACGCTTGAA AAAGAATATT TAGTTAATCC CAATAATGAA
 GACACAAAAA AAACAAGTAG AACAGAAAAA AAGGTATATA AAAATATTAA AATACAAGAA
 AATAAAGAGA GCTATGAAAT TATAGGTCAA TTGGACAAAA AAACGAAAAA AATAGAGTTT
 AAAAAAGTTG ATGAAGGTAA ACGTATATCT GATGCAGAAG GTAATGTGTA TGGTGATTTT
 GGTGGTAAAT AG

EF034-4 (SEQ ID NO:132)

KEN GNLLNASSFP LILTTIIEKE EDLTKGSIFF
 NKDKTMTLEK EYLVNPNND TKKTSRTEKK VYKNIQIEN KESYEIIGQL DKKTKKIEFK
 KVDEGKRISD AEGNVYGDFG GK

EF035-1 (SEQ ID NO:133)

TAAACGAGAG GTGAGTTTAT GAAAACAAAA ATCGGAAAAA CAGTTATCTT GTCAGCATTT
 TTATTCACAA GTTTCCTTTT ACTGAGTGGT TGTACCTCGG CTGGCGAAGA GATGGAAAAA
 ACAATTGATC GACAGAAAGA AAAAGTCGAT AAAACGGTCG ATAAGCAGAA ACATAAAAAAT
 GAAAATTCCA TGGAAAGTTA CGACGAAAAA GTTGACCGTT CTTTAGATAG TCAAGAAGAC
 AAAATCGATA CTA CTGAGTA A

EF035-2 (SEQ ID NO:134)

MKTKI GKTIVLSAFL FTSFLLLSGC TSAGEEMEKT IDRQKEKVDK TVDKQKHKNE
 NSMESYDEKV DRSLDSQEDK IDTTE

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF035-3 (SEQ ID NO:135)

GATGGAAAAA

ACAAATGATC GACAGAAAGA AAAAGTCGAT AAAACGGTCG ATAAGCAGAA ACATAAAAAT
 GAAAATCCA TGGAAAGTTA CGACGAAAAA GTTGACCGTT CTTTAGATAG TCAAGAAGAC
 AAAATCGATA CTACTGAG

EF035-4 (SEQ ID NO:136)

MEKT IDRQKEKVDK TVDKQKHKNE
 NSMESYDEKV DRSLDSQEDK IDTTE

EF036-1 (SEQ ID NO:137)

TAATTTTCAA GTCCTACATA TAATGGTAAA ATAGAATGGA TTGAAATTAA TTGGAGGAAT
 AATGAATCGA TGAAAAAAG ATTGCTATTA TTTATTTGGTT TGGCAAGTAT ACTTACTTTG
 ACAGGATGTG CAAAATGGAT TGATCGTGGT GAATCCATCA CAGCGGTAGG CTCATCAGCT
 TTACAACCAT TAGTAGAGAC AGCGAGTGAG GAATATCAAA GCCAAAATCC GGAAGATTT
 ATTAATGTCC AAGGTGGCGG AAGCGGAACA GGTCTGAGTC AAGTCCAATC TGGCGCGGTA
 GACATTGGTA ATTCTGATTT ATTTGCAGAA GAGAAAAAGG GCATCAAAGC GGAAGACTTA
 ATTGATCATA AAGTTGCTGT CGTTGGGATT ACACCAATCG TTAACAAAAA TGTCGGTGTC
 AAAGATATCT CAATGGAAAA TTAAAGAAA ATCTTTTGTAG GTGAAGTAAC AAATGGA
 GAATTTGGCG GGAAAGACCA AAAAATTGTT ATTTTGAATA GAGCGGCCGG TAGTGGTACG
 CGTGCGACTT TTGAAAAGTG GGTCTTGGGA GATAAACAG CCATTTCGTGC GCAAGAACAA
 GATTCCAGCG GCATGGTTTCG TTCCATTGTT TCTGATACAC CAGGAGCGAT TAGTTATACC
 GCATTTTCAT ATGTTACTGA TGAAGTAGCT ACGTTAAGTA TTGATGGTGT TCAGCCAACA
 GATGAAAATG TAATGAACAA TAAATGGATT ATTTGGTCTT ATGAACACAT GTACACTCGT
 AAAAATCCAA GTGATTTAAC CAAAGAGTTT TTAGACTTTA TGTTGTCAGA TGATATCCAA
 GAACGTGTGA TTGGTCAATT AGGGTATATT CCTGTTTCGA AAATGGAAAT TGAACGGGAT
 TGGCAAGGAA ATGTCATTAA ATAA

EF-36-2 (SEQ ID NO:138)

MKKRLLLF IGLASILTITL CKAkWIDRGE SITAVGSSAL
 QPLVETASEE YQSQNPRFI NVQGGSGTG LSQVQSGAVD IGNSDLFAEE KKGIIKAEDLI
 DHKVAVVGIT PIVNKNVGK DISMENLKKI FLGEVTNWKE LGGKDQKIVI LNRAAGSGTR
 ATFEKWVLGD KTAIRAQEQD SSGMVRSIVS DTPGAISYTA FSYVTDEVAT LSIDGVQPTD
 ENVMNNKWII WSYEHMYTRK NPSDLTKEFL DFMLSDDIQE RVIGQLGYIP VSKMEIERDW
 QGNVIK

EF036-3 (SEQ ID NO:139)

GAT TGATCGTGGT GAATCCATCA CAGCGGTAGG CTCATCAGCT
 TTACAACCAT TAGTAGAGAC AGCGAGTGAG GAATATCAAA GCCAAAATCC GGAAGATTT
 ATTAATGTCC AAGGTGGCGG AAGCGGAACA GGTCTGAGTC AAGTCCAATC TGGCGCGGTA
 GACATTGGTA ATTCTGATTT ATTTGCAGAA GAGAAAAAGG GCATCAAAGC GGAAGACTTA
 ATTGATCATA AAGTTGCTGT CGTTGGGATT ACACCAATCG TTAACAAAAA TGTCGGTGTC
 AAAGATATCT CAATGGAAAA TTAAAGAAA ATCTTTTGTAG GTGAAGTAAC AAATGGA
 GAATTTGGCG GGAAAGACCA AAAAATTGTT ATTTTGAATA GAGCGGCCGG TAGTGGTACG
 CGTGCGACTT TTGAAAAGTG GGTCTTGGGA GATAAACAG CCATTTCGTGC GCAAGAACAA
 GATTCCAGCG GCATGGTTTCG TTCCATTGTT TCTGATACAC CAGGAGCGAT TAGTTATACC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCATTTTCAT ATGTTACTGA TGAAGTAGCT ACGTTAAGTA TTGATGGTGT TCAGCCAACA
 GATGAAAATG TAATGAACAA TAAATGGATT ATTTGGTCTT ATGAACACAT GTACACTCGT
 AAAAATCCAA GTGATTTAAC CAAAGAGTTT TTAGACTTTA TGTTGTCAGA TGATATCCAA
 GAACGTGTGA TTGGTCAATT AGGGTATATT CCTGTTTCGA AAATGGAAAT TGAACGGGAT
 TGGCAAGGAA ATGTCATTAA A

EF036-4 (SEQ ID NO:140)

IDRGE SITAVGSSAL

QPLVETASEE YQSQNPRFI NVQGGSGTG LSQVQSGAVD IGNSDLFAEE KKGIIKAEDLI
 DHKVAVVGIT PIVNKNVGK DISMENLKKI FLGEVTNWKE LGGKDQKIVI LNRAAGSGTR
 ATFEKWVLGD KTAIRAQEQD SSGMVRSIVS DTPGAISYTA FSYVTDEVAT LSIDGVQPTD
 ENVMNNKWII WSYEHMYTRK NPSDLTKEFL DFMLSDDIQE RVIGQLGYIP VSKMEIERDW
 QGNVIK

EF037-1 (SEQ ID NO:141)

TGAGTGTATG ATTACTCATT TCCCTTTGAA TCAGTTATGA TAAAGGAAGA AATAAATAAA
 TTTTTTGGAG GGATTTTCAT GAAAATGTCT AAAGTACTCA CCACTGTTTT GACGGCAACT
 GCTGCTCTTG TGTTGCTTAG TGCTTGTTCA TCTGATAAAA AAACAGATAG TAGTTCCTAGT
 AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTCGC AGCTACTGAC
 AATGTCACCT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT
 TCCAACGATG TCTATCGTAA ATTAGCACCT TATTCCCAAG ATGATAATAA AAAAGTAACT
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA ATAA

EF037-2 (SEQ ID NO:142)

MKMSK VLTIVLTATA ALVLLSACSS DKKTDSSTSS
 KETANSSTEV VSGASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLALY SQDDNKKVTA EYEITVPKLI VSSNFNIVH GTVKGDIEVK ANGFTLNGTK
 VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF037-3 (SEQ ID NO:143)

AACAGATAG TAGTTCCTAGT
 AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTCGC AGCTACTGAC
 AATGTCACCT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT
 TCCAACGATG TCTATCGTAA ATTAGCACCT TATTCCCAAG ATGATAATAA AAAAGTAACT
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA A

EF037-4 (SEQ ID NO:144)

TDSSSSS

KETANSSTEV VSGASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLALY SQDDNKKVTA EYEITVPKLI VSSNFNIVH GTVKGDIEVK ANGFTLNGTK

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF038-1 (SEQ ID NO:145)

TAATGGCCAT TTCGTCTACT AATAAAGAGG ATGAAGCTAC TCAAATGGCG TTGGCAATGG
 AACAAGGATC ATAAAAAAGG AGAAGTGAGC ATGAAAAAAG TACTACCTTT TATTGCCTTA
 GTCGGCTTGT TATTGTGTGC AGGTTGTGGA ACAGATATGA AAAAGATATT GACTGCCGAT
 GGTGGTAAAT GGGAACTAGA AAATAAAAGT CCAACTACTA CTTACACTTT TTTTGATGAT
 GAAACTTTTT CGAGGTATAA TTCAAAAATT AGTGATAGTG GAACGTACTC TTACGATGAA
 AATAATAAAA AACTCACTTT GGATATAAAA AATAAAGAAC AATTAAATAAT GGAAAAATGTT
 GAATATAAAG ACGGTAAATT AAAAGGTGAA ATTGAGGCG AGAAGGACTC TGATAAAAAA
 TNGAATAAGA GGTGCTTTTG A

EF038-2 (SEQ ID NO:146)

M KLLKWRWQWN KDHKKGEVSM KKVLPFIALV GLLLLSGCGT DMKKILTADG
 GKWELENKSP TTTYTFFDDE TFSRYNSKIS DSGTYSYDEN NKKLTLDIKN KEQLIMENVE
 YKDGKLGKEI GGEKDSKKX NKRCL

EF038-3 (SEQ ID NO:147)

TTGTGGA ACAGATATGA AAAAGATATT GACTGCCGAT
 GGTGGTAAAT GGGAACTAGA AAATAAAAGT CCAACTACTA CTTACACTTT TTTTGATGAT
 GAAACTTTTT CGAGGTATAA TTCAAAAATT AGTGATAGTG GAACGTACTC TTACGATGAA
 AATAATAAAA AACTCACTTT GGATATAAAA AATAAAGAAC AATTAAATAAT GGAAAAATGTT
 GAATATAAAG ACGGTAAATT AAAAGGTGAA ATTGAGGCG AGAAGGACTC TGATAAAAAA
 TNGAATAAGA GGTGCTTTTG A

EF038-4 (SEQ ID NO:148)

CGT DMKKILTADG
 GKWELENKSP TTTYTFFDDE TFSRYNSKIS DSGTYSYDEN NKKLTLDIKN KEQLIMENVE
 YKDGKLGKEI GGEKDSKKX NKRCL

EF039-1 (SEQ ID NO:149)

TAAATATATC AAAAAGAAAA AAGGGGATTA CCAACCATGA AAAAGAAAAA AGTTTTTAGT
 GCGCTTACCT TATTAACCTT TAGTACGTTG TTGATTGCAG GCTGTGCTGG CGGAGCCAAC
 TCTGCAACAG ATAAATCAAG TGCAGCTAGC TCAAGCACTG CAGTCTCTAG TTCAGCAGAA
 GCAGCTAAAG AGCAATCAAA AGGACAAGAA TTAACAGAAA TTTTATCCAG TACTGATTGG
 CAAGGCACAA AAGTTTACGA CAAAAATNAT AATAATTTAA CAGCAGAAAA TGCTAATTTT
 ATTGGTTTAG CAAAATATGA TGGTGAAACA GGTTTTTATG AATTTTTCGA CAAAGAAACA
 GGTGAAACCC GTGGCGATGA AGGCACATTC TTTGTGACAG ACGATGGCGA AAAGCGTATC
 TTAATTTCCG ATACACAAAA CTATCAAGCG GTGGTCGATT TAACGGAAGT GACGAAAGAT
 AAATTTACCT ATAAGCGAAT GGGTAAAGAT AAAGACGGGA AAGATGTAGA AGTCTTTGTA
 GAACATATCC CTTATTCTGA CGAGAAATTA ACCTTTACGA ACGGCCGTAA AGATTTAGAA
 ACAGAACTG GCAAGATTGT TACCAATGAA CCTGGGGATG ACATTTTAGG GGCCACATTA
 TGGAATGGCA CGAAAGTTTT AGATGAAGAC GGTAACGATG TTAGTGAAGC AAATAAAATG
 TTTATTAGTT TAGCGAAATT TGATAATAAA ACAAGTAAAT ATGAATTCTT TGATTTAGAA
 ACGGGTAAAA CACGTGGAGA TTTTGGTTAC TTCCAAGTAA TTGATAATAA CAAAATCCGT
 GCTCACGTTT CAATTGGTGA CAATAAATAT GGAGCTGCAT TAGAATTAAC AGAATTAAAT
 GATAAACGTT TTACGTATAC ACGAATGGGT AAAGACAACA ATGGCAAAGA AATTAAAGTC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTTGTAGAAC ATGAACCATA TGAAGGAGAC TTTACGCCAG ACTTCACGTT CTAA

EF039-2 (SEQ ID NO:150)

MKKKKVFS LTLTTFSTLL IAGCAGGANS ATDKSSAASS STAVSSSAEA
 AKEQSKGQEL TEILSSTDWQ GTKVYDKNXN NLTAENANFI GLAKYDGETG FYEFFDKETG
 ETRGDEGTFE VTDDGEKRIL ISDTQNYQAV VDLTEVTKDK FTYKRMGKDK DGKDVEVFVE
 HIPYSDEKLT FTNGRKDLET ETGKIVTNEP GDDILGATLW NGTKVLDEDEG NDVTEANKMF
 ISLAKFDNKT SKYEFFDLET GKTRGDFGYF QVIDNNKIRA HVSIGDNKYG AALELTELND
 KRFTYTRMGK DNNGKEIKVF VEHEPYEGDF TPDFTF

EF039-3 (SEQ ID NO:151)

TGCAACAG ATAAATCAAG TGCAGCTAGC TCAAGCACTG CAGTCTCTAG TTCAGCAGAA
 GCAGCTAAAG AGCAATCAAA AGGACAAGAA TTAACAGAAA TTTTATCCAG TACTGATTGG
 CAAGGCACAA AAGTTTACGA CAAAAATNAT AATAATTTAA CAGCAGAAAA TGCTAATTTT
 ATTGGTTTAG CAAAATATGA TGGTGAAACA GGTTTTATG AATTTTTCGA CAAAGAAACA
 GGTGAAACCC GTGGCGATGA AGGCACATTC TTTGTGACAG ACGATGGCGA AAAGCGTATC
 TTAATTTTCG ATACACAAA CTATCAAGCG GTGGTCGATT TAACGGAAGT GACGAAAGAT
 AAATTTACCT ATAAGCGAAT GGGTAAAGAT AAAGACGGGA AAGATGTAGA AGTCTTTGTA
 GAACATATCC CTTATTCTGA CGAGAAATTA ACCTTTACGA ACGGCCGTAA AGATTTAGAA
 ACAGAACTG GCAAGATTGT TACCAATGAA CCTGGGGATG ACATTTTAGG GGCCACATTA
 TGAATGGCA CGAAAGTTTT AGATGAAGAC GGTAACGATG TACTGAAGC AAATAAAATG
 TTTATTAGTT TAGCGAAATT TGATAATAAA ACAAGTAAAT ATGAATTCTT TGATTTAGAA
 ACGGGTAAAA CACGTGGAGA TTTTGGTTAC TTCCAAGTAA TTGATAATAA CAAAATCCGT
 GCTCACGTTT CAATTGGTGA CAATAAATAT GGAGCTGCAT TAGAATTAAC AGAATTAAT
 GATAACGTT TTACGTATAC ACGAATGGGT AAAGACAACA ATGGCAAAGA AATTAAGTC
 TTTGTAGAAC ATGAACCATA TGAAGGAGAC TTTACGCCAG ACTTCACGTT CTAA

EF039-4 (SEQ ID NO:152)

ATDKSSAASS STAVSSSAEA
 AKEQSKGQEL TEILSSTDWQ GTKVYDKNXN NLTAENANFI GLAKYDGETG FYEFFDKETG
 ETRGDEGTFE VTDDGEKRIL ISDTQNYQAV VDLTEVTKDK FTYKRMGKDK DGKDVEVFVE
 HIPYSDEKLT FTNGRKDLET ETGKIVTNEP GDDILGATLW NGTKVLDEDEG NDVTEANKMF
 ISLAKFDNKT SKYEFFDLET GKTRGDFGYF QVIDNNKIRA HVSIGDNKYG AALELTELND
 KRFTYTRMGK DNNGKEIKVF VEHEPYEGDF TPDFTF

EF040-1 (SEQ ID NO:153)

TAGATTAGAA CCACTGGAGA AAAATCTCAT ATTTCTCTCG AGGAAAGGAA GTTGAGCACA
 ATGAACAAAA AAATTTTAAT GGGGCTATTA AGTGTCTGTA CCATTCCATT ACTTGCTGCG
 TGTCAGGAG GAGAAACACC TTCCGCAGCG TCAAAAAATA GTCAAACGGT GACTACTCAA
 AGTAGTGCAA AACTGAAAG CACCAGTACA ACCCGTTCGG TAGCTCAAAC AACATCAAAA
 GAGGAAGTGA AAGAACCGAT GAAGACCTAT GAAGTGGGTG CGCTTTTAGA AGCAGCCAAT
 CAACGAGATA CGAAGAAGGT CAAGGAAATT TTACAAGATA CTACTTATCA AGTGAGATGA
 GTCGACACAG AAGGCAACAC ACCGCTCAAT ATCGCTGTTT ACAATAATGA CATTGAGATT
 GCAAAAGCGT TGATTGATCG GGGTGCCGAT ATTAATCTGC AAAACAGCAT TAGTGATAGT
 CCCTATCTTT ATGCGGGAGC GCAAGGACGT ACGGAGATT TAGCGTATAT GTTAAACAT
 GCGACCCAG ATTTAAATAA GCATAACCGT TACGGTGGCA ATGCGTTAAT TCCGGCAGCT
 GAAAAAGGAC ATATTGACAA TGTGAAGCTC TTGTTAGAAG ATGGACGAGA AGACATAGAT
 TTCCAAAATG ACTTTGGCTA TACAGCATTG ATTGAGGCAG TGGGGTTACG TGAAGGGAAC
 CAACTTTACC AAGATATTGT AAAATTGTTA ATGGAAAATG GTGCGGATCA ATCCATTAAA
 GACAATTCTG GTCGAACAGC AATGGACTAT GCCAATCAAA AAGGTTATAC GGAAATTAGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAATTTTAG CACAGTACAA CTAA

EF040-2 (SEQ ID NO:154)

M NKKILMGLLS VVTIPLLAAC QGGETPSAAS KNSQTVTTQS
 SAKTESTSTT RSVAQTTSKE EVKEPMKTYE VGALLEAANQ RDTKKVKEIL QDTTYQVDEV
 DTEGNTPLNI AVHNNNDIEIA KALIDRGADI NLQNSISDSP YLYAGAQRGT EILAYMLKHA
 TPDLNKHNRY GGNALIPAAE KGHIDNVKLL LEDGREDIDF QNDFGYTALI EAVGLREGNQ
 LYQDIVKLLM ENGADQSIKD NSGRTAMDYA NQKGYTEISK ILAQYN

EF040-3 (SEQ ID NO:155)

AGCG TCAAAAAATA GTCAAACGGT GACTACTCAA
 AGTAGTGCAA AAACGTAAAG CACCAGTACA ACCCGTTCGG TAGCTCAAAC AACATCAAAA
 GAGGAAGTGA AAGAACCGAT GAAGACCTAT GAAGTGGGTG CGCTTTTAGA AGCAGCCAAT
 CAACGAGATA CGAAGAAGGT CAAGGAAATT TTACAAGATA CTACTTATCA AGTGGATGAA
 GTCGACACAG AAGGCAACAC ACCGCTCAAT ATCGCTGTTC ACAATAATGA CATTGAGATT
 GCAAAAGCGT TGATTGATCG GGGTGCCGAT ATTAATCTGC AAAACAGCAT TAGTGATAGT
 CCCTATCTTT ATGCGGGAGC GCAAGGACGT ACGGAGATTT TAGCGTATAT GTTAAACAT
 GCGACCCAG ATTTAAATAA GCATAACCGT TACGGTGGCA ATGCGTTAAT TCCGGCAGCT
 GAAAAAGGAC ATATTGACAA TGTGAAGCTC TTGTTAGAAG ATGGACGAGA AGACATAGAT
 TTCCAAATG ACTTTGGCTA TACAGCATTG ATTGAGGCAG TGGGGTTACG TGAAGGGAAC
 CAACTTTACC AAGATATTGT AAAATTGTTA ATGGAAATG GTGCGGATCA ATCCATTAAA
 GACAATTCTG GTCGAACAGC AATGGACTAT GCCAATCAAA AAGGTTATAC GGAAATTAGT
 AAAATTTTAG CACAGTACAA C

EF040-4 (SEQ ID NO:156)

AS KNSQTVTTQS
 SAKTESTSTT RSVAQTTSKE EVKEPMKTYE VGALLEAANQ RDTKKVKEIL QDTTYQVDEV
 DTEGNTPLNI AVHNNNDIEIA KALIDRGADI NLQNSISDSP YLYAGAQRGT EILAYMLKHA
 TPDLNKHNRY GGNALIPAAE KGHIDNVKLL LEDGREDIDF QNDFGYTALI EAVGLREGNQ
 LYQDIVKLLM ENGADQSIKD NSGRTAMDYA NQKGYTEISK ILAQYN

EF041-1 (SEQ ID NO:157)

TAATTATTAA NNTCTGATTT TTCAGAAAAT ACAGATTGCA TTATTTTAGG AGGCAACACT
 ATGAAATTGA AAAAGTCATT AACATTCCGT GTGATTACAT TATTTAGCGT AACAACTTTA
 GCGGCTTGTG GAGGCGGCGG AACGTCAGAT AGCTCAAGCG CGTCTGGTGG CCGTAAGGCA
 AGTGGCGAAC AAGTTTTACG TGTCACAGAA CAACAAGAAA TGCCAACAGC TGATTTATCA
 CTAGCAACAG NCAGAAATAG TTTTATTGCA TTAAATAATG TATATGAAGG AATTTATCGT
 TTAGACAAAG ATAACAAAGT CCAACCTGCA GGTGCAGCGG AAAAAGCAGA AGTTTCTGAA
 GATGGACTAA CATACAAAAT TAAATTAAAT AAAGATGCAA AATGGTCAGA CCGTAAACCA
 GTGACTGCTA ATGACTATGT TTACGGATGG CAACGAACAG TTGATCCAGC GACAGCTTCT
 GAATATGCTT ATCTGTATGC CTCTGTAAAA AATGGTGATG CCATTGCTAA AGGGGAAAAA
 GATAAATCAG AATTAGGAAT TAAAGCAGTC AGTGATACAG AATTAGAAAT CACTTTAGAA
 AAAGCAACAC CATACTTTGA TTACTTATTA GCTTTCCCAT CATTCTTCCC GCAACGTCAA
 GACATTGTGG AAAAAATATG TAAAAATTAT GCATCAAACA GCGAAAGTGC TGTCTACAAAT
 GGTCCATTCTG TCTTAGACGG CTTTGATGGT CCTGGTACAG ATACAAAATG GTCATTCAAG
 AAAAACGATC AATATTGGGA TAAAGATACT GTGAAACTGG ACTCAGTAGA TGTGAATGTC
 GTGAAAGAAT CACCAACCGC GTTGAACCTG TTCCAAGATG GACAAACAGA CGATGTCGTT
 CTTTCTGGTG AATTAGCCCA ACAAATGGCC AATGACCCAG CTTTGTGTAG TCAAAAAGAA
 GCATCAACAC AATATATGGA ACTAAATCAA CGTGATGAAA AATCACCATT TAGAAATGCG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AACTTACGTA AAGCAATTTT TTACTIONAATC GACCGTAAAG CGTTAGTTGA ATCAATCCTT
AGGGGATGG

EF041-2 (SEQ ID NO:158)

M KLKSLTFGV ITLFSVITLA ACGGGGTSDS SSASGGGKAS
GEQVLRVTEQ QEMPTADLSL ATXRISFIAL NNVYEGYRL DKDNKVQPAG AAEKAEVSED
GLTYKIKLNK DAKWSDGKPV TANDYVYGWQ RTVDPATASE YAYLYASVKN GDAIAKGEKD
KSELGIKAVS DTELEITLEK ATPYFDYLLA FPSFFPQRQD IVEKYGKNYA SNSESAVYNG
PFVLDGFDGP GTDTKWSFKK NDQYWDKDTV KLDSVDVNVV KESPTALNLF QDGQTDVVV
SGELAQQMAN DPAFVSQKEA STQYMELNQR DEKSPFRNAN LRKAISYSID RKALVESILR
GW

EF041-3 (SEQ ID NO:159)

TTGTG GAGGCGGCGG AACGTCAGAT AGCTCAAGCG CGTCTGGTGG CGGTAAGGCA
AGTGGCGAAC AAGTTTTACG TGTCACAGAA CAACAAGAAA TGCCAACAGC TGATTTATCA
CTAGCAACAG NCAGAATTAG TTTTATTGCA TTAAATAATG TATATGAAGG AATTTATCGT
TTAGACAAAG ATAACAAAGT CCAACCTGCA GGTGCAGCGG AAAAAGCAGA AGTTTCTGAA
GATGGACTAA CATAAAAAT TAAATTAAAT AAAGATGCAA AATGGTCAGA CGGTAAACCA
GTGACTGCTA ATGACTATGT TTACGGATGG CAACGAACAG TTGATCCAGC GACAGCTTCT
GAATATGCTT ATCTGTATGC CTCTGTAAAA AATGGTGATG CCATTGCTAA AGGGGAAAAA
GATAAATCAG AATTAGGAAT TAAAGCAGTC AGTGATACAG AATTAGAAAT CACTTTAGAA
AAAGCAACAC CATACTTTGA TTACTTATTA GCTTTCCCAT CATTCTTCCC GCAACGTCAA
GACATTGTGG AAAAATATGG TAAAAATTAT GCATCAACA GCGAAAGTGC TGTCTACAAT
GGTCCATTCC TCTTAGACGG CTTTGATGGT CCTGGTACAG ATACAAAATG GTCATTCAAG
AAAAACGATC AATATTGGGA TAAAGATACT GTGAAACTGG ACTCAGTAGA TGTGAATGTC
GTGAAAGAAT CACCAACCGC GTTGAACCTG TTCCAAGATG GACAAACAGA CGATGTCGTT
CTTTCTGGTG AATTAGCCCA ACAAATGGCC AATGACCCAG CTTTGTGTAG TCAAAAAGAA
GCATCAACAC AATATATGGA ACTAAATCAA CGTGATGAAA AATCACCATT TAGAAATGCC
AACTTACGTA AAGCAATTTT TTACTIONAATC GACCGTAAAG CGTTAGTTGA ATCAATCCTT
AGGGGATGG

EF041-4 (SEQ ID NO:160)

CGGGGTSDS SSASGGGKAS
GEQVLRVTEQ QEMPTADLSL ATXRISFIAL NNVYEGYRL DKDNKVQPAG AAEKAEVSED
GLTYKIKLNK DAKWSDGKPV TANDYVYGWQ RTVDPATASE YAYLYASVKN GDAIAKGEKD
KSELGIKAVS DTELEITLEK ATPYFDYLLA FPSFFPQRQD IVEKYGKNYA SNSESAVYNG
PFVLDGFDGP GTDTKWSFKK NDQYWDKDTV KLDSVDVNVV KESPTALNLF QDGQTDVVV
SGELAQQMAN DPAFVSQKEA STQYMELNQR DEKSPFRNAN LRKAISYSID RKALVESILR
GW

EF044-1 (SEQ ID NO:161)

TAAGATAAAA TTAGTTATAG CGTCTATAGG AGGAATAGTA TGAAAAAATT AGTTTGTGTT
ATTTTAGTTA TTTTTTTAAC AGGTGTAGT TCTCAAAAAG CGAATGAACC TAAAAACAA
GAAAATTCTA CCAATCATAC AACATCAATA AAAAGCAGTA CTAATCATT CAGTTCTAGC
ATAGAAACAA GCTCTAATAA TAACTAAAA GAACTTCAG AAAGTGCCAG CACCACTCAA
ACTTCGTCAA AGTCGAAAAA TGAAGTATCT ACAAATGTCG AAGAAGCAAA TTCTTTAGAA
GCAACACCTT ATGCTGTGCA TCTTAGTAGC TTAAACAATC CACTCGTATT TAATTTTAAA
GGAATGAATG TGCCAACCTC AATTACGTTA GAGAACTTAA ATTCAACACC AACTGCTACC
TTCCGAACAA AATTGTTTGG GGCTGAAAAAT GGTCAAGTGA AAGAAGCCAT TAATAAATAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAGCTATCTA TAAATACAAT TCCTACAAAA GAGATTAGAA TATTTTCAGC GGCCGATAAC
 AGTATTTCGCA CCGTTAAAGT AAATACAGAA TTAATTTTAG GAACATAATAT TTCTTCAAAC
 GATGAACAAA ATAGATCGGG CACTTTTATAC TTATTCAACA ATAAAAATGG TTCGATATCT
 TTAATCACTC CTAACACGCG TGGCAATGTT ACGGATGATC AAAAAGACGT TATGCTAGAA
 GTAATTCAAT AA

EF044-2 (SEQ ID NO:162)

MKKLVCVI LVIFLTGCGS QKANEPKKQE NSTNHTTSIK SSTNHYSSSI
 ETSSNNKLKE TSESASTTQT SSKSKNEVST NVEEANSLEA TPYAVDLSSL NNPLVFNFKG
 MNVPTSITL NLNSTPTATF RTKLFGAENG QVKEAINKYE LSINTIPTKE IRIFSAADNS
 IRTVKVNTL ILGTNISSND EQNRSGLTYL FNNKNGSISL ITPNYAGNVT DDQKDVMLEV
 IQ

EF044-3 (SEQ ID NO:163)

TTGTAGT TCTCAAAAAG CGAATGAACC TAAAAACAA
 GAAATTTCTA CCAATCATAC AACATCAATA AAAAGCAGTA CTAATCATTA CAGTTCTAGC
 ATAGAAACAA GCTCTAATAA TAAACTAAAA GAAACTTCAG AAAGTGCCAG CACCACTCAA
 ACTTCGTCAA AGTCGAAAAA TGAAGTATCT ACAAATGTCG AAGAAGCAAA TTCTTTAGAA
 GCAACACCTT ATGCTGTGCGA TCTTAGTAGC TTAAACAATC CACTCGTATT TAATTTTAAA
 GGAATGAATG TGCCAACCTC AATTACGTTA GAGAACTTAA ATTCAACACC AACTGCTACC
 TTCCGAACTA AATTGTTTGG GGCTGAAAAT GGTCAAGTGA AAGAAGCCAT TAATAAATAT
 GAGCTATCTA TAAATACAAT TCCTACAAAA GAGATTAGAA TATTTTCAGC GGCCGATAAC
 AGTATTTCGCA CCGTTAAAGT AAATACAGAA TTAATTTTAG GAACATAATAT TTCTTCAAAC
 GATGAACAAA ATAGATCGGG CACTTTTATAC TTATTCAACA ATAAAAATGG TTCGATATCT
 TTAATCACTC CTAACACGCG TGGCAATGTT ACGGATGATC AAAAAGACGT TATGCTAGAA
 GTAATTCAA

EF044-4 (SEQ ID NO:164)

CSS QKANEPKKQE NSTNHTTSIK SSTNHYSSSI
 ETSSNNKLKE TSESASTTQT SSKSKNEVST NVEEANSLEA TPYAVDLSSL NNPLVFNFKG
 MNVPTSITL NLNSTPTATF RTKLFGAENG QVKEAINKYE LSINTIPTKE IRIFSAADNS
 IRTVKVNTL ILGTNISSND EQNRSGLTYL FNNKNGSISL ITPNYAGNVT DDQKDVMLEV
 IQ

EF045-1 (SEQ ID NO:165)

TAGCCAAAAA ATGAGGGAGG AAAAGAGATG AACAAGAAAC GGATTTTAGG TGCAATCACG
 TTAGCTTCTG TGTTAGTATT CGGGTTAGCT GCATGTGGTG GCGGCAATAA AGGCGGGGGC
 AATAAAGCAA CGGAAACAGA AGACATTTCA AAAATGCCAA TCGCTGTTAA AAATGATAAA
 AAAGCAATTG ATGGCGGTAC ATTAGATGTC GCTGTAGTTA TGGATACACA ATTCCAAGGA
 CTTTTCCAGC AAGAATTTTA TCAAGACAAC TATGATGCAC AATACATGCT TCCAACGGTA
 CAGCCATTAT TTAACAATGA TGCAGACTTT AAGATTGTCG ATGGGGGTCC TGCGGATCTG
 AAATTAGATG AAGATGCCAA TACAGCAACC ATTAAATTAC GTGACAATTT GAAATGGTCT
 GACGGTAAAG ATGTGACAGC CGATGACGTG ATTTTCTCTT ATGAAGTCAT TGGTCATAAA
 GACTATACAG GGATTCTGTTA TGATGATAAC TTTACGAATA TTGTTGGCAT GGAAGACTAC
 CATGATGGTA AATCGCCAAC CATTCTGTCG ATAGAAAAAG TCAATGATAA AGAAGTTAAA
 ATCACTTATA AAGAAGTTCA CCCAGGAATG CAACAATTAG GTGGCGGTGT TTGGGGCTCA
 GTTTTACCAA AACATGCCTT TGAAGGAATT GCTGTTAAAG ACATGGAATC AAGCGATGCA
 GTTCGTAAAA ACCCTGTGAC TATTGGACCA TACTACATGA GTAATATTGT GACAGGTGAA
 TCTGTTGAAT ACCTACCAA TGAGCATTAC TACGGTGGTA AACCTAAATT AGATAAATTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTGTTCAAAT CTGTTCCCTC TGCAGCATT GTAGAAGCGA TGAAAGCGAA ACAATACGAT
 ATTGCATTAT CAATGCCAAC AGATACGTAT CCAACATACA AAGATACTGA AGGGTATCAA
 ATCTTAGGAC GTCCCGAACA AGCCTACACG TATATTGGCT TTAAAAATGGG TACGTTTGAC
 AAAGAAACAA ATACAGTGAA ATACAATCCA AAAGCTAAAA TGGCAGATAA AAGCTTACGT
 CAAGCCATGG GCTATGCAAT TGACAATGAT GCAGTCGGCC AAAAATTCTA CAACGGCTTA
 CGAACAGGGG CAACAACGTT AATCCCACCA GTCTTCAAGA GCTTGCATGA TAGCGAAGCG
 AAAGGCTATA CGCTTGATTT AGACAAAGCG AAAAAATTAT TAGACGATGC TGGTTATAAA
 GACGTAGACG GCGATGGCAT TCGCGAAGAC AAAGAAGGCA AACCCTAGA AATCAAGTTT
 GCTTCAATGT CAGGCGGCGA AACTGCACAA CCACCTGCTG ATTACTATGT CCAACAATGG
 AAAGAAATTG GCTTAAACGT AACGTATACA ACAGGACGCT TAATTGATTT CCAAGCATTC
 TATGATAAAT TGAAAAATGA TGACCCAGAA GTAGATATCT ATCAAGGCGC GTGGGGCACA
 GGTTACAGATC CTTACCAAC CGGCTTATAT GGTCCAACT CAGCCTTTAA CTATACACGT
 TTTGAGTCAG AAGAAAAATC TAAATTACTT GATGCGATTG ATTCAAAGC ATCATTGAT
 GAAGAAAAAC GTAAAAAGC CTTCTACGAT TGGCAAGAGT ATGCCATTGA TGAAGCGTTT
 GTAATCCCAA CGCTTTACAG AAATGAAGTC TTGCCGTGCA ACGACCGTGT AGTTGACTTT
 ACTTGGGCAG TTGATACGAA AGATAATCCA TGGGCAACGG TGGGTGTCAC AGCAGACTCA
 CGGAAATAA

EF045-2 (SEQ ID NO:166)

MN KKRILGAIL ASVLVFLA CCGGNKGGN KATETEDISK MPIAVKNDKK
 AIDGGTLDVA VMDTQFQGL FQQEFYQDNY DAQYMLPTVQ PLFNNDADFK IVDGGPADLK
 LDEDANTATI KLRDNLKWSG GKDVTADDVI FSYEVIGHKD YTGIRYDDNF TNIVGMEDYH
 DGKSPITISGI EKVNDKEVKI TYKEVHPGMQ QLGGGVWGSV LPKHAFEGIA VKDMESSDAV
 RKNPVITIGPY YMSNIVTGES VEYLPNEHYG GKGPKLDKLV FKSVPASIV EAMKAKQYDI
 ALSMPTDTYP TYKDTGYQI LGRPEQAYTY IGFKMGTFDK ETNTVKYNPK AKMADKSLRQ
 AMGYAIDNDA VGQKFYNGLR TGATTLIPPV FKSLHDSEAK GYTLDLKAK KLLDDAGYKD
 VDGDGIREDK EGKPLEIKFA SMSGGETAQP LADYVYQWK EIGLNVYTTT GRLIDFQAFY
 DKLKNDDPEV DIYQGAWGTG SDPSPTGLYG PNSAFNYTRF ESEENTKLLD AIDSASFDE
 EKRKKAIFYDW QEYAIDEAFV IPTLYRNEVL PVNDRVVDFT WAVDTKDNPW ATVGVTADSR
 K

EF045-3 (SEQ ID NO:167)

ATGTGGTG GCGGCAATAA AGGCGGGGGC
 AATAAGCAA CGGAAACAGA AGACATTTCA AAAATGCCAA TCGCTGTAA AAATGATAAA
 AAAGCAATTG ATGGCGGTAC ATTAGATGTC GCTGTAGTTA TGGATACACA ATTCCAAGGA
 CTTTTCCAGC AAGAATTTTA TCAAGACAAC TATGATGCAC AATACATGCT TCCAACGGTA
 CAGCCATTAT TTAACAATGA TGCAGACTTT AAGATTGTCG ATGGGGGTCC TCGGATCTG
 AAATTAGATG AAGATGCCAA TACAGCAACC ATTAAATTAC GTGACAATTT GAAATGGTCT
 GACGGTAAAG ATGTGACAGC CGATGACGTG ATTTTCTCTT ATGAAGTCAT TGGTCATAAA
 GACTATACAG GGATTCGTTA TGATGATAAC TTTACGAATA TTGTTGGCAT GGAAGACTAC
 CATGATGGTA AATCGCCAAC CATTTCTGGC ATAGAAAAAG TCAATGATAA AGAAGTTAAA
 ATCACTTATA AAGAAGTTCA CCCAGGAATG CAACAATTAG GTGGCGGTGT TTGGGGCTCA
 GTTTTACCAA AACATGCCTT TGAAGGAATT GCTGTTAAAG ACATGGAATC AAGCGATGCA
 GTTCGTAAAA ACCCTGTGAC TATTGGACCA TACTACATGA GTAATATTGT GACAGGTGAA
 TCTGTTGAAT ACCTACCAA TGAGCATTAC TACGGTGGTA AACCTAAATT AGATAAATTA
 GTGTTCAAAT CTGTTCCCTC TGCAGCATT GTAGAAGCGA TGAAAGCGAA ACAATACGAT
 ATTGCATTAT CAATGCCAAC AGATACGTAT CCAACATACA AAGATACTGA AGGGTATCAA
 ATCTTAGGAC GTCCCGAACA AGCCTACACG TATATTGGCT TTAAAAATGGG TACGTTTGAC
 AAAGAAACAA ATACAGTGAA ATACAATCCA AAAGCTAAAA TGGCAGATAA AAGCTTACGT
 CAAGCCATGG GCTATGCAAT TGACAATGAT GCAGTCGGCC AAAAATTCTA CAACGGCTTA
 CGAACAGGGG CAACAACGTT AATCCCACCA GTCTTCAAGA GCTTGCATGA TAGCGAAGCG
 AAAGGCTATA CGCTTGATTT AGACAAAGCG AAAAAATTAT TAGACGATGC TGGTTATAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GACGTAGACG GCGATGGCAT TCGCGAAGAC AAAGAAGGCA AACCCTAGA AATCAAGTTT
 GCTTCAATGT CAGGCGGCGA AACTGCACAA CCACTTGCTG ATTACTATGT CCAACAATGG
 AAAGAAATTG GCTTAAACGT AACGTATACA ACAGGACGCT TAATTGATTT CCAAGCATTC
 TATGATAAAT TGAAAAATGA TGACCCAGAA GTAGATATCT ATCAAGGCGC GTGGGGCACA
 GGTTTCAGATC CTTACCAAC CGGCTTATAT GGTCCAACT CAGCCTTTAA CTATACACGT
 TTTGAGTCAG AAGAAAATAC TAAATTACTT GATGCGATTG ATTCAAAAGC ATCATTTGAT
 GAAGAAAAAC GTAAAAAGC CTTCTACGAT TGGCAAGAGT ATGCCATTGA TGAAGCGTTT
 GTAATCCCAA CGCTTTACAG AAATGAAGTC TTGCCTGTCA ACGACCGTGT AGTTGACTTT
 ACTTGGGCAG TTGATACGAA AGATAATCCA TGGGCAACGG TGGGTGTCAC AGCAGACTCA
 CGGAAA

EF045-4 (SEQ ID NO:168)

CGGGNKGGGN KATETEDISK MPIAVKNDKK
 AIDGGTLDA VMDTQFQGL FQQEFYQDNY DAQYMLPTVQ PLFNNDADFK IVDGGPADLK
 LDEDANTATI KLRDNLKWSG GKDVTTADDVI FSYEVIGHKD YTGIRYDDNF TNIVGMEDYH
 DGKSPITISGI EKVNDEKVKI TYKEVHPGMQ QLGGGVWGSV LPKHAFEGIA VKDMESSDAV
 RKNPVTIGPY YMSNIVTGES VEYLPNEHYH GGKPKLDKLV FKSVPASIV EAMKAKQYDI
 ALSMPTDTYP TYKDTEGYQI LGRPEQAYTY IGFKMGTFDK ETNTVKYNPK AKMADKSLRQ
 AMGYAIDNDA VGQKFYNGLR TGATTLIPPV FKSLHDSEAK GYTLDLDKAK KLLDDAGYKD
 VDGDIREDK EGKPLEIKFA SMSGGETAQP LADYYVQQWK EIGLNVYTTT GRLIDFQAFY
 DKLKNDDEPV DIYQGAWGTG SDPSPTGLYG PNSAFNYTRF ESEENTKLLD AIDSKASFDE
 EKRRKAFYDW QEYAIDEAFV IPTLYRNEVL PVNDRVVDFT WAVDTKDNPW ATVGVTADSR
 K

EF046-1 (SEQ ID NO:169)

TAGGAGGATA TAATGAAAAA AAAACTTATT GTACTATTGT TAGCCTTATT TTTAACGGCA
 TGTAAGTAATA ATACTGGGGG AAAAAATAGC GACGCTTCAT CTACTGAAGT ATCAACTAAG
 CAGCAAACTA CCCAGTCTTC TAAAAAGAT AGTAGTAATC CGGACACAAC ACCAACTTCT
 ACATCATCTA TAACAATTGA AACAACCGAG AATTTAAAGA ATAGAGAATT GAATCCAACA
 GATGATGTTT CAAAAACTAG ACGACAATTG TATGAACAAG GAATTAACAG TTCAACAATT
 ACGGATAAAG AACTAAAGGA ATATATATCA GAGGCTAAAG AACAAAAGAA AGATGTCATT
 AATTATATTA AGCAAAAA

EF046-2 (SEQ ID NO:170)

MKKKLIV LLLALFLTAC SNNTGGKNSD ASSTEVSTKQ QTTQSSKKDS SNPDTTPTST
 SSITIIETTEN LKNRELNPTD DVSKTRRQLY EQGINSSTIT DKELKEYISE AKEQKKDVIN
 YIKQK

EF046-3 (SEQ ID NO:171)

A
 TGTAAGTAATA ATACTGGGGG AAAAAATAGC GACGCTTCAT CTACTGAAGT ATCAACTAAG
 CAGCAAACTA CCCAGTCTTC TAAAAAGAT AGTAGTAATC CGGACACAAC ACCAACTTCT
 ACATCATCTA TAACAATTGA AACAACCGAG AATTTAAAGA ATAGAGAATT GAATCCAACA
 GATGATGTTT CAAAAACTAG ACGACAATTG TATGAACAAG GAATTAACAG TTCAACAATT
 ACGGATAAAG AACTAAAGGA ATATATATCA GAGGCTAAAG AACAAAAGAA AGATGTCATT
 AATTATATTA AGCAAAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF046-4 (SEQ ID NO:172)

C SNNTGGKNSD ASSTEVSTKQ QTTQSSKKDS SNPDTPPTST
 SSITTIETTEN LKNRELNPTD DVSKTRRQLY EQGINSSTIT DKELKEYISE AKEQKKDVIN
 YIKQK

EF047-1 (SEQ ID NO:173)

TAGGGAAAAC AAGGAGGAAT TCTTATGAAA AAGATAGGGC TTATTTCTAG TGCTTTTCTT
 TTAACCCTTG CTTTAGCAGC ATGCGGCGGC GGAAAAAGTA CAGAAAATAC GGATAGTCGT
 TCCAGTGCTG CGGAAAGTAC CACAGTCGAG AGTACAAAAG CATCTGCTAC AAAAGAATCA
 AGTAGCAAAG CAACAACAAA ATCTAGTGAT GCGAAACCGT CAGGAACAAC AACAGCTGAT
 TCGAAAGCAA CAGCTTCTTC TACGAAGGAA GCGGCAAATA ATGGCTCAGC AGAGAAGCAA
 TCACCAGCGA AAAATGCGAA TCCAGATGAC CAAGCCAACC AAGTGCTTAA CCAGCTAGCA
 AACATGTTTC CTGGTCAAGG CTTACCGCAG GCAATTTTAA CGAGTCAAAC GAATAACTTT
 TTAAGTGCAG CGACAACCTC ACAAGCGGAT CAAAACAATT TCCGTGTTTT ATATTATGCA
 GAAAAAGAAG CGATTCCAGT GAATGATGCA CGTGTCATC AGTTAACGCC AATTAGTTCT
 TTTGAGAAAA AAACATATGG CTCTGATGCC GAAGCAAAAA ATGCAGTGAA CCAAATCATT
 GACAATGGCG GTCAACCACT AGATTTAGGT TACAATATTA CTGGGTATAA ACAAGGGGCG
 GCAGGTTCTA GTTACTTATC TTGGCAAGAA GGCAATTGGA GTTTAGTCGT ACGGGCCTCA
 AATATCAATG GTGAATCGCC TGATGATTTA GCGAAAAATG TTGTCAACAT TTTGGAACAA
 GAAACATTAC CAGCACCGAA TACCGTTGGT CAAATCACAC TGAACGTGGC AGGAACCACT
 GACTATAATC GAAACTCAGT AGTTTGGCAA GCCGGTACAG TCGTTTACTC TGTCCATCAT
 TTTGACCCAA TTCAAGCAGT GAAGATGGCA ACATCAATGT AA

EF047-2 (SEQ ID NO:174)

MKK IGLISSAFLL TLALAACGGG KSTENTDSRS SAAESTTVES TKASATKES
 SKATTKSSDA KPSGTTTTADS KATASSTKEA ANNGSAEKQS PAKNANPDDQ ANQVLNQLAN
 MFPGQGLPQA ILTSQTNNFL TAATTSQADQ NNFRVLYAE KEAIPVNDAR VNQLTPISSE
 EKKTYGSDAE AKNAVNIID NGGQPVDLGY NITGYKQGA GSSYLSWQEG NWSLVVRASN
 INGESPDDL A KNVVNILEQE TLPAPNTVGQ ITLNVAGTTD YNRNSVVWQA GTVVYSVHHF
 DPIQAVKMAT SM

EF047-3 (SEQ ID NO:175)

ATGCGGCGGC GGAAAAAGTA CAGAAAATAC GGATAGTCGT
 TCCAGTGCTG CGGAAAGTAC CACAGTCGAG AGTACAAAAG CATCTGCTAC AAAAGAATCA
 AGTAGCAAAG CAACAACAAA ATCTAGTGAT GCGAAACCGT CAGGAACAAC AACAGCTGAT
 TCGAAAGCAA CAGCTTCTTC TACGAAGGAA GCGGCAAATA ATGGCTCAGC AGAGAAGCAA
 TCACCAGCGA AAAATGCGAA TCCAGATGAC CAAGCCAACC AAGTGCTTAA CCAGCTAGCA
 AACATGTTTC CTGGTCAAGG CTTACCGCAG GCAATTTTAA CGAGTCAAAC GAATAACTTT
 TTAAGTGCAG CGACAACCTC ACAAGCGGAT CAAAACAATT TCCGTGTTTT ATATTATGCA
 GAAAAAGAAG CGATTCCAGT GAATGATGCA CGTGTCATC AGTTAACGCC AATTAGTTCT
 TTTGAGAAAA AAACATATGG CTCTGATGCC GAAGCAAAAA ATGCAGTGAA CCAAATCATT
 GACAATGGCG GTCAACCACT AGATTTAGGT TACAATATTA CTGGGTATAA ACAAGGGGCG
 GCAGGTTCTA GTTACTTATC TTGGCAAGAA GGCAATTGGA GTTTAGTCGT ACGGGCCTCA
 AATATCAATG GTGAATCGCC TGATGATTTA GCGAAAAATG TTGTCAACAT TTTGGAACAA
 GAAACATTAC CAGCACCGAA TACCGTTGGT CAAATCACAC TGAACGTGGC AGGAACCACT
 GACTATAATC GAAACTCAGT AGTTTGGCAA GCCGGTACAG TCGTTTACTC TGTCCATCAT
 TTTGACCCAA TTCAAGCAGT GAAGATGGCA ACATCAATGT AA

EF047-4 (SEQ ID NO:176)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CGGG KSTENTDSRS SAAESTTVES TKASATKES

SKATTKSSDA KPSGTTTADS KATASSTKEA ANNGSAEKQS PAKNANPDDQ ANQVLNQLAN
 MFPQGGLPQA ILTSQTNNFL TAATTSQADQ NNFRVLYYAE KEAIPVNDAR VNQLTPISSF
 EKKTYGSDAE AKNAVNQIID NGGQPVDLGY NITGYKQGAA GSSYLSWQEG NWSLVVRASN
 INGESPDDLA KNVVNILEQE TLPAPNTVGQ ITLNVAGTTD YNRNSVWVQA GTVVYSVHHF
 DPIQAVKMAT SM

EF048-1 (SEQ ID NO:177)

TAAGGAGAAA AGTTCATGAA AAAAAGAAAG GTTTTATTTA CAGCAGTTAT GGTATTGGCA
 GGATTACAGT TGCTAAGTGG TTGCGGCAAA ACAGAAGCTT CGGCAAATGA TACGGTAGTC
 TTGCGCTATG CGTATGCTAG TAATAGCCAA CCAGTTATCG ATTCTATGAA GAAATTCGGT
 GAATTAGTAG AGGAAAAAAC AGATGGTAAA GTTCAAATG AATATTTTCC AGATGGTCAA
 TTAGGAGGAG AAACAGAACT AATTGAATTA ACACAAACAG GTGCAATTGA TTTTGCAAAG
 GTCAGTGGAT CAGCATTAGA AAGTTTTTCT AAAGATTATT CTGTATTGTC CATTCCGTAT
 ATTTTTGATA ATGAAAAACA TTTTTTTAAA GTAATGGATA ATCAAGCGCT AATGCAACCA
 GTGTATGATT CTACAAAAAA ATTAGGATTT GTTGGTTTAA CTTATTATGA CTCTGGTCAA
 CGAAGTTTTT ATATGAGCAA AGGGCCTGTT ACATCTCCAG ATGATTGAA AGGTAAAAAA
 ATTCGGGTCA TGCAAAGTGA AACCGCCATC AAAATGGTAG AACTTTTAGG GGGTTCGCCA
 GTACCTATGG GTAGTTCGGA AGTATATACT TCTCTACAAT CTAATCTAAT CAACGGTGCA
 GAGAATAATG AGTTCGTTTT ATATACAGCT GGTCATGGTG GTGTGGCTAA GTATTATTCT
 TATGATGAGC ATACTCGAGT GCCAGATATT GTGATTATGA ACGAGGGAAC AAAAGAACGT
 TTGACAGCGA AACAAGAACA AGCGATTGAA GAAGCAGCAA AAGAATCGAC CGCTTTTGAA
 AAAACGGTCT TTAAAGAAGC GGTGAAGAA GAAAAGAAAA AAGCACAAGC AGAATATGGC
 GTTGTGTTCA ATCAAGTAGA CAGTGAACCA TTCCAAAAAC TTGTTCAACC GTTGCATGAA
 TCATTCAAAA ATAGCTCAGA ACATGGCGAA CTGTATCAGG CTATTCGCCA GTTGGCGGAC
 TAA

EF048-2 (SEQ ID NO:178)

MKKRKV LFTAVMVLG LQLLSGCGKT EASANDTVVL RYAYASNSQP VIDSMKKFGE
 LVEEKTGKQV QIEYFPDQQL GGETELIELT QTGAIDFAKV SGSALSFPSK DYSVFAIPYI
 FDNEKHFFKV MDNQALMQPV YDSTKKLGFV GLTYYDSGQR SFYMSKGPVT SPDDLKGGKI
 RVMQSETAIK MVELLGGSPV PMGSSEVYTS LQSNLINGAE NNEFVLYTAG HGGVAKYYSY
 DEHTRVPDIV IMNEGTKERL TAKQEQAIEE AAKESTAFEG TVFKEAVEEE KKKAQAEYGV
 VFNQVDSEPF QKLVPPLHES FKNSSHEGEL YQAIRQLAD

EF048-3 (SEQ ID NO:179)

TTGCGGCAAA ACAGAAGCTT CGGCAAATGA TACGGTAGTC
 TTGCGCTATG CGTATGCTAG TAATAGCCAA CCAGTTATCG ATTCTATGAA GAAATTCGGT
 GAATTAGTAG AGGAAAAAAC AGATGGTAAA GTTCAAATG AATATTTTCC AGATGGTCAA
 TTAGGAGGAG AAACAGAACT AATTGAATTA ACACAAACAG GTGCAATTGA TTTTGCAAAG
 GTCAGTGGAT CAGCATTAGA AAGTTTTTCT AAAGATTATT CTGTATTGTC CATTCCGTAT
 ATTTTTGATA ATGAAAAACA TTTTTTTAAA GTAATGGATA ATCAAGCGCT AATGCAACCA
 GTGTATGATT CTACAAAAAA ATTAGGATTT GTTGGTTTAA CTTATTATGA CTCTGGTCAA
 CGAAGTTTTT ATATGAGCAA AGGGCCTGTT ACATCTCCAG ATGATTGAA AGGTAAAAAA
 ATTCGGGTCA TGCAAAGTGA AACCGCCATC AAAATGGTAG AACTTTTAGG GGGTTCGCCA
 GTACCTATGG GTAGTTCGGA AGTATATACT TCTCTACAAT CTAATCTAAT CAACGGTGCA
 GAGAATAATG AGTTCGTTTT ATATACAGCT GGTCATGGTG GTGTGGCTAA GTATTATTCT
 TATGATGAGC ATACTCGAGT GCCAGATATT GTGATTATGA ACGAGGGAAC AAAAGAACGT
 TTGACAGCGA AACAAGAACA AGCGATTGAA GAAGCAGCAA AAGAATCGAC CGCTTTTGAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAACGGTCT TTAAGAAGC GGTGAAGAA GAAAAGAAA AAGCACAAGC AGAATATGGC
 GTTGTGTTCA ATCAAGTAGA CAGTGAACCA TTCCAAAAAC TTGTTCAACC GTTGCATGAA
 TCATTCAAAA ATAGCTCAGA ACATGGCGAA CTGTATCAGG CTATTGCCA GTTGGCGGAC
 TAA

EF048-4 (SEQ ID NO:180)

CGKT EASANDTVVL RYAYASNSQP VIDSMKKFGE
 LVEEKTGDKV QIEYFPDGL GGETELIELT QTGAIDFAKV SGSALSFESK DYSVFAIPYI
 FDNEKHFFKV MDNQALMQPV YDSTKKLGFV GLTYYDSGQR SFYMSKGPVT SPDDLKGGKI
 RVMQSETAIK MVELLGGSPV PMGSSEVYTS LQSNLINGAE NNEFVLYTAG HGGVAKYYSY
 DEHTRVPDIV IMNEGTKERL TAKQEQAIEE AAKESTAF EK TVFKEAVEEE KKKAQAEYGV
 VFNQVDSEPF QKLVPPLHES FKNSSEHGEL YQAIRQLAD

EF049-1 (SEQ ID NO:181)

TGAGACTCTT TCTTTTTCAA AATGAGGTAT GGTATAGTTA TAACAGANAT AAAACTANAA
 AAAACAGGAG TGCATAAGAG AATGAAGAAA AACTAATCT TAGCTGCAGC GGGCGCAATG
 GCCGTTTTTC GTTTAGCAGC GTGTTCAAGC GGTTCAAAAG ATATCGCAAC AATGAAAGGT
 TCAACAATTA CTGTTGATGA TTTTATAAAC CAAATTAAAG AACAAAGCAC TAGCCAACAA
 GCGTTTAGCC AAATGGTTAT TTATAAAGTC TTTGAAGAAA AATATGGCGA CAAAGTAACT
 GACAAAGANA TTCAAAAAAA CTTTGACGAA GCCAAAGAAC AAGTAGAAGC ACAAGGCGGA
 AAGTTCTCTG ATGCATTAAA ACAAGCTGGT TTAAGTAAA AAACATTCAA GAAACAGTTA
 AAACAAAGAG CAGCCTATGA TGCAGGTCTA AAAGCCCACT TAAAAATTAC AGATGAAGAC
 TTAACAAACAG CTTGGGCAAG TTTCCATCCA GAAGTAGAAG CACAAATTAT CCAAGTTGCT
 TCAGAAGATG ATGCCAAAGC TGCAAGAAA GAAATCACTG ACGGCGGCGA TTTCACAAAA
 ATTGCTAAAG AAAAATCAAC AGATACTGCT ACGAAAAAAG ATGGCGGTAA AATTAAATTT
 GATTCAAG CAACAACCTGT TCCTGCCGAA GTTAAAGAAG CTGCCTTCAA ATTAAAGAT
 GGCGAAGTGT CAGAACCAAT TGCTGCAACA AATATGCAAA CCTACCAAAAC AACCTACTAT
 GTAGTGAAAA TGACGAAAAA CAAAGCAAAA GGCAATGACA TGAACCTTA TGAAGAGAG
 ATCAAGAAAA TTGTGAAGA AACAAAATTA GCCGATCAA CATTGTGTTT GAAAGTCATT
 AGTGACGAAT TAAAGCGGC CAATGTGAAA ATTAAAGATG ATGCCTTCAA GAACGCTTTA
 GCAGGCTACA TGCAAACTGA ATCTTCAAGC GCTTCTTCAG AGAAAAAGA ATCAAAATCA
 AGTGATTCTA AAACAAGCGA TACCAAAACA AGCGACTCTG AAAAAGCAAC AGATTCTTCA
 AGCAAAACAA CAGAACTCTT TTCTAAATAA

EF049-2 (SEQ ID NO:182)

MKKK LILAAAGAMA VFSLAACSSG SKDIATMKGS
 TITVDDFYNQ IKEQSTSQA FSQMVIYKFV EEKYGDKVTD KXIQKNFDEA KEQVEAQGGK
 FSDALKQAGL TEKTFKKQLK QRAAYDAGLK AHLKITDEDL KTAWASFHPE VEAQIIQVAS
 EDDAKAVKKE ITDGGDFTKI AKEKSTDAT KKGKIKFD SQATTVP AEV KEAAFKLKDG
 EVSEPIAATN MQTYQTTYV VKMTKNKAKG NDMKPYEKEI KKIAEETKLA DQTFVSKVIS
 DELKAANVKI KDDAFKNALA GYMQTESSA SSEKKESKSS DSKTSDTKTS DSEKATDSSS
 KTTESSSK

EF049-3 (SEQ ID NO:183)

GTGTTCAAGC GGTTCAAAAG ATATCGCAAC AATGAAAGGT
 TCAACAATTA CTGTTGATGA TTTTATAAAC CAAATTAAAG AACAAAGCAC TAGCCAACAA
 GCGTTTAGCC AAATGGTTAT TTATAAAGTC TTTGAAGAAA AATATGGCGA CAAAGTAACT
 GACAAAGANA TTCAAAAAAA CTTTGACGAA GCCAAAGAAC AAGTAGAAGC ACAAGGCGGA
 AAGTTCTCTG ATGCATTAAA ACAAGCTGGT TTAAGTAAA AAACATTCAA GAAACAGTTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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AAACAAAGAG CAGCCTATGA TGCAGGTCTA AAAGCCCACT TAAAAATTAC AGATGAAGAC
TTAAAAACAG CTTGGGCAAG TTTCCATCCA GAAGTAGAAG CACAAATTAT CCAAGTTGCT
TCAGAAGATG ATGCCAAAGC TGTCAAGAAA GAAATCAC TG ACGGCGGCGA TTTCACAAAA
ATTGCTAAAG AAAAATCAAC AGATACTGCT ACGAAAAAAG ATGGCGGTAA AATTAAATTT
GATTACAAAG CAACAACGTG TCCTGCCGAA GTTAAAGAAG CTGCCTTCAA ATTAAAAGAT
GGCGAAGTGT CAGAACCAAT TGCTGCAACA AATATGCAAA CCTACCAAAC AACCTACTAT
GTAGTGAAAA TGACGAAAAA CAAAGCAAAA GGCAATGACA TGAAACCTTA TGAAAAAGAG
ATCAAGAAAA TTGCTGAAGA AACAAAATTA GCCGATCAAA CATTTGTTTC GAAAGTCATT
AGTGACGAAT TTTAAGCGGC CAATGTGAAA ATTAAAGATG ATGCCTTCAA GAACGCTTTA
GCAGGCTACA TGCAAACTGA ATCTTCAAGC GCTTCTTCAG AGAAAAAGA ATCAAAATCA
AGTGATTCTA AAACAAGCGA TACCAAAACA AGCGACTCTG AAAAAGCAAC AGATTCTTCA
AGCAAAACAA CAGAATCTTC TTCTAAATAA

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EF049-4 (SEQ ID NO:184)

CSSG SKDIATMKGS

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TITVDDFYNG IKEQSTSQQA FSQMVYKVF EEKYGDKVTD KXIQKNFDEA KEQVEAQGGK
FSDALKQAGL TEKTFKKQLK QRAAYDAGLK AHLKITDEDL KTAWASFHPE VEAQIIQVAS
EDDAKAVKKE ITDGGDFTKI AKEKSTDAT KKDGGKIKFD SQATTVPAEV KEAAFKLKD G
EVSEPIAATN MQTYQTTYV VKMTKNKAKG NDMKPYEKI KKIAEETKLA DQTFVSKVIS
DELKAANVKI KDDAFKNALA GYMQTESSA SSEKKESKSS DSKTSDTKTS DSEKATDSSS
KTTESSSK

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EF050-1 (SEQ ID NO:185)

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TAGGGTCTGG AAAAGCAGTC AACTGACTTC TTTTCCAAGC CCTTTTTTAG TTCATCGCAG
AAAGGATGNA AAAAAATGAA CATGCCCAAA AATATCNGTT ATTTTCTTTT GCTAATGGGT
CTGTCTCTAT TATTAAGTGC TTGCCAAATT GGGGCAACTA CGAAGGATGA CAACCAAGCC
GCCACAAAAG AAGCAACTGT TGAGTTAAAC CGCACACAA CACCAACGCT TTTTTTTCAT
GGTTACGCAG GAATAAAAA TTCGTTTGGC TCGTTACTGC ATCGCTTGA GAAACAAGGT
GCCACAAC TC AAGAATTAGT GCTACTCGTT AAACCTGATG GGACCGTGGT TAAAGAGCGA
GGAGCTTTAA GTGGCAAAGC GACGAATCCC AGTGTTCAAG TTCTATTTGA AGATAATAAA
AACAAATGAAT GGAATCAAAC AGAATGGATA AAAACACAT TACTCTATTT ACAAAAAAAT
TATCAAGTGA ACAAAGCCAA TATTGTCTGG CACTCTATGG GTGGTGTTAG TGGTTTACGT
TATTTAGGAA CCTATGGGCA AGATACATCG TTACCTAAAA TTGAAAAATT CGTCAGCATT
GGAGCACCTT TCAATGATTT TATTGATACG AGTCAACAGC AAACCATCGA AACGGAAC TA
GAAAACGGCC CCACAGAAAA AAGTAGCCGC TATTTGGATT ATCAAGAGAT GATTAATGTT
GTTCAGAAA AACTGCCCAT TTTATTAATT GGTGGTCAAT TAAGTCCAAC AGATTTAAGT
GATGGAACGG TGCCGTTATC TAGTGCCTTA GCAGTCAACG CCTTGCTAAG ACAGCGAGGA
ACTCAAGTCA CTAGCCAGAT TATTAAAGGA GAAAATGCAC AACATAGTCA ATTACATGAA
AATCCTGAAG TAGATCAATT GCTAATCGAA TTTCTATGGC CGAGTAAAAA ATAG

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EF050-2 (SEQ ID NO:186)

MNMPKN IXYSLLMGL VLLSACQIG ATTKDDNQAA

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TKEATVELNR TTTPTLFFHG YAGTKNSFGS LLHRLEKQGA TTQELVLLVK PDGTVVKERG
ALSGKATNPS VQVLFEDNKN NEWNQTEWIK NTLlyLQKNY QVNKANIVGH SMGGVSGRLY
LGTYGQDTSI PKIEKFVSIG APFNDFIDTS QQTIETELE NGPTEKSSRY LDYQEMINVV
PEKLPILLIG QLSPTDLSD GTVPLSSALA VNALLRQRGT QVTSQIIKGE NAQHSQ LHEN
PEVDQLLIEF LWPSKK

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EF050-3 (SEQ ID NO:187)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTGCCAAATT GGGGCAACTA CGAAGGATGA CAACCAAGCC
 GCCACAAAAG AAGCAACTGT TGAGTTAAAC CGCACAACAA CACCAACGCT TTTTTCAT
 GGTACGCAG GAACTAAAAA TTCGTTTGGC TCGTTACTGC ATCGCTTGGA GAAACAAGGT
 GCCACAACCTC AAGAATTAGT GCTACTCGTT AAACCTGATG GGACCGTGGT TAAAGAGCGA
 GGAGCTTTAA GTGGCAAAGC GACGAATCCC AGTGTTCAG TTCTATTGTA AGATAATAAA
 AACAAATGAAT GGAATCAAAC AGAATGGATA AAAACACAT TACTCTATTT ACAAAAAAAT
 TATCAAGTGA ACAAAGCCAA TATTGTCGGG CACTCTATGG GTGGTGTTAG TGGTTTACGT
 TATTTAGGAA CCTATGGGCA AGATACATCG TTACCTAAAA TTGAAAAATT CGTCAGCATT
 GGAGCACCTT TCAATGATTT TATTGATACG AGTCAACAGC AAACCATCGA AACGGAACCTA
 GAAAACGGCC CCACAGAAAA AAGTAGCCGC TATTTGGATT ATCAAGAGAT GATTAATGTT
 GTTCCAGAAA AACTGCCCAT TTTATTAATT GGTGGTCAAT TAAGTCCAAC AGATTTAAGT
 GATGGAACGG TGCCGTTATC TAGTGCCTTA GCAGTCAACG CCTTGCTAAG ACAGCGAGGA
 ACTCAAGTCA CTAGCCAGAT TATTAAAGGA GAAAATGCAC AACATAGTCA ATTACATGAA
 AATCCTGAAG TAGATCAATT GCTAATCGAA TTTCTATGGC CGAGTAAAAA ATAG

EF050-4 (SEQ ID NO:188)

CQIG ATTKDDNQAA

TKEATVELNR TTTPTLFFHG YAGTKNSFGS LLHRLEKQGA TTQELVLLVK PDGTVVKERG
 ALSGKATNPS VQVLFEDNKN NEWNQTEWIK NTLLYLQKNY QVKNANIVGH SMGGVSGRLRY
 LGTYGQDTSI PKIEKFVSIG APFNDFIDTS QQQTIELE NGPTEKSSRY LDYQEMINVV
 PEKLPILLIG GQLSPTDLSD GTVPLSSALA VNALLRQRGT QVTSQIIKGE NAQHSQLEHN
 PEVDQLLIEF LWPSKK

EF051-1 (SEQ ID NO:189)

TAAAAAGAAA GAGGCGTTCA AATGTCTAAA CAAAAAAGG CTGTGTTCTT GCTTAGTTTA
 TTCAGTTTAG TTGCCCTAAT TGCTGCATGT ACAAATCAGC CGCAAAAAGA AACAGTTTCA
 ACAAAAAAAG AAGAAATAAC CCTTGCGGCA GCAGCTAGCT TAGAATCAGT CATGGAGAAG
 AAAATTATTC CAGCCTTTGA AAAAGAGCAT CCAGATATTC AGGTAACTGG AACCTATGAT
 AGTTCTGGAA AATTACAGAT GCAAATTGAA AAAGGCCTAA AAGCCGATGT ATTTTCTCTCA
 GCTTCGACAA AACAAATGAA TGCATTGGTT GCAGAAAAAC TAATTAATAA AAAAAGTGTC
 GTTCCTTTAT TGA AAAACCA GTCGTTCTT ATTGTGCCTA ACCAAGATCA AGCAAAGTGG
 CATGATTTTT CTGATTTTAA AAAAGCCCAA ATGATAGCAA TTGGTGATCC TGCAAGTGTT
 CCAGCTGGTC AATATGCCGA AGAAGGCTTA AAAGCTTTAG GCGCTTGGTC TTATGTAGAA
 AAACACGCAA GCTTTGGCAC GAATGTAACA GAAGTCCTTG AATGGGTAGC TAATGCAAGT
 GCAGAAGCTG GCTTAGTTTA TGCGACAGAT GCAGCAACCA ATTCAAAAGT AGCGATTGTT
 GCGGCCATGC CTGAAGCTGT TTTGAAAAAG CCAATTATCT ATCCAGTTGG TAAAGTTGCC
 GCCTCTAAGA AACAAAAATC AGCAGATGCT TTTTTAAATT TTTTACAGAG TCAACAATGC
 AGAAAAATATT TTGANAATAT TGGCTTTAAG TTAACAAAGT AG

EF051-2 (SEQ ID NO:190)

MSKQ KKAFLLSLF SLVALIACT NQPQKETVST KKEEITLAAA ASLESVMEKK
 IIPAFEKEHP DIQVTGYDYS SGKLQMIEK GLKADVFFSA STKQMNALVA EKLINKKSVV
 PLENQLVLI VPNDQAKWH DFSDLKKAQM IAIGDPASVP AGQYAEGLK ALGAWSYVEK
 HASFGTNVTE VLEWVANASA EAGLVYATDA ATNSKVAIVA AMPEAVLKKP IIPVGVKVA
 SKKQKSADAF LNFLQSQQCR KYFXNIGFKL TK

EF051-3 (SEQ ID NO:191)

ATGT ACAAATCAGC CGCAAAAAGA AACAGTTTCA
 ACAAAAAAAG AAGAAATAAC CCTTGCGGCA GCAGCTAGCT TAGAATCAGT CATGGAGAAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAATTATTC CAGCCTTTGA AAAAGAGCAT CCAGATATTC AGGTAAC TGG AACCTATGAT
 AGTTCTGGAA AATTACAGAT GCAAATTGAA AAAGGCCTAA AAGCCGATGT ATTTTCTCA
 GCTTCGACAA AACAAATGAA TGCATTGGTT GCAGAAAAC TAATTAATAA AAAAAGTGTC
 GTTCCTTTAT TGGAAAACCA GCTCGTTCTT ATTGTGCCTA ACCAAGATCA AGCAAAGTGG
 CATGATTTTT CTGATTTAAA AAAAGCCCAA ATGATAGCAA TTGGTGATCC TGCAAGTGTT
 CCAGCTGGTC AATATGCCGA AGAAGGCTTA AAAGCTTTAG GCGCTTGGTC TTATGTAGAA
 AAACACGCAA GCTTTGGCAC GAATGTAACA GAAGTCCTTG AATGGGTAGC TAATGCAAGT
 GCAGAAGCTG GCTTAGTTTA TGCGACAGAT GCAGCAACCA ATTCAAAAGT AGCGATTGTT
 GCGGCCATGC CTGAAGCTGT TTTGAAAAG CCAATTATCT ATCCAGTTGG TAAAGTTGCC
 GCCTCTAAGA AACAAAAATC AGCAGATGCT TTTTAAATTT TTTTACAGAG TCAACAATGC
 AGAAAATATT TTGANAATAT TGGCTTTAAG TTAACAAAGT AG

EF051-4 (SEQ ID NO:192)

CT NQPQKETVST KKEEITLAAA ASLESVMEKK
 IIPAFEKEHP DIQVTGYDYS SGKLQMQIEK GLKADVFFSA STKQMNALVA EKLINKKSVV
 PLENQLVLI VPNQDQAKWH DFSDLKKAQM IAIGDPASVP AGQYAEGLK ALGAWSYVEK
 HASFGTNVTE VLEWVANASA EAGLVYATDA ATNSKVAIVA AMPEAVLKKP IIPVGVKVA
 SKKQKSADAF LNFLQSQQR KYFXNIGFKL TK

EF052-1 (SEQ ID NO:193)

TAAAGTAGGA GAAGCGCAAG CGAAAAAAGT GAATCAATCG GCAGCGTATC AAGTAGTGAT
 CCCACAATGG GTACCATGGG TAGCATTATC TTTGACAGTA GCACTTGCTG GATTGATTGC
 TTACTTAGTT CGTCGTGGAG AGAAGTGGA AAACGAAGGG GAAGTGACAT AATGAGANGA
 NGAAATCTTC NGTTTTTATT ATTGTTGGTT CTATTAATTT ATATTCCTCA AACAACTTAT
 GCAGAAAAA GGGAGACCAC AGAAGTCGGA ATCGGGTTTA CAAAACTTC AGACATACCA
 TCAAAAAATA ATCCAGTTGT GAATGTATTG CCGCAAACAA CCATTCAATC GCTATCAATC
 GTTCGTAGCA GAACGCAAAT AAAAAGATTA CCTAAACTG GTGACAATCG AATAACTTGG
 CTAAGCTGGT TTGGCATATT GTTTTAAATA AGTAGTTTTT GGCTGTTTCT ATTTAGACAA
 TTATGTAGAA AAGGAGAATA A

EF052-2 (SEQ ID NO:194)

MRXX
 NLXFLLLLVL LIYIPQTTYA ENRETTEVGI GFTKTS DIPS KKNPVVNVLP QTTIQSL SIV
 RSRTQIKRLP KTGDNRITWL SWFGILFLIS SFWLFLRQL CRKGE

EF052-3 (SEQ ID NO:195)

AGAAAATA GGGAGACCAC AGAAGTCGGA ATCGGGTTTA CAAAACTTC AGACATACCA
 TCAAAAAA ATCCAGTTGT GAATGTATTG CCGCAAACAA CCATTCAATC GCTATCAATC
 GTTCGTAGCA GAACGCAAAT AAAAAGAT

EF052-4 (SEQ ID NO:196)

ENRETTEVGI GFTKTS DIPS KKNPVVNVLP QTTIQSL SIV
 RSRTQIKR

EF053-1 (SEQ ID NO:197)

TAGTCATGGC ACCATAACAA GGAGGAGAGA AGTGAGATGA AAAAATACCT TTTGCTTAGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TGTTTTTTAG GTCTTTTCAG CTTCTGTCAT TCAGACACTG CGTTTGGAGA AGCAGCTTAT
 GAAAATAGTG GTGTTGTCTC CTTTTATGGA ACGTATGAAT ATCCACAGA AGAGTCGACA
 ACAGCGACTA GTAATTCTTC CACAACGACC GAACCCACCA AGCCAGCTGA CGGAGGCGCT
 TCATCCGTCC TTTCTTCTGG CGTATATGGA TCGCGACAAG GAAGATTACC AGCGACAGGT
 ACCACCAATC AAGCACCATT TATTTATTG GGAATCAGCC TTATCACTAT AGGCATATTA
 TTTATTAAAA GGAGAAGAGA AGATGAAAAA AACAGTATTA GCAGTAGTAG GGATTGTAGG
 ATTTAG

EF053-2 (SEQ ID NO:198)

MKKYLLLS SC FLGLFSFCHS DTAFGEAAEY NSGVVSFYGT YEYPTEESTT
 ATSNSSTTTE PTKPADGGAS SVLSSGVYGS RQRLPATGT TNQAPFIYLG ISLITIGILF
 IKRRREDEKN SISSSRDCRI

EF053-3 (SEQ ID NO:199)

TTTGGAGA AGCAGCTTAT
 GAAAATAGTG GTGTTGTCTC CTTTTATGGA ACGTATGAAT ATCCACAGA AGAGTCGACA
 ACAGCGACTA GTAATTCTTC CACAACGACC GAACCCACCA AGCCAGCTGA CGGAGGCGCT
 TCATCCGTCC TTTCTTCTGG CGTATATGGA TCGCGACAAG GAAGA

EF053-4 (SEQ ID NO:200)

FGEAAEY NSGVVSFYGT YEYPTEESTT
 ATSNSSTTTE PTKPADGGAS SVLSSGVYGS RQGR

EF054-1 (SEQ ID NO:201)

TAAATAAAAA ATTATTTGGA GGAAATTACA ATGAAAAAAA TTATTTTATC AAGCTTGTTT
 AGTGCAGTAC TAGTATTCGG TGGCGGAAGT ATAACAGCAT TCGCTGACGA TTTAGGACCA
 ACAGATCCAG CAACTCCACC AATTACCGAA CCAACTGATT CTAGTGAACC TACGAATCCT
 ACTGAGCCGG TGGATCCTGC AGAACCGCCA GTAATACCAA CTGATCCAAC AGAACCAAGC
 AAGCCAACCG AGCCTACAAC ACCGAGTGAG CCAGAAAAGC CAACAGAACC AACAACGCCA
 ATTGATCCTG GAACGCCGGT TGAACCGACT GAACCAAGCG AGCCAACAGA ACCTAGTCAA
 CCAACCGAGC CTACAACACC AAGCGAACCA GAAAAACCTG TTA CTCCAGA ACAACCGAAA
 GAACCAACTC AACCAGTGAT TCCAGAAAAA CCAGCAGAAC CAGAAACACC AAAAACTCCT
 GAACAGCCCA CTAAACCAAT AGACGTAGTC GTTACACCTA GTGGAGAAAT TGATAAAACG
 AATCAATCGG CAGGAACACA ACCAAGTATT CCTATTGAAA CAAGCAACTT AGCGGAGGTA
 ACACATGTAC CAAGTGAAAC TACTCCAATT ACAACAGAAG CTGGGGAAGA AATTGTAGCA
 GTAGATAAAG GTGTTCCGTT AACCAAAACA CCAGAAGGAT TAAAAACCAAT TAGCAGCTCG
 TATAAGGTTT TACCTAGCGG AAACGTTGAG GTAAAAGCAA GTGATGGAAA AATGAAAGTA
 TTGCCACATA CAGGAGAGAA ATTCACACTC CTTTCTCTG TATTGGGAAG CTTCTTTGTA
 TTAATTTTCAG GATTCTTTTT CTTTAAAAAG AATAAGAAAA AAGCTTAA

EF054-2 (SEQ ID NO:202)

M KKIILSSLS AVLVFGGSI TAFADDLGPT DPATPPITEP TDSSEPTNPT
 EPVDPAEPPV IPTDPTPSK PTEPTTSEP EKPTPTPI DPGTPVEPTE PSEPTPSQP
 TEPPTPSEPE KPVTPPEPKP PTQVPIEKP AEPETPKTPE QPTKPIDVVV TPSGEIDKTN
 QSAGTQPSIP IETSNLAEVT HVPSETTPI TEGEEIVAV DKGVPILKTP EGLKPISSSY
 KVLPSGNVEV KASDGKMKVL PHTGEKFTLL FSVLGSFFVL ISGFFFFKKN KKKA

EF054-3 (SEQ ID NO:203)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

A

ACAGATCCAG CAACTCCACC AATTACCGAA CCAACTGATT CTAGTGAACC TACGAATCCT
 ACTGAGCCGG TGGATCCTGC AGAACCGCCA GTAATACCAA CTGATCCAAC AGAACCAAGC
 AAGCCAACCG AGCCTACAAC ACCGAGTGAG CCAGAAAAGC CAACAGAACC AACACGCCA
 ATTGATCCTG GAACGCCGGT TGAACCGACT GAACCAAGCG AGCCAACAGA ACCTAGTCAA
 CCAACCGAGC CTACAACACC AAGCGAACCA GAAAAACCTG TTACTIONCAGA ACAACCGAAA
 GAACCAACTC AACCAGTGAT TCCAGAAAAA CCAGCAGAAC CAGAAACACC AAAAACTCCT
 GAACAGCCCA CTAACCAAT AGACGTAGTC GTTACACCTA GTGGAGAAAT TGATAAAACG
 AATCAATCGG CAGGAACACA ACCAAGTATT CCTATTGAAA CAAGCAACTT AGCGGAGGTA
 ACACATGTAC CAAGTGAAAC TACTCCAATT ACAACAGAAG CTGGGGAAGA AATTGTAGCA
 GTAGATAAAG GTGTTCCGTT AACCAAAACA CCAGAAGGAT TAAAACCAAT TAGCAGCTCG
 TATAAGGTTT TACCTAGCGG AAACGTTGAG GTAAAAGCAA GTGATGGAAA AATGAAAGTA

T

EF054-4 (SEQ ID NO:204)

DDLGP DPATPPITEP TDSSEPTNPT
 EPVDPAPPPV IPTDPTEPSK PTEPTTPSEP EKPTEPTTPI DPGTPVEPTE PSEPTEPSQP
 TEPPTPSEPE KPVTPPEPKE PTQVPIPEKP AEPETPKTPE QPTKPIDVVV TPSGEIDKTN
 QSAGTQPSIP IETSNLAEVT HVPSETTPIT TEAGEEIVAV DKGVPLTKTP EGLKPISSSY
 KVLPSGNVEV KASDGKMKV

EF055-1 (SEQ ID NO:205)

TAACAAAAGG TTGTTTTGTC TTTCTTGTGT AAAAGGGCAA GAAAGGCTAG CGAGTTAAAA
 GGAGGTTTTT CAATGAAAAA AAAGCGTTAT TTAATGATTG TGTGTCTACT ATCTTCTCCT
 AGTTTTTTTA TAAATGTTGA AGCGTCTGAT GGTGGTTCTA GTTCGGTGGG GATTGAATTT
 TACCAAAATC CGAGAACACC CGCTCCTAAA GATCCCCAC CGAAAACAGA TGCGCCAGCT
 GCTGATCCCA AGGAACCAGC TGCTCCTCCG CAAGGAGATC AACGAAGTGG TGTTTCGACA
 CAGACCACCA CAACTGGCTC AACGCTCCCT CGTACAGGGA GCAAGAGTCA GGCAAATTTG
 AGCATTTCTN GNTTCGCCTT AATCGGTTTG GCGGGAATCG TACATAGAAA GAAGGGACGA
 CATGAAGCAA ACTAA

EF055-2 (SEQ ID NO:206)

MKKKRYL MIVCLLSSPS FFINVEASDG GSSSVGIEFY
 QNPRTPAPKD PPPKTDAPAA DPKEPAGPPQ GDQRSGGSTQ TTTTGSTLPR TGSKSQANLS
 ILXFALIGLA GIVHRKKGRH EAN

EF055-3 (SEQ ID NO:207)

AGCGTCTGAT GGTGGTTCTA GTTCGGTGGG GATTGAATTT
 TACCAAAATC CGAGAACACC CGCTCCTAAA GATCCCCAC CGAAAACAGA TGCGCCAGCT
 GCTGATCCCA AGGAACCAGC TGCTCCTCCG CAAGGAGATC AACGAAGTGG TGTTTCGACA
 CAGACCACCA CAACTGGCTC AACG

EF055-4 (SEQ ID NO:208)

SDG GSSSVGIEFY
 QNPRTPAPKD PPPKTDAPAA DPKEPAGPPQ GDQRSGGSTQ TTTTGST

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF056-1 (SEQ ID NO:209)

TAAATGAAAA AAAAGCGTTA TTTAATAAATT GCGTGTTTAC TATTTTCCCC TAGTTTTTTT
ATAAATGTTG AAGCATCTGA GGGTGGTTCT AGTTCGGTGG GAATTGAATT TTACCAAAT
CCGGCAACAC CCGCTCCTAA AGATGCCCCA CCGAAAACAG ATGAGCCAGC TCGGATCCC
AAGGAACCAG CTGGTCCTCT GCAAGGAGAT CAACGAAGTG GTGGTTCGAC ACAGACCACC
ACAGCTGGCT CGCAGCTCCC TCGTACAGGA AGCAAGAGTC AGGCAAACCT GAGCATTCTT
GGTCTTGTCT TGATTGTCT TGTCCGAATG GTCCAGAGAA AGAAGGGACG ACATGAAGCA
AACTAA

EF056-2 (SEQ ID NO:210)

MKKKRYLIIA CLLFSPSFFI NVEASEGGSS SVGIEFYQNP ATPAPKDAPP KTDEPAADPK
EPAGPLQGDQ RSGGSTQTTT AGSQLPRTGS KSQANLSILG LVLIGLVGMV QRKKGRHEAN

EF056-3 (SEQ ID NO:211)

ATCTGA GGGTGGTTCT AGTTCGGTGG GAATTGAATT TTACCAAAT
CCGGCAACAC CCGCTCCTAA AGATGCCCCA CCGAAAACAG ATGAGCCAGC TCGGATCCC
AAGGAACCAG CTGGTCCTCT GCAAGGAGAT CAACGAAGTG GTGGTTCGAC ACAGACCACC
ACAGCTGGCT CGCAG

EF056-4 (SEQ ID NO:212)

SEGGSS SVGIEFYQNP ATPAPKDAPP KTDEPAADPK
EPAGPLQGDQ RSGGSTQTTT AGSQ

EF057-1 (SEQ ID NO:213)

TAATGTTTAT TGGCTGGGCC AGTCAATGTT GAAAATGGGG AAGGAGGAAT TCAGATGAAA
ATCATAAAAA GGTTTAGTTT GGTATGTTTA GGGCTATTGA TCATTGGGTT GCNAACAAAA
AGCGNTATGG CTGAAGAAAA TAATTATGAA TCAAATGGTC AAGCGAGCTT CTATGGTACC
TACGTTTATG AGAATGAAAA AGAGTCAAAT GACGTAGCGT ATACCCAACA ATCAGAAGAA
CAGGGAAGAA ACAATTTAGC TGCTTCTGGA CAAGCAGTTT TACCTAAAC AGGCGAGTCT
GAAAATCCGC TGTATTCCTT GATAGGAGTT AGTTTGTGG GGATAGTCAT TTATTTAATT
AATAAAATGA AACGAGAGAA GGAGTTTATT TAA

EF057-2 (SEQ ID NO:214)

MKI IKRFSVLCLG LLIIGLXTKS XMAEENNYES NGQASFYGT
VYENEKESND VAYTQQSEEQ GRNNLAASGQ AVLPKTGESE NPLYSIGVS LLGIVYILIN
KMKREKEFI

EF057-3 (SEQ ID NO:215)

AAA TAATTATGAA TCAAATGGTC AAGCGAGCTT CTATGGTACC
TACGTTTATG AGAATGAAAA AGAGTCAAAT GACGTAGCGT ATACCCAACA ATCAGAAGAA
CAGGGAAGAA ACAATTTAGC TGCTTCTGGA CAAGCAGTTT

EF057-4 (SEQ ID NO:216)

EENNYES NGQASFYGT
VYENEKESND VAYTQQSEEQ GRNNLAASGQ AV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF058-1 (SEQ ID NO:217)

TGAAGAACGT TCTATTTGGT TGACGATTGC AGGCCTGCTA ATCATTGGGA TGGTAGTCAT
 TTGGCTATTT TATCAAAAAC AAAAAAGAGG AGAGAGAAAA TGAAGCAATT AAAAAAGTT
 TGGTACACCG TTAGTACCTT GTTACTAATT TTGCCACTTT TCACAAGTGT ATTAGGGACA
 ACAACTGCAT TTGCAGAAGA AAATGGGGAG AGCGCACAGC TCGTGATTCA CAAAAAGAAA
 ATGACGGATT TACCAGATCC GCTTATTCAA AATAGCGGGA AAGAAATGAG CGAGTTTGAT
 AAATATCAAG GACTGGCAGA TGTGACGTTT AGTATTTATA ACGTGACGAA CGAATTTTAC
 GAGCAACGAG CGGCAGGCGC AAGCGTTGAT GCAGCTAAAC AAGCTGTCCA AAGTTTAACT
 CCTGGGAAAC CTGTTGCTCA AGGAACCACC GATGCAAAATG GGAATGTCAC TGTTTCAGTTA
 CCTAAAAAAC AAAATGGTAA AGATGCAGTG TATACCATTA AAGAAGAACC AAAAGAGGGT
 GTAGTTGCTG CTACGAATAT GGTGGTGGCG TTCCCAGTTT ACGAAATGAT CAAGCAACA
 GATGGTTCCCT ATAAATATGG AACAGAAGAA TTAGCGGTTG TTCATATTTA TCCTAAAAAT
 GTGGTAGCCA ATGATGGTAG TTTACATGTG AAAAAAGTAG GAACTGCTGA AAATGAAGGA
 TTAAATGGCG CAGAATTTGT TATTTCTAAA AGCGAAGGCT CACCAGGCAC AGTAAATAT
 ATCCAAGGAG TCAAAGATGG ATTATATACA TGGACAACGG ATAAAGAACA AGCAAAACGC
 TTTATTACTG GGAAAAGTTA TGAAATTTGGC GAAAAATGATT TCACAGAAGC AGAGAATGGA
 ACGGGAGAAT TAACAGTTAA AAATCTTGAG GTTGGTTCCG ATATTTTAGA AGAAGTAAAA
 GCTCCAAATA ATGCAGAAAT AATTGAAAAAT CAAACAAAAA CACCATTTAC AATTGAAGCA
 AACAATCAAA CACCTGTTGA AAAACAGTC AAAAATGATA CCTCTAAAGT TGATAAAACA
 ACACCAAGCT TAGATGGTAA AGATGTGGCA ATTGGCGAAA AAATTAAATA TCAAATTTCT
 GTAAATATTC CATTGGGGAT TGCAGACAAA GAAGGCGACG CTAATAAATA CGTCAAATTC
 AATTTAGTTG ATAAACATGA TGCAGCCTTA ACTTTTGATA ACGTGACTTC TGGAGAGTAT
 GCTTATGCGT TATATGATGG GGATACAGTG ATTGCTCCTG AAAATTATCA AGTGACTGAA
 CAAGCAAATG GCTTCACTGT CGCCGTTAAT CCAGCGTATA TTCCTACGCT AACACCAGGC
 GGCACACTAA AATTCTGTTT CTTTATGCAT TTAAATGAAA AAGCAGATCC TACGAAAGGC
 TTTAAAAATG AGGCGAATGT TGATAACCGT CATACCGACG ACCAAACACC ACCAACTGTT
 GAAGTTGTGA CAGGTGGGAA ACGTTTCATT AAAGTCGATG GCGATGTGAC AGCGACACAA
 GCCTTGGCGG GAGCTTCCTT TGTCTGCCGT GATCAAAACA GCGACACAGC AAATTATTTG
 AAAATCGATG AAACAACGAA AGCAGCAACT TGGGTGAAAA CAAAAGCTGA AGCAACTACT
 TTTACAACAA CGGCTGATGG ATTAGTTGAT ATCACAGGCG TTAAATACGG TACCTATTAT
 TTAGAAGAAA CTGTAGCTCC TGATGATTAT GTCTTGTTAA CAAATCGGAT TGAATTTGTG
 GTCAATGAAC AATCATATGG CACAACAGAA AACCTAGTTT CACCAGAAAA AGTACCAAAC
 AAACACAAAG GTACCTTACC TTCAACAGGT GGCAAAGGAA TCTACGTTTA CTTAGGAAGT
 GGCGCAGTCT TGCTACTTAT TGCAGGAGTC TACTTTGCTA GACGTAGAAA AGAAAATGCT
 TAA

EF058-2 (SEQ ID NO:218)

MKQLKKVW YTVSTLLIL PLFTSVLGTT
 TFAEENGES AQLVIHKKKM TDLDPDPLIQN SGKEMSEFDK YQGLADVTF S IYNTNEFYE
 QRAAGASVDA AKQAVQSLTP GKPVAQGT TD ANGNVTVQLP KKQNGKDAVY TIKEEPKEGV
 VAATNMVVA F PVYEMIKQTD GSYKYGTEEL AVVHIYPKNV VANDGSLHVK KVGTAENEGL
 NGAEFVSKS EGSPGTVKYI QGVKDGLYTW TTDKEQAKRF ITGKSYEIGE NDFTEAENGT
 GELTVKNLEV GSYILEEVA PNNAELIENQ TKTPFTIEAN NQTPVEKTVK NDTSKVDKTT
 PSLDGKDAI GEKIKYQISV NIPLGIADKE GDANKYVKFN LVDKHDAA LT FDNVTSGEYA
 YALYDGD TVI APENYQVTEQ ANGFTVAVNP AYIPTLT PPG TLKFVYFMHL NEKADPTKGF
 KNEANVDNGH TDDQTPPTVE VVTGGKRFIK VDGDTVATQA LAGASFVVRD QNSDTANYLK
 IDETTKAATW VKTKAEATTF TTTADGLVDI TGLKYGTYYL EETVAPDDYV LLTNRIEFV V
 NEQSYGT TEN LVSPEKVPNK HKGTLPSTGG KGIYVYLGSG AVLLLIAGVY FARRRKENA

EF058-3 (SEQ ID NO:219)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AGAAGA AAATGGGGAG AGCGCACAGC TCGTGATTCA CAAAAAGAAA
 ATGACGGATT TACCAGATCC GCTTATTCAA AATAGCGGA AAGAAATGAG CGAGTTTGAT
 AAATATCAAG GACTGGCAGA TGTGACGTTT AGTATTATATA ACGTGACGAA CGAATTTTAC
 GAGCAACGAG CGGCAGGCGC AAGCGTTGAT GCAGCTAAAC AAGCTGTCCA AAGTTTAACT
 CCTGGGAAAC CTGTTGCTCA AGGAACCACC GATGCAAAATG GGAATGTCAC TGTTCAGTTA
 CCTAAAAAAC AAAATGGTAA AGATGCAGTG TATACCATTA AAGAAGAACC AAAAGAGGGT
 GTAGTTGCTG CTACGAATAT GGTGGTGGCG TTCCCAAGTTT ACGAAATGAT CAAGCAAACA
 GATGGTTCCCT ATAAATATGG AACAGAAGAA TTAGCGGTTG TTCATATTTA TCCTAAAAAT
 GTGGTAGCCA ATGATGGTAG TTTACATGTG AAAAAAGTAG GAACTGCTGA AAATGAAGGA
 TTAAATGGCG CAGAATTTGT TATTTCTAAA AGCGAAGGCT CACCAGGCAC AGTAAAAATAT
 ATCCAAGGAG TCAAAGATGG ATTATATACA TGGACAACGG ATAAAGAACA AGCAAAACGC
 TTTATTACTG GGAAAAGTTA TGAAATTGCG GAAAATGATT TCACAGAAGC AGAGAATGGA
 ACGGGAGAAT TAACAGTTAA AAATCTTGAG GTTGGTTTCGT ATATTTTAGA AGAAGTAAAA
 GCTCCAAATA ATGCAGAAAT AATTGAAAAT CAAACAAAA CACCATTTAC AATTGAAGCA
 AACAATCAAA CACCTGTTGA AAAACAGTC AAAAATGATA CCTCTAAAGT TGATAAAACA
 ACACCAAGCT TAGATGTAA AGATGTGGCA ATTGGCGAAA AAATTAAATA TCAAATTTCT
 GTAAATATTCT CATTGGGGAT TGCAGACAAA GAAGGCGACG CTAATAAATA CGTCAAATTC
 AATTTAGTTG ATAAACATGA TGCAGCCTTA ACTTTTGATA ACGTGACTTC TGGAGAGTAT
 GCTTATGCGT TATATGATGG GGATACAGTG ATTGCTCCTG AAAATTATCA AGTGACTGAA
 CAAGCAAATG GCTTCACTGT CGCCGTTAAT CCAGCGTATA TTCCTACGCT AACACCAGGC
 GGCACACTAA AATTCGTTTA CTTTATGCAT TTAAATGAAA AAGCAGATCC TACGAAAGGC
 TTTAAAAATG AGGCGAATGT TGATAACGGT CATACCGACG ACCAAACACC ACCAAGCTGT
 GAAGTTGTGA CAGGTGGGAA ACGTTTCATT AAAGTCGATG GCGATGTGAC AGCGACACAA
 GCCTTGGCGG GAGCTTCCTT TGTCGTCCGT GATCAAAACA GCGACACAGC AAATTATTTG
 AAAATCGATG AAACAACGAA AGCAGCAACT TGGGTGAAAA CAAAAGCTGA AGCAACTACT
 TTTACAACAA CGGCTGATGG ATTAGTTGAT ATCACAGGCG TTAAATACGG TACCTATTAT
 TTAGAAGAAA CTGTAGCTCC TGATGATTAT GTCTTGTTAA CAAATCGGAT TGAATTTGTG
 GTCAATGAAC AATCATATGG CACAACAGAA AACCTAGTTT CACCAGAAAA AGTACCAAAC
 AAACACAAAG GTACCTTACC T

EF058-4 (SEQ ID NO:220)

EENGES AQLVIHKKKM TDLDPDPLIQN SGKEMSEFDK YQGLADVTF S IYNTNEFYE
 QRAAGASVDA AKQAVQSLTP GKPVAQGTDD ANGNVTVQLP KKQNGKDAVY TIKEEPKEGV
 VAATNMVAVF PVYEMIKQTD GSYKYGTEEL AVVHIYPKNV VANDGSLHV KVGTAENEGL
 NGAEFVSKS EGSPGTVKYI QGVKDGlyTW TTDKEQAKRF ITGKSYEIGE NDFTEAENGT
 GELTVKNLEV GSYILEEVKA PNNAELIENQ TKTPFTIEAN NQTPVEKTVK NDTSKVDKTT
 PSLDGKDVAI GEKIKYQISV NIPLGIADKE GDANKYVKFN LVDKHDAAALT FDNVTSGEYA
 YALYDGDTVI APENYQVTEQ ANGFTVAVNP AYIPTLTGPG TLKFVYFMHL NEKADPTKGF
 KNEANVDNGH TDDQTPPTVE VVTGGKRFIK VDGDTVATQA LAGASFVVRD QNSDTANYLK
 IDETTKAATW VKTKAEATTF TTTADGLVDI TGLKYGTYYL EETVAPDDYV LLTNRIEFV
 NEQSYGTTEN LVSPEKVPNK HKGT

EF059-1 (SEQ ID NO:221)

TAGATTGGAA GAATGAAAT GAAAAAATG ATTATTATTG CCTTATTCAG TACAAGCCTT
 TTAGCAGGGG GAAGCAGTGT TTCTGCTTAT GCGCAAGAAT CAGAAGGAAA TCTTGGTGAA
 ACAACAGGGA GTGTTTTACC AGATGAACCG AATGTACCAA CTGACCCAAT AACGCCAAGT
 GAGCCAGAGC AACCAACAGA GCCAAGTACA CCAGAGCAAC CATCGGAACC GTCAACACCA
 ACCGAACCTA GTGAGCCTTC AAAACCGACG GATCCTTCGT TACCAGACGA ACCGAGCGTA
 CCAACAGAGC CAACAACGCC AAGTAAGCCA GAGCAACCAA CAGAGCCAAC AACGCCAAGT
 GTACCAGAGC AACCAACAGA GCCAAGTGTA CCAGAAAAAC CAGTAGAACC AAATAAACCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACCGAGCCAG AAAAGCCTGT GCCAGTTGTT CCTGAAAAAC CAGTTGTACC ACAACAACCA
 GAGCAACCAA CAGATGTGGT GGTAAAGCCA AATGGAGAAA TTGCAACAGG AGAATCTACA
 CAACAGCCAA CTGTTCCAAT TGAAACGAAT AACCTTTCAG AAGTAACACA TGTCCCAACT
 GTGACGACAC CGATTGAAAC AGCAAGCGGA GAAGCAATTG TCGCAGTGGA TAAGGGCGTT
 CCTTTAACAC AAACGGCTGA TGGATTAAAA CCGATTAAAA GTGAATATAA AGTATTACCA
 AGTGGCAATG TACAAGTGAA AAGTGCTGAC GGAAAAATGA AAGTACTTCC TTACACTGGT
 GAAAAAATGG GCATAATTGG GTCAATCGCT GGTGTATGTT TGAAGTATTT ATCAGGAATC
 TTAATTTATA AAAAACGTAA AGTGTAG

EF059-2 (SEQ ID NO:222)

MKKMI IIALFSTSL AGSSVSAYA QESEGNLGET TGSVLPDEPN VPTDPITPSE
 PEQPTPESTP EQPSEPSTPT EPSEPSKPTD PSLPDEPSVP TEPTTPSKPE QPTEPTPSV
 PEQPTPEPSVP EKPVEPNKPT EPEKVPVVP EKPVPVQPE QPTDVVVKPN GEIATGESTQ
 QPTVPIETNN LSEVTHVPTV TTPLETASGE AIVAVDKGVP LTQTADGLKP IKSEYKVLPS
 GNVQVKSADG KMKVLPYTGE KMGIIIGSIAG VCLTVLSGIL IYKKRKV

EF059-3 (SEQ ID NO:223)

AGAAGGAAA TCTTGGTGAA
 ACAACAGGGA GTGTTTACC AGATGAACCG AATGTACCAA CTGACCCAAT AACGCCAAGT
 GAGCCAGAGC AACCACAGA GCCAAGTACA CCAGAGCAAC CATCGGAACC GTCAACACCA
 ACCGAACCTA GTGAGCCTTC AAAACCGACG GATCCTTCGT TACCAGACGA ACCGAGCGTA
 CCAACAGAGC CAACAACGCC AAGTAAGCCA GAGCAACCAA CAGAGCCAAC AACGCCAAGT
 GTACCAGAGC AACCACAGA GCCAAGTGTA CCAGAAAAAC CAGTAGAACC AAATAAACCA
 ACCGAGCCAG AAAAGCCTGT GCCAGTTGTT CCTGAAAAAC CAGTTGTACC ACAACAACCA
 GAGCAACCAA CAGATGTGGT GGTAAAGCCA AATGGAGAAA TTGCAACAGG AGAATCTACA
 CAACAGCCAA CTGTTCCAAT TGAAACGAAT AACCTTTCAG AAGTAACACA TGTCCCAACT
 GTGACGACAC CGATTGAAAC AGCAAGCGGA GAAGCAATTG TCGCAGTGGA TAAGGGCGTT
 CCTTTAACAC AAACGGCTGA TGGATTAAAA CCGATTAAAA GTGAATATAA AGTATTACCA
 AGTGGCAATG TACAAGTGAA AAGTGCTGAC GGAAAAATGA AAGTAC

EF059-4 (SEQ ID NO:224)

EGNLGET TGSVLPDEPN VPTDPITPSE
 PEQPTPESTP EQPSEPSTPT EPSEPSKPTD PSLPDEPSVP TEPTTPSKPE QPTEPTPSV
 PEQPTPEPSVP EKPVEPNKPT EPEKVPVVP EKPVPVQPE QPTDVVVKPN GEIATGESTQ
 QPTVPIETNN LSEVTHVPTV TTPLETASGE AIVAVDKGVP LTQTADGLKP IKSEYKVLPS
 GNVQVKSADG KMKV

EF060-1 (SEQ ID NO:225)

TGAAAAATAG ACAAGGAGCA CGCGATGATG ACAATGAAAA GTAAAGGGTC ACTTCTGGTG
 ACGTTGGGAA TACTTTTAAC CGTTGGCATT GCGAGTCTAA TTGTTTCTTC TGAGAGTTTT
 GCAGAGAAG TAGGGCAAAC GAATATCGGT GTAACGTTCT ATGGAGGAAA AGAGCCACTA
 AAAACGGAAG GTGTCATTAA GCCAATAGAG CAACCACTCA CTGATAAAGA TAAAAAACG
 TCACAACAAC AAGACAAAGT GAGCAGAAAA ACCACTGCTA AAACGAATCC GACTAATGCA
 CAGACGTCAT TACCAAGGAC AGGTGAACGA AATAGCACGT GGCTTTACAG CCTTGGTATT
 GCCTGTTTAC TCGTAGTACT AACAAGTTTC TATTATTGTA ATAAAAAAG GAAAAAGGAA
 AAATAA

EF060-2 (SEQ ID NO:226)

MMT MKSKGSLVLT LGILLTVGIA SLIVSSESFA EEVGQTNIGV TFYGGKEPLK

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TEGVIKPIEQ PVTDKDKKTS QQQDKVSRKT TAKTNPTNAQ TSLPRTGERN STWLYSLGIA
 CLLVVLTSFY YLNKKRKKEK

EF060-3 (SEQ ID NO:227)

AGAAGAAG TAGGGCAAAC GAATATCGGT GTAACGTTCT ATGGAGGAAA AGAGCCACTA
 AAAACGGAAG GTGTCATTAA GCCAATAGAG CAACCAGTCA CTGATAAAGA TAAAAAACG
 TCACAACAAC AAGACAAAGT GAGCAGAAAA ACCACTGCTA AAACGAATCC GACTAATGCA
 CAGACGTCAT

EF060-4 (SEQ ID NO:228)

EEVGQTNIGV TFYGGKEPLK
 TEGVIKPIEQ PVTDKDKKTS QQQDKVSRKT TAKTNPTNAQ TS

EF061-1 (SEQ ID NO:229)

TAATGGAACG ACCGACAGAA GAAGATTTTG AACTTACAAA TTAAAATTAA AATGGAGGAA
 ATAATGATGA AAAAAATTCT TTTTGCTAGT TTATTTAGTG CCACACTACT ATTTGGGGGA
 AGTGAAATTT CTGCTTTTGC ACAAGAAATT ATCCCTGATG ATACTACGAC ACCGCCCAT
 GAAGTACCAA CAGAACCAAG TACACCAGAA AAGCCAACAG ATCCAACACC GCCAATTGAG
 CCACCTGTAG ACCCTGTAGA GCCACCTATT ACACCAACGG AGCCAACAGA ACCGACAGAG
 CCGACAACAC CAACAGAACC TACAACCTCT ACAGAGCCAA GTGAACCAGA ACAACCAACG
 GAGCCAAGTA AACCAGTAGA ACCTGAAAAA CCAGTTACAC CAAGCAAACC AGCAGAACCC
 GAAAAAATG TGACACCAAC TAAACCAACA GAATCTGAAA AACCAGTACA ACCAGCAGAA
 CCAAGCAAGC CAATCGACGT TGTGTGTAACG CCAACAGGGG AATTAAATCA CGCTGGAAAT
 GGTACACAAC AGCCAACAGT CCCTATTGAA ACAAGTAATT TGGCAGAAAT CACGCACGTG
 CCTAGTGTAA CAACACCTAT TACAACCTACA GACGGAGAAA ACATTGTAGC TGTAGAAAAA
 GGTGTTCCAC TTACACAAAC AGCAGAAGGG TTAAAACCTA TTCAATCNAG TTACAAAGTA
 TTGCCTAGCG GAAATGTAGA AGTAAAAGGT AAGGACGGTA AAATGAAGGT TTTACCATAC
 ACAGGTGAAG AAATGAATAT CTTTTTATCT GCCGTAGCG TATCTTGTCT GTAG

EF061-2 (SEQ ID NO:230)

MMKKILFASL FSATLLFGGS EISAFQEI PDDTTTPPIE
 VPTEPSTPEK PTDPTPIEP PVDPEPPIT PTEPTEPTEP TTPTEPTTPT EPSEPEQPT
 PSKPVEPEKP VTPSKPAEP KTVTPTKPTE SEKPVQPAEP SKPIDVVVTP TGELNHAGNG
 TQOPTVPIET SNLAEITHVP SVTTPIITTD GENIVAVEKG VPLTQTAEGL KPIQSSYKVL
 PSGNVEVKGK DGKMKVLPYT GEEMNIFLSA VAVSCL

EF061-3 (SEQ ID NO:231)

GAAATTT CTGCTTTTGC ACAAGAAATT ATCCCTGATG ATACTACGAC ACCGCCCAT
 GAAGTACCAA CAGAACCAAG TACACCAGAA AAGCCAACAG ATCCAACACC GCCAATTGAG
 CCACCTGTAG ACCCTGTAGA GCCACCTATT ACACCAACGG AGCCAACAGA ACCGACAGAG
 CCGACAACAC CAACAGAACC TACAACCTCT ACAGAGCCAA GTGAACCAGA ACAACCAACG
 GAGCCAAGTA AACCAGTAGA ACCTGAAAAA CCAGTTACAC CAAGCAAACC AGCAGAACCC
 GAAAAAATG TGACACCAAC TAAACCAACA GAATCTGAAA AACCAGTACA ACCAGCAGAA
 CCAAGCAAGC CAATCGACGT TGTGTGTAACG CCAACAGGGG AATTAAATCA CGCTGGAAAT
 GGTACACAAC AGCCAACAGT CCCTATTGAA ACAAGTAATT TGGCAGAAAT CACGCACGTG
 CCTAGTGTAA CAACACCTAT TACAACCTACA GACGGAGAAA ACATTGTAGC TGTAGAAAAA
 GGTGTTCCAC TTACACAAAC AGCAGAAGGG TTAAAACCTA TTCAATCNAG TTACAAAGTA
 TTGCCTAGCG GAAATGTAGA AGTAAAAGGT AAGGACGGTA AAATGAAGGT TT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF061-4 (SEQ ID NO:232)

QEII PDDTTTPPIE

VPTEPSTPEK PTDPTPIEP PVDPEPPIT PTEPTEPTEP TTPTEPTTPT EPSEPEQPT
 PSKPVEPEKP VTPSKPAEPE KTVTPTKPTE SEKPVQPAEP SKPIDVVVTP TGELNHAGNG
 TQQPTVPIET SNLAEITHVP SVTTPITTTD GENIVAVEKG VPLTQTAEGL KPIQSSYKVL
 PSGNVEVKGK DGKMKV

EF062-1 (SEQ ID NO:233)

TGATTCTTGA AGCAACAAAT GAAAGCAAAA AAACAATATA AGACATATAA AGCTAAGAAT
 CACTGGGGTAA CTGTCCCTAT TCTTTTCTA AGTGTGTTAG GAGCCGTAGG ATTAGCTACT
 GATAATGTAC AAGCCGCGGA ATTAGATACG CAACCAGAAA CAACGACGGT TCAACCCAAT
 AACCCCGACC TGCAGTCAGA AAAGGAAACA CCTAAAACGG CAGTATCTGA AGAAGCAACA
 GTACAAAAAG ACACACTTTC TCAACCGACC AAAGTAGAAG AAGTAGCGCC AGAAAATAAA
 GGTACTGAAC AAAGTTCAGC TACCCCAAAT GATACCACAA ACGCGCAACA ACCAACAGTA
 GGAGCTGAAA AATCAGCACA AGAACAACCA GTAGTAAGCC CTGAAACAAC CAATGAACCT
 CTAGGCGAGC CAACAGAAGT TGCACCAGCT GAAAATGAAG TGAATAAATC AACGTCCATT
 CCTAAAGAAT TTGAAACACC AGACGTTGAT AAAGCAGTTG ATGAAGTAAA AAAAGATCCA
 AACATTACCG TTGTTGAAAA ACCAGCAGAA GACTTAGGCA ACGTTTCTTC TAAAGATTTA
 GCTGCAAAAG AAAAGAAGT AGACCAACTA CAAAAGAAGC AAGCGAAAAA GATTGCCCAA
 CAAGCAGCTG AATTAAAAAGC CAAAAATGAA AAAATTGCCA AAGAAAAATGC AGAAATTGCG
 GCAAAAAACA AAGCNGAAAA AGAGCGNTAN GANAAAGAAG TCGCNGAATA CAACAAGCAT
 AAGAACGAAA ACAGCTATGT CAATGAAGCG ATTAGTAAAA ACCTAGTGTT CGATCAATCT
 GTCGTGACGA AAGACACTAA AATTTCCGTCG ATTAAGGCGG GAAAAATTTAT CAAAGCAACT
 GATTTTAATA AAGTAAATGC AGGGGATTCA AAAGATATCT TTACAAAATT ACGGAAAGAT
 ATGGGNGGGA AAGNTACTGG CAACTCCAG AATTCCTTTG TAAAAGAGGC AAATCTTGGG
 TCTAATGGTG GGTATGCGGT TCTTTTAGAA AAAAATAAAC CAGTGACAGT GACCTATACA
 GGACTAAACG CTAGTTATTT AGGACGTAAA ATTACAAAAG CAGAATTTGT TTATGAACATA
 CAATCCTCAC CAAGCCAAAG TGGAACGTTA AATGCAGTAT TTTCAAACGA TCCGATTATC
 ACNGCTTTTA TTGGTACAAA CAGAGTCAAT GGTAAAGGATG TTAACACACG CTTAACGATT
 AAGTTCTTTG ATGCGTCAGG TAAAGAAGTA CTACCAGATA AAGATAGTCC ATTTGCGTAT
 GCGCTGTCTT CTTTAAATTC AAGTTTAACG AATAAAGGTG GCCATGCGGA ATTTGTTTCT
 GATTTTGGGG CNAACAATGC GTTCAAATAC ATTAATGGNT CNTATGTGAA AAAACAAGCG
 GATGGAATAA TTTACTCACC GGAAGATATT GACTATGGCA CAGGACCTTC TGGATTGAAA
 AATAGTGATT GGGACGCTGT AGGTCACAAG AATGCCTACT TTGGTTCAGG TGTAGGTCTA
 GCNAATGNC GTATTTCTTT TTCTTTTGGT ATGACAACAA AAGGAAAAAG TAATGTGCCT
 GTATCTAGTG CGCAATGGTT TGCTTTAGN ACTAECTTAA ATGCGCAATC AGTGAAGCCT
 ATTTTCAATT ATGGGAATCC AAAAGAACCA GAAAAAGCAA CGATTGAATT CAATNGATAC
 AAAGCCAATG TCGTTCCTGT NCTTGTGCCN AATAAAGAAG TCACTGATGG NCAGAAAAAT
 NTCAATGATT TAAATGTGAA NCGTGGCGAT TCTTTACAAT ACATGTGAC AGGGGATACG
 ACAGAACTTG CCAAAGTAGA TCCAAAAACA GTAACNAAAC AAGGGATTCTG AGATACNTTT
 GATGCAGAAA AAGTGACGAT TGATTTATCC AAAGTGAAAG TTTATCAAGC AGACGCAAGT
 CTNAACGANA AAGACTNAAA AGCTGTTGCT GCAGCNATTA ATTCAGGAAN AGCTAAAGAC
 GTGACTGCTT CTTATGANCT CAATTTAGAT CAAAACACCG TCACAGCAAT GATGAAAACC
 AACGCNGACG GNTCNGTTGT TTTAGCAATG GGGTATAAAT ATTTACTTGT CTTGCCGTTT
 GTAGTAAAAA ATGTAGAAGG CGATTTTGAA AATACAGCTG TTCAGCTGAC AAANGATGNG
 GAAACGGTAA CAAATACAGT GTTAACCAT GTGCCAGGTA GTAACTCCTTC CAAAGATGTA
 AAAGCAGATA AAAACGGTAC AGTTGGCAGT GTTTCTCTAC ATGATAAAGA TATTCCGTTA
 CAAACAAAAA TTTATTATGA AGTGAAATCT TCCGAACGTC CAGCNAACTA TGGCGGAATN
 ACNGAAGAAT GGGGCATGAA TGATGTCTTG GACACGACCC ATGATCGTTT CACAGGNAAA
 TGGCACGCTA TTACNAANTA TGACCTTAAA GTAGGGGANA AAACGTTAAA AGCAGGAACA
 GATATTTCTG CCTACATTCT TTTAGAAAAC AAAGACAATA AAGACTTGAC GTTTACNATG
 AATCAAGCAT TATTGGCNGC NTTAAATGAA GGAAGCAATA AAGTAGGCAA ACAAGCTTGG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCTGTGTATC TGGAAGTCGA ACGGATNAAA ACAGGTGACG TAGAAAACAC GCAAACAGAA
 AACTACAACA AAGAGCTTGT NCGTTC TAAT ACNGTGGTGA CGCATACNCC TGATGATCCA
 AAACCAACCA AAGCCGTTCA TAACAAGAAA GGGGAAGANA TTAANCATGG AAAAGTNGCT
 CGTGGTGTATG TTCTTTCTTA TGAAATGACN TGGGACTTAA AAGGGTACGA TAAAGACTTT
 GCCTTTGATA CAGTCGATCT TGCACAGGC GTTCTTTCT TCGATGATTA CGATGAAACG
 AANGTGACAC CAATCAAAGA CTTACTTCGT GTCAAAGATT CTAAAGGGGN AGACATTACG
 AACCAGTTCA CGATCTCNTG GGACGATGCC AAAGGCACGG TGACNATNTC TGCCAAAGAC
 CCACAAGCCT TTATTCTAGC GNATGGTGGG CAAGAATTGC GTGTAACNCT CCCTACAAAA
 GTCAAAGCCG ATGTTTCTGG NGATGTTTAT AATTTCAGCGG AACAAAATAC ATTTGGNCAA
 CGAATTAAAA CCAATACNGT TGTCAACCAT ATTCCAAAAG TGAANCCTAA AAAAGACGTG
 GTTATTAAAG TNGGTGACAA ACAAAGTCAA AATGGNGCCA CAATCAAATT AGGGGAGAAN
 TTCTTCTATG AATTTACAAG TAGTGACATT CCTGCAGAAAT ACGCTGGNGT TGTGGAAGAA
 TGGTTCGATTA GCGATAAACT AGACGTCAAA CATGACAAAT TTAGTGGCCA ATGGTCTGTG
 TTTGCCAATT CTAATTTTGT TTTAGCAGAC GGAACCAAAG TGAATAAAGG GGACGACATT
 TCGAAACTAT TCACGATGAC CTTTGAACAA GGGGTAGTGA AAATCACGGC CAGTCAAGCC
 TTTTNGATG CGATGAATCT AAAAGAAAAC AAAAACGTTG CACACTCATG GAAAGCGTTC
 ATTGGTGTAG AACGAATTGC GGCAGGAGAC GTTTACAACA CAATCGAAGA ATCTTTCAAC
 AATGAGAAGA TTAAACNAA TACGGTAGTG ACNCATACGC CAGAAAAACC ACAAACNCCA
 CCAGAAAAAA CAGTGATTGT ACCACCAACA CCAAAAACAC CGCAAGCACC AGTAGAGCCA
 TTAGTGGTAG AAAAGGCAAG TGTNGTGCCA GAATTGCCGC AAACAGGCGA AAAACAAAAT
 GTCTTATTAA CGGTAGCTGG TAGTTTAGCC GCAATGCTTG GCTTAGCAGG CTTAGGCTTT
 AAACGTAGAA AAGAAACAAA ATAA

EF062-2 (SEQ ID NO:234)

MKAKK QYKTYKAKNH WVTVPILFLS VLGAVGLATD NVQAAELDTQ PETTTVQPNN
 PDLQSEKETP KTAVSEEATV QKDTTSQPTK VEEVAPENKG TEQSSATPND TTNAQQPTVG
 AEKSAQEOPV VSPETTNEPL GQPTVEPAE NEVNKSTSIP KEFETPDVVK AVDEVKKDPN
 ITVVEKPAED LGNVSSKDLA AKEKEVDQLQ KEQAKKIAQQ AAELKAKNEK TAKENAEIAA
 KNKAERERXX KEVAEYNKHK NENSYVNEAI SKNLVFDQSV VTKDTKISSI KGGKFIKATD
 FNKVNAGDSK DIFTKLKRD M GCKXTGNFQN SFVKEANLGS NNGYAVLLEK NKPVTVTYTG
 LNASYLGRKI TKAEFVYELQ SSPSQSGTLN AVFSNDPIIT AFIGTNRVNG KDVKTRLTIK
 FFDASGKEVL PDKDSPFAYA LSSLNSSLTN KGGHAEFVSD FGANNAFKYI NGSYVKKQAD
 GKFYSPEDID YGTGPSGLKN SDWDAVGHKN AYFGSGVGLA NGRISFSFGM TTKGKSNVPV
 SSAQWFAXT NLNAQSVKPI FNYGNPKPE KATIEFNXYK ANVVPVLVPN KEVTDGQKNX
 NDLNVXRGDS LQYIVTGDIT ELAKVDPKTV TKQGIRDFTD AEKVTIDLSK VKVYQADASL
 NXKDXXAVAA AINSXKXADV TASYXLNLDQ NTVTAMMKTN ADGSSVVLAMG YKYLVLPLFV
 VKNVEGDFEN TAVQLTXDGE TVTNTVINHV PGSNPSKDVK ADKNGTVGSV SLHDKDIPLQ
 TKIYYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTGKW HAITXYDLKV GXKTLKAGTD
 ISAYILLENK DNKDLTFTMN QALLAALNEG SNKVGKQAWS VYLEVERXKT GDVENTQTEN
 YNKELVRSNT VVTHTPDDPK PTKAVHNKKG EXIXHGKVAR GDVLSYEMTW DLKGYDKDFA
 FDTVDLATGV SFFDDYDETX VTPIKDLLRV KDSKXGDITN QFTISWDDAK GTVTXSAKDP
 QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFGQR IKTNTVVNHI PKVXPKKDVV
 IKVGDKQSQN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISDKLDVKH DKFSGQWSVF
 ANSNFVLADG TKVNKGDDIS KLFTMTFEQG VVKITASQAF XDAMNLKENK NVAHSWKAFI
 GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPQTPP EKTIVIPPTP KTPQAPVEPL
 VVEKASVPE LPQTGEKQNV LLTVAGSLAA MLGLAGLGFK RRKETK

EF062-3 (SEQ ID NO:235)

TGATTCTTGA AGCAACAAAT GAAAGCAAAA AAACAATATA AGACATATAA AGCTAAGAAT
 CACTGGGTAA CTGTCCCTAT TCTTTTCTA AGTGTGTTAG GAGCCGTAGG ATTAGCTACT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

| | | | | | |
|-------------|-------------|-------------|-------------|------------|------------|
| GATAATGTAC | AAGCCGCGGA | ATTAGATACG | CAACCAGAAA | CAACGACGGT | TCAACCCAAT |
| AACCCCGACC | TGCAGTCAGA | AAAGGAAACA | CCTAAAACGG | CAGTATCTGA | AGAAGCAACA |
| GTACAAAAAG | ACACTACTTC | TCAACCGACC | AAAGTAGAAG | AAGTAGCGCC | AGAAAATAAA |
| GGTACTGAAC | AAAGTTCAGC | TACCCCAAAT | GATACCACAA | ACGCGCAACA | ACCAACAGTA |
| GGAGCTGAAA | AATCAGCACA | AGAACAACCA | GTAAGTAAAG | CTGAAACAAC | CAATGAACCT |
| CTAGGGCAGC | CAACAGAAGT | TGCACCAGCT | GAAAATGAAG | TGAATAAATC | AACGTCCATT |
| CCTAAAGAAT | TTGAAACACC | AGACGTTGAT | AAAGCAGTTG | ATGAAGTAAA | AAAAGATCCA |
| AACATTACCG | TTGTTGAAAA | ACCAGCAGAA | GACTTAGGCA | ACGTTTCTTC | TAAAGATTTA |
| GCTGCAAAAG | AAAAAGAAGT | AGACCAACTA | CAAAAAGAAG | AAGCGAAAAA | GATTGCCCCA |
| CAAGCAGCTG | AATTAAAAGC | CAAAAATGAA | AAAATTGCCA | AAGAAAATGC | AGAAATTGCG |
| GCAAAAAACA | AAGCNGAAAA | AGAGCGNTAN | GANAAAGAAG | TCGCGAATA | CAACAAGCAT |
| AAGAACGAAA | ACAGCTATGT | CAATGAAGCG | ATTAGTAAAA | ACCTAGTGT | CGATCAATCT |
| GTCGTGACGA | AAGACACTAA | AATTTCTGTC | ATTAAAGCGC | GAAAAATTAT | CAAAGCAACT |
| GATTTTAAATA | AAGTAAATGC | AGGGGATTCA | AAAGATATCT | TTACAAAATT | ACGGAAGAT |
| ATGGGNGGGA | AAGNTACTGG | CAACTTCCAG | AATTCCTTTG | TAAAAGAGGC | AAATCTTGGG |
| TCTAATGGTG | GGTATGCGGT | TCTTTTAGAA | AAAAATAAAC | CAGTGACAGT | GACCTATACA |
| GGAGTAAAGC | CTAGTTATTT | AGGACGTAAA | ATTACAAAAG | CAGAATTTGT | TTATGAACTA |
| CAATCCTCAC | CAAGCCAAAG | TGGAACGTTA | AATGCAGTAT | TTTCAAACGA | TCCGATTATC |
| ACNGCTTTTA | TTGGTACAAA | CAGAGTCAAT | GGTAAGGATG | TTAAAACACG | CTTAACGATT |
| AAGTTCCTTG | ATGCGTCAGG | TAAAGAAGTA | CTACCAGATA | AAGATAGTCC | ATTTGCGTAT |
| GCGCTGTCTT | CTTTAAATTC | AAGTTTAACG | AATAAAGGTG | GCCATGCGGA | ATTTGTTTCT |
| GATTTTGGGG | CNAACAATGC | GTTCAAATAC | ATTAATGGNT | CNTATGTGAA | AAAACAAGCG |
| GATGGAATAT | TTTACTCACC | GGAAGATATT | GACTATGGCA | CAGGACCTTC | TGGATTGAAA |
| AATAGTGATT | GGGACGCTGT | AGGTCAACAAG | AATGCCTACT | TTGGTTCAGG | TGTAGGTCTA |
| GCNAATGGNC | GTATTTCCCT | TTCTTTTGGT | ATGACAACAA | AAGGAAAAAG | TAATGTGCCT |
| GTATCTAGTG | CGCAATGGTT | TGCCTTTAGN | ACTAATTTAA | ATGCGCAATC | AGTGAAGCCT |
| ATTTTCAATT | ATGGGAATCC | AAAAGAACCA | GAAAAAGCAA | CGATTGAATT | CAATNGATAC |
| AAAGCCAAATG | TCGTTCCCTGT | NCTTGTGCCN | AATAAAGAAG | TCACTGATGG | NCAGAAAAAT |
| NTCAATGATT | TAAATGTGAA | NCGTGGCGAT | TCTTTACAAT | ACATTGTGAC | AGGGGATACG |
| ACAGAATTTG | CCAAAGTAGA | TCCAAAAACA | GTAACNAAAC | AAGGGATTTC | AGATACNITT |
| GATGCAGAAA | AAGTGACGAT | TGATTTATCC | AAAGTGAAAG | TTTATCAAGC | AGACGCAAGT |
| CTNAACGANA | AAGACTNAAA | AGCTGTTGCT | GCAGCNATTA | ATTGAGGAAN | AGCTAAAGAC |
| GTGACTGCTT | CTTATGANCT | CAATTTAGAT | CAAAACACCG | TCACAGCAAT | GATGAAAACC |
| AACGCNGACG | GNTCNGTTGT | TTTAGCAATG | GGGTATAAAT | ATTTACTTGT | CTTGCCGTTT |
| GTAGTGAAAA | ATGTAGAAGG | CGATTTTGAA | AATACAGCTG | TTCAGCTGAC | AAANGATGGN |
| GAAACGGTAA | CAAATACAGT | GATTAACCAT | GTGCCAGGTA | GTAATCCTTC | CAAAGATGTA |
| AAAGCAGATA | AAAACGGTAC | AGTTGGCAGT | GTTTCTCTAC | ATGATAAAGA | TATTCCGTTA |
| CAAAACAAAA | TTTATTATGA | AGTGAAATCT | TCCGAACGTC | CAGCNAACTA | TGGCGGAATN |
| ACNGAAGAAT | GGGGCATGAA | TGATGTCTTG | GACACGACCC | ATGATCGTTT | CACAGGNAAA |
| TGGCACGCTA | TTACNAANTA | TGACCTTAAA | GTAGGGGANA | AAACGTTAAA | AGCAGGAACA |
| GATATTTCTG | CCTACATTCT | TTTAGAAAAC | AAAGACAATA | AAGACTTGAC | GTTTACNATG |
| AATCAAGCAT | TATTGGCNGC | NTTAAATGAA | GGAAGCAATA | AAGTAGGCAA | ACAAGCTTGG |
| TCTGTGTATC | TGGAAGTCGA | ACGGATNAAA | ACAGGTGACG | TAGAAAACAC | GCAAACAGAA |
| AACTACAACA | AAGAGCTTGT | NCGTTCTAAT | ACNGTGGTGA | CGCATACNCC | TGATGATCCA |
| AAACCAACCA | AAGCCGTTCA | TAACAAGAAA | GGGGAAGANA | TTAANCATGG | AAAAGTNGCT |
| CGTGGTGATG | TTCTTTCTTA | TGAAATGACN | TGGGACTTAA | AAGGGTACGA | TAAAGACTTT |
| GCCTTTGATA | CAGTCGATCT | TGCGACAGGC | GTTTCTTTCT | TCGATGATTA | CGATGAAACG |
| AANGTGACAC | CAATCAAAGA | CTTACTTCGT | GTCAAAGATT | CTAAAGGGGN | AGACATTACG |
| AAACAGTTCA | CGATCTCNTG | GGACGATGCC | AAAGGCACGG | TGACNATNTC | TGCCAAAGAC |
| CCACAAGCCT | TTATTCTAGC | GNATGGTGGG | CAAGAAATTGC | GTGTAACNCT | CCCTACAAAA |
| GTCAAAGCCG | ATGTTTCTGG | NGATGTTTAT | AATTCAGCGG | AACAAAATAC | ATTTGGNCAA |
| CGAATTAAAA | CCAATACNGT | TGTCAACCAT | ATTCCAAAAG | TGAANCCTAA | AAAAGACGTG |
| GTTATTAAAG | TNGGTGACAA | ACAAAGTCAA | AATGGNGCCA | CAATCAAATT | AGGGGAGAAN |
| TTCTTCTATG | AATTTACAAG | TAGTGACATT | CCTGCAGAAT | ACGCTGGNGT | TGTGGAAGAA |

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TGGTCGATTA GCGATAAACT AGACGTCAAA CATGACAAAT TTAGTGGCCA ATGGTCTGTG
 TTTGCCAATT CTAATTTTGT TTTAGCAGAC GGAACCAAAG TGAATAAAGG GGACGACATT
 TCGAAACTAT TCACGATGAC CTTTGAACAA GGGGTAGTGA AAATCACGGC CAGTCAAGCC
 TTTTNGATG CGATGAATCT AAAAGAAAAC AAAACGTTG CACACTCATG GAAAGCGTTC
 ATTGGTGTAG AACGAATTGC GGCAGGAGAC GTTTACAACA CAATCGAAGA ATCTTTCAAC
 AATGAGAAGA TTAAACNAA TACGGTAGTG ACNCATACGC CAGAAAAACC ACAAACNCCA
 CCAGAAAAAA CAGTGATTGT ACCACCAACA CCAAAAACAC CGCAAGCACC AGTAGAGCCA
 TTAGTGGTAG AAAAGGCAAG TG

EF062-4 (SEQ ID NO:236)

AELDTQ PETTTVQPNP
 PDLQSEKETP KTAVSEETV QKDTTSQPTK VEEVAPENKG TEQSSATPND TTNAQQPTVG
 AEKSAEQEPV VSPETTNEPL GQPTEVAPAE NEVNKSTSIP KEFETPDVDK AVDEVKKDPN
 ITVVEKPAED LGNVSSKDLA AKEKEVDQLQ KEQAKKIAQQ AAELKAKNEK IAKENAEIAA
 KNKAEKERXX KEVAEYNKHK NENSYVNEAI SKNLVFDQSV VTKDTKISSI KGGKFIKATD
 FNKVNAGDSK DIFTKLRRKDM GGKXTGNFQN SFVKEANLGS NGGYAVLLEK NKPVTVTYTG
 LNASYLGRKI TKAEFVYELQ SSPSQSGTLN AVFSNDPIIT AFIGTNRVNG KDVKTRLTIK
 FFDASGKEVL PDKDSPFAYA LSSLNSSLTN KGGHAEFVSD FGANNAPFYI NGSYVKKQAD
 GKFYSPEDID YGTGP SGLKN SDWDAVGHN AYFGSGVGLA NGRISFSFGM TTKGKSNVPV
 SSAQWFAFXT NLNAQSVKPI FNYGNPKEPE KATIEFNXYK ANVVPVLVPN KEVTDGQKNX
 NDNLVXRGDS LQYIVTGDIT ELAKVDPKTV TKQGIRDITD AEKVTIDLSK VKVYQADASL
 NXKDXKAVAA AINSXKAKDV TASYXLNLDQ NTVTAMMKTN ADGSVVLAMG YKYLVLVLPFV
 VKNVEGDFFEN TAVQLTXDGE TVTNTVINHV PGSNPSKDVK ADKNGTVGSV SLHDKDIPLO
 TKIYYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTGKW HAITXYDLKV GXKTLKAGTD
 ISAYILLENK DNKDLTFMTN QALLAALNEG SNKVGKQAWS VYLEVERXKT GDVENTQTEN
 YNKELVRSNT VVTHTPDDPK PTKAVHNKKG EXIXHGKVAR GDVLSYEMTW DLKGYDKDFA
 FDTVLDLATGV SFFDDYDETX VTPIKDLLRV KDSKGXIDTN QFTISWDDAK GTVTXSAKDP
 QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFGQR IKTNTVNNHI PKVXPKKDVV
 IKVGDKQSQN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISDKLDVKH DKFSGQWSVF
 ANSNFVLADG TKVNKGDDIS KLFTMTFEQG VVKITASQAF XDAMNLKENK NVAHSWKAFI
 GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPQTPP EKTIVIPPTP KTPQAPVEPL
 VVEKASV

EF063-1 (SEQ ID NO:237)

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 CACTGGGTAA CTGTCCCTAT TCTTTTCTA AGTGTGTTAG GAGCCGTAGG ATTAGCTACT
 GATAATGTAC AAGCCGCGGA ATTAGATACG CAACCAGAAA CAACGACGGT TCAACCCAAT
 AACCCCGACC TGCAGTCAGA AAAGGAAACA CCTAAAACGG CAGTATCTGA AGAAGCAACA
 GTACAAAAAG ACACTACTTC TCAACCGACC AAAGTAGAAG AAGTAGCGCC AGAAAAATAA
 GGTACTGAAC AAAGTTCAGC TACCCCAAAT GATACCACAA ACGCGCAACA ACCAACAGTA
 GGAGCTGAAA AATCAGCACA AGAACAACCA GTAGTAAGCC CTGAAACAAC CAATGAACCT
 CTAGGGCAGC CAACAGAAGT TGCACCAGCT GAAAATGAAG TGAATAAATC AACGTCCATT
 CCTAAGAAT TTGAAACACC AGACGTTGAT AAAGCAGTTG ATGAAGTAAA AAAAGATCCA
 AACATTACCG TTGTTGAAAA ACCAGCAGAA GACTTAGGCA ACGTTTCTTC TAAAGATTTA
 GCTGCAAAAAG AAAAAGAAAGT AGACCAACTA CAAAAAGAAC AAGCGAAAAA GATTGCCCAA
 CAAGCAGCTG AATTAAAAAGC CAAAAATGAA AAAATTGCCA AAGAAAAATGC AGAAATTGCG
 GCAAAAAACA AAGCNGAAAA AGAGCGNTAN GANAAAGAAG TCGCNGAATA CAACAAGCAT
 AAGAACGAAA ACAGCTATGT CAATGAAGCG ATTAGTAAAA ACCTAGTGTT CGATCAATCT
 GTCGTGACGA AAGACACTAA AATTTCTGTCG ATTAAAGGCG GAAAATTTAT CAAAGCAACT
 GATTTTAAATA AAGTAAATGC AGGGGATTCA AAAGATATCT TTACAAAATT ACGGAAAGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

| | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|
| ATGGGNGGGA | AAGNTACTGG | CAACTTCCAG | AATTCCCTTTG | TAAAAGAGGC | AAATCTTGGG |
| TCTAATGGTG | GGTATGCGGT | TCTTTTAGAA | AAAAATAAAC | CAGTGACAGT | GACCTATACA |
| GGACTAAACG | CTAGTTATTT | AGGACGTAAA | ATTACAAAAG | CAGAATTTGT | TTATGAACTA |
| CAATCCTCAC | CAAGCCAAAAG | TGGAACGTTA | AATGCAGTAT | TTTCAAACGA | TCCGATTATC |
| ACNGCTTTTA | TTGGTACAAA | CAGAGTCAAT | GGTAAGGATG | TTAAAACACG | CTTAACGATT |
| AAGTTCCTTG | ATGCGTCAGG | TAAAGAAGTA | CTACCAGATA | AAGATAGTCC | ATTGCGTAT |
| GCGCTGTCTT | CTTTAAATTC | AAGTTTAAACG | AATAAAGGTG | GCCATGCGGA | ATTGTTTCT |
| GATTTTGGGG | CNAACAATGC | GTTCAAATAC | ATTAATGGNT | CNTATGTGAA | AAAACAAGCG |
| GATGGAAAAT | TTTACTCACC | GGAAGATATT | GACTATGGCA | CAGGACCTTC | TGGATTGAAA |
| AATAGTGATT | GGGACGCTGT | AGGTCACAAG | AATGCCTACT | TTGGTTCAGG | TGTAGGTCTA |
| GCNAATGGNC | GTATTTCTTT | TTCTTTTGGT | ATGACAACAA | AAGGAAAAAG | TAATGTGCCT |
| GTATCTAGTG | CGCAATGGTT | TGCCTTTAGN | ACTAACTTAA | ATGCGCAATC | AGTGAAGCCT |
| ATTTTCAATT | ATGGGAATCC | AAAAGAACCA | GAAAAAGCAA | CGATTGAATT | CAATNGATAC |
| AAAGCCAATG | TCGTTCCCTGT | NCTTGTGCCN | AATAAAGAAG | TCACTGATGG | NCAGAAAAAT |
| NTCAATGATT | TAAATGTGAA | NCGTGGCGAT | TCTTTACAAT | ACATTGTGAC | AGGGGATACG |
| ACAGAACTTG | CCAAAGTAGA | TCCAAAAACA | GTAACNAAAC | AAGGGATTCTG | AGATACNTTT |
| GATGCAGAAA | AAGTGACGAT | TGATTTATCC | AAAGTGAAAG | TTTATCAAGC | AGACGCAAGT |
| CTNAACGANA | AAGACTNAAA | AGCTGTTGCT | GCAGCNATTA | ATTCAAGGAAN | AGCTAAAGAC |
| GTGACTGCTT | CTTATGANCT | CAATTTAGAT | CAAAACACCG | TCACAGCAAT | GATGAAAAACC |
| AACCGNACG | GNTCNGTTGT | TTTAGCAATG | GGGTATAAAT | ATTTACTTGT | CTTGCCGTTT |
| GTAGTGAAAA | ATGTAGAAGG | CGATTTTGAA | AATACAGCTG | TTCAGCTGAC | AAANGATGGN |
| GAAACGGTAA | CAAAATACAGT | GATTAACCAT | GTGCCAGGTA | GTAATCCTTC | CAAAGATGTA |
| AAAGCAGATA | AAAACGGTAC | AGTTGGCAGT | GTTTCTCTAC | ATGATAAAGA | TATTCCGTTA |
| CAACAAAAAA | TTTATTATGA | AGTGAAATCT | TCCGAACGTC | CAGCNAACTA | TGGCGGAATN |
| ACNGAAGAAT | GGGGCATGAA | TGATGTCTTG | GACACGACCC | ATGATCGTTT | CACAGGNAAA |
| TGGCAGCGTA | TTACNAANTA | TGACCTTAAA | GTAGGGGANA | AAACGTTAAA | AGCAGGAACA |
| GATATTTCTG | CCTACATCTT | TTTAGAAAAAC | AAAGACAATA | AAGACTTGAC | GTTTACNATG |
| AATCAAGCAT | NTTAAATGAA | NTTAAATGAA | GGAAGCAATA | AAGTAGGCAA | ACAAGCTTGG |
| TCTGTGTATC | TGGAAGTCGA | ACCGATNAAA | ACAGGTGACG | TAGAAAAACAC | GCAAACAGAA |
| AACTACAACA | AAGAGCTTGT | NCGTTCCTAAT | ACNGTGGTGA | CGCATACNCC | TGATGATCCA |
| AAACCAACCA | AAGCCGTTCA | TAACAAGAAA | GGGGAAGANA | TTAANCATGG | AAAAGTNGCT |
| CGTGGTGATG | TTCTTTCTTA | TGAAATGACN | TGGGACTTAA | AAGGGTACGA | TAAAGACTTT |
| GCCCTTGATA | CAGTCGATCT | TGCGACAGGC | GTTTCTTTCT | TCGATGATTA | CGATGAAACG |
| AANGTGACAC | CAATCAAAGA | CTTACTTCGT | GTCAAAGATT | CTAAAGGGGN | AGACATTACG |
| AACCAGTTCA | CGATCTCNTG | GGACGATGCC | AAAGGCACGG | TGACNATNTC | TGCCAAAGAC |
| CCACAAGCCT | TTATTCTAGC | GNATGGTGGG | CAAGAATTGC | GTGTAACNCT | CCCTACAAAA |
| GTCAAAGCCG | ATGTTTCTGG | NGATGTTTAT | AATTCAGCGG | AACAAAATAC | ATTTGGNCAA |
| CGAATTAATA | CCAATACNGT | TGTCAACCAT | ATTCCAAAAG | TGAANCCCTAA | AAAAGACGTG |
| GTTATTAATA | TNGGTGACAA | ACAAAGTCAA | AATGGNGCCA | CAATCAAATT | AGGGGAGAA |
| TTCTTCTATG | AATTTACAAG | TAGTGACATT | CCTGCAGAAT | ACGCTGGNGT | TGTGGAAGAA |
| TGGTCGATTA | GCGATAAACT | AGACGTCAAA | CATGACAAAT | TTAGTGCCCA | ATGGTCTGTG |
| TTTGCCAAAT | CTAATTTTGT | TTTAGCAGAC | GGAACCAAAG | TGAATAAAGG | GGACGACATT |
| TCGAAACTAT | TCACGATGAC | CTTTGAACAA | GGGTTAGTGA | AAATCACGGC | CAGTCAAGCC |
| TTTTTTNGATG | CGATGAATCT | AAAAGAAAAAC | AAAAACGTTG | CACACTCATG | GAAAGCGTTC |
| ATTGGTGTAG | AACGAATTGC | GGCAGGAGAC | GTTTACAACA | CAATCGAAGA | ATCTTTCAAC |
| AATGAGAAGA | TTAAAACNAA | TACGGTAGTG | ACNCATACGC | CAGAAAAACC | ACAAACNCCA |
| CCAGAAAAAA | CAGTGATTGT | ACCACCAACA | CCAAAAACAC | CGCAAGCACC | AGTAGAGCCA |
| TTAGTGGTAG | AAAAGGCAAG | TGTNGTGCCA | GAATTGCCGC | AAACAGGCCA | AAAACAAAAT |
| GTCTTATTAA | CGGTAGCTGG | TAGTTTAGCC | GCAATGCTTG | GCTTAGCAGG | CTTAGGCTTT |
| AAACGTAGAA | AAGAAACAAA | ATAA | | | |

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

MKAKK QYKTYKAKNH WVTVPILFLS VLGAVGLATD NVQAAELDTQ PETTTVQPNN
 PDLQSEKETP KTAVSEEATV QKDTTSQPTK VEEVAPENKG TEQSSATPND TTNAQQPTVG
 AEKSAQEQPV VSPETTNEPL GQPTEVAPAE NEVNKSTSIP KEFETPDVVK AVDEVKKDPN
 ITVVEKPAED LGNVSSKDLA AKEKEVDQLQ KEQAKKIAQQ AAELKAKNEK IAKENAEIAA
 KNKAEKERXX KEVAEYNKHK NENSYVNEAI SKNLVFDQSV VTKDTKISSI KGGKFIKATD
 FNKVNAGDSK DIFTKLKDKM GGKXTGNFQN SFVKEANLGS NGGYAVLLEK NKPVTVTYTG
 LNASYLGRKI TKAEFVYELQ SSPSQSGTLN AVFSNDPIIT AFIGTNRVNG KDVKTRLTIK
 FFDASGKEVL PDKDSPFAYA LSSLNSSLTN KGGHAEFVSD FGANNAFKYI NGSYVKKQAD
 GKFYSPEDID YGTGPSGLKN SDWDAVGHN AYFGSGVGLA NGRISFSFGM TTKGKSNVPV
 SSAQWFAXT NLNAQSVKPI FNYGNPKEPE KATIEFNXYK ANVVPVLVPN KEVTDGQKNX
 NDLNVXRGDS LQYIVTGDIT ELAKVDPKTV TKQGIRDFTD AEKVTIDLKSK VKVYQADASL
 NXKDXKAVAA AINSXGAKDV TASYXLNLDQ NTVTAMMKTN ADGSVVLAMG YKYLVLPLFV
 VKNVEGDFEN TAVQLTXDGE TVTNTVINHV PGSNPSKDVK ADKNGTVGSV SLHDKDIPLO
 TKIYYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTGKW HAITXYDLKV GXKTLKAGTD
 ISAYILLENK DNKDLTFTMN QALLAALNEG SNKVGKQAWS VYLEVERXKT GDVENTQTEN
 YNKELVRSNT VVTHTPDDPK PTKAVHNKKG EXIXHGKVAR GDVLSYEMTW DLKGYDKDFA
 FDTVLDATGV SFFDDYDETX VTPIKDLLRV KDSKXGDIITN QFTISWDDAK GTVTXSAKDP
 QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFGQR IKTNTVVNHI PKVXPKKDVV
 IKVGDQSQSN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISDKLDVKH DKFSGQWSVF
 ANSNFVLADG TKVNGGDDIS KLFTMTFEQG VVKITASQAF XDAMNLKENK NVAHSWKAFI
 GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPQTPP EKTIVVPPTP KTPQAPVEPL
 VVEKASVPE LPQTGEKQNV LLTVAGSLAA MLGLAGLGFK RRKETK

EF063-3 (SEQ ID NO:239)

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 GTACAAAAAG ACACACTTTC TCAACCGACC AAAGTAGAAG AAGTAGCGCC AGAAAATAAA
 GGTACTGAAC AAAGTTCAGC TACCCCAAAT GATACCACAA ACGCGCAACA ACCAACAGTA
 GGAGCTGAAA AATCAGCACA AGAACAACCA GTAGTAAGCC CTGAAACAAC CAATGAACCT
 CTAGGGCAGC CAACAGAAGT TGCACCAGCT GAAAATGAAG TGAATAAATC AACGTCCATT
 CCTAAGAAT TTGAAACACC AGACGTTGAT AAAGCAGTTG ATGAAGTAAA AAAAGATCCA
 AACATTACCG TTGTTGAAAA ACCAGCAGAA GACTTAGGCA ACGTTTCTTC TAAAGATTTA
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 CAAGCAGCTG AATTAAAAAGC CAAAAATGAA AAAATTGCCA AAGAAAATGC AGAAATTGCG
 GCAAAAAACA AAGCNGAAAA AGAGCGNTAN GANAAAGAAG TCGCNGAATA CAACAAGCAT
 AAGAACGAAA ACAGCTATGT CAATGAAGCG ATTAGTAAAA ACCTAGTGTG CGATCAATCT
 GTCGTGACGA AAGACACTAA AATTTCTGTCG ATTAAAGGCG GAAAATTTAT CAAAGCAACT
 GATTTTAAATA AAGTAAATGC AGGGGATTCA AAAGATATCT TTACAAAATT ACGGAAAGAT
 ATGGGNGGGA AAGNTACTGG CAACTTCCAG AATTCCTTTG TAAAAGAGGC AAATCTTGGG
 TCTAATGGTG GGTATGCGGT TCTTTTAGAA AAAAATAAAC CAGTGACAGT GACCTATACA
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 ACNGCTTTTA TTGCTACAAA CAGAGTCAAT GGTAAGGATG TTAAAAACAG CTTAACGATT
 AAGTTCTTTG ATGCGTCAGG TAAAGAAGTA CTACCAGATA AAGATAGTCC ATTTGCGTAT
 GCGCTGTCTT CTTTAAATTC AAGTTTAAACG AATAAAGGTG GCCATGCGGA ATTTGTTTCT
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 GTATCTAGTG CGCAATGGTT TGCCTTTAGN ACTAACTTAA ATGCGCAATC AGTGAAGCCT
 ATTTTCAATT ATGGGAATCC AAAAGAACCA GAAAAAGCAA CGATTGAATT CAATNGATAC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAGCCAATG TCGTTCCTGT NCTTGTGCCN AATAAAGAAG TCACTGATGG NCAGAAAAAT
 NTCAATGATT TAAATGTGAA NCGTGGCGAT TCTTTTACAAT ACATTGTGAC AGGGGATACG
 ACAGAACTTG CCAAAGTAGA TCCAAAAACA GTAACNAAAC AAGGGATTTCG AGATACNTTT
 GATGCAGAAA AAGTGACGAT TGATTTATCC AAAGTG

EF063-4 (SEQ ID NO:240)

ELDTQ PETTTVQPNN

PDLQSEKETP KTAVSEEATV QKDTTSQPTK VEEVAPENKG TEQSSATPND TTNAQQPTVG
 AEKSAQEOPV VSPETTNEPL GQPTVAPAE NEVNKSTSIP KEFETPDVDK AVDEVKKDPN
 ITVVEKPAED LGNVSSKDLA AKEKEVDQLQ KEQAKKIAQQ AAELKAKNEK IAKENAEIAA
 KNKAERKXX KEVAEYNKHK NENSYVNEAI SKNLVFDQSV VTKDTKISSI KGGFKIKATD
 FNKNVAGDSK DIFTKLKRD M GGKXTGNFQN SFVKEANLGS NGGYAVLLEK NKPVTVTYTG
 LNASYLGRKI TKAEFVYELQ SSPSQSGTLN AVFSNDPIIT AFIGTNRVNG KDVKTRLTIK
 FFDASGKEVL PDKDSPFAYA LSSLNSSLTN KGGHAEFVSD FGANNAFKYI NGSYVKKQAD
 GKFPSPEDID YGTGPSGLKN SDWDVAVGHKN AYFGSGVGLA NGRISFSFGM TTKGKSNVPV
 SSAQWFAFXT NLNAQSVKPI FNYGNPKEPE KATIEFNXYK ANVVPVLVPN KEVTDGQKNX
 NDLNVXRGS LQYIVTGDIT ELAKVDPKTV TKQGIRDTFD AEKVTIDLSK V

EF064-1 (SEQ ID NO:241)

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 CACTGGGTAA CTGTCCCTAT TCTTTTCTA AGTGTGTTAG GAGCCGTAGG ATTAGCTACT
 GATAATGTAC AAGCCGCGGA ATTAGATACG CAACCAGAAA CAACGACGGT TCAACCCAAT
 AACCCCGACC TGCAGTCAGA AAAGGAAACA CCTAAAACGG CAGTATCTGA AGAAGCAACA
 GTACAAAAAG ACACACTTTC TCAACCGACC AAAGTAGAAG AAGTAGCGCC AGAAAATAAA
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 CCTAAGAAT TTGAAACACC AGACGTTGAT AAAGCAGTTG ATGAAGTAAA AAAAGATCCA
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 GCTGCAAAAAG AAAAAGAAGT AGACCAACTA CAAAAAGAAC AAGCGAAAAA GATTGCCCAA
 CAAGCAGCTG AATTAAAAAGC CAAAAATGAA AAAATTGCCA AAGAAAATGC AGAAATTGCG
 GCAAAAAACA AAGCNGAAAA AGAGCGNTAN GANAAAGAAG TCGCNGAATA CAACAAGCAT
 AAGAACGAAA ACAGCTATGT CAATGAAGCG ATTAGTAAAA ACCTAGTGTT CGATCAATCT
 GTCGTGACGA AAGACACTAA AATTTCGTG ATTAAGGCG GAAAAATTAT CAAAGCAACT
 GATTTTAATA AAGTAAATGC AGGGGATTCA AAAGATATCT TTACAAAATT ACGGAAAGAT
 ATGGNGGGA AAGNTACTGG CAACTTCCAG AATTCCTTTG TAAAAGAGGC AAATCTGGG
 TCTAATGGTG GGTATGCGGT TCTTTTAGAA AAAAATAAAC CAGTGACAGT GACCTATACA
 GGACTAAACG CTAGTTATTT AGGACGTAAA ATTACAAAAG CAGAATTGTT TTATGAACTA
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 ACNGCTTTTA TTGGTACAAA CAGAGTCAAT GGTAAGGATG TTAAAACACG CTTAACGATT
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 GATTTTGGGG CNAACAATGC GTTCAAATAC ATTAATGGNT CNTATGTGAA AAAACAAGCG
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 AATAGTGATT GGGACGCTGT AGGTACAAG AATGCCTACT TTGGTTTCAAG TGTAGGTCTA
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 ACAGAACTTG CCAAAGTAGA TCCAAAAACA GTAACNAAAC AAGGGATTTCG AGATACNTTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GATGCAGAAA AAGTGACGAT TGATTTATCC AAAGTGAAAG TTTATCAAGC AGACGCAAGT
 CTNAACGANA AAGACTNAAA AGCTGTTGCT GCAGCNATTA ATTCAGGAAN AGCTAAAGAC
 GTGACTGCTT CTTATGANCT CAATTTAGAT CAAAACACCG TCACAGCAAT GATGAAAACC
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 GTAGTGAAAA ATGTAGAAGG CGATTTTGAA AATACAGCTG TTCAGCTGAC AAANGATGGN
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 AAAGCAGATA AAAACGGTAC AGTTGGCAGT GTTTCTCTAC ATGATAAAGA TATTCCGTTA
 CAAACAAAAA TTTATTATGA AGTGAAATCT TCCGAACGTC CAGCNAACTA TGGCCGAATN
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 GATATTTCTG CCTACATTCT TTTAGAAAAC AAAGACAATA AAGACTTGAC GTTTACNATG
 AATCAAGCAT TATTGGCNGC NTTAAATGAA GGAAGCAATA AAGTAGGCAA ACAAGCTTGG
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 AACTACAACA AAGAGCTTGT NCGTTCATAT ACNGTGGTGA CGCATACNCC TGATGATCCA
 AAACCAACCA AAGCCJTTCA TAACAAGAAA GGGGAAGANA TTAANCATGG AAAAGTNGCT
 CGTGGTGATG TTCCTTCTTA TGAAATGACN TGGGACTTAA AAGGGTACGA TAAAGACTTT
 GCCTTTGATA CAGTCGATCT TGGCAGAGGC GTTTCTTTCT TCGATGATTA CGATGAAACG
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 TCGAAACTAT TCACGATGAC CTTTGAACAA GGGGTAGTGA AAATCACGGC CAGTCAAGCC
 TTTTNGATG CGATGAATCT AAAAGAAAAC AAAAAACGTTG CACACTCATG GAAAGCGTTC
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 AATGAGAAGA TTAACACNAA TACGGTAGTG ACNCATACGC CAGAAAAACC ACAAACNCCA
 CCAGAAAAAA CAGTGATTGT ACCACCAACA CCAAAAACAC CGCAAGCACC AGTAGAGCCA
 TTAGTGGTAG AAAAGGCAAG TGTNGTGCCA GAATTGCCGC AAACAGGCGA AAAACAAAAT
 GTCTTATTAA CGGTAGCTGG TAGTTTAGCC GCAATGCTTG GCTTAGCAGG CTTAGGCTTT
 AAACGTAGAA AAGAAACAAA ATAA

EF064-2 (SEQ ID NO:242)

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 PDLQSEKETP KTAVSEETV QKDTTSQPTK VEEVAPENKG TEQSSATPND TTNAQQPTVG
 AEKSAQEOPV VSPETTNEPL GQPTVAPAE NEVNKSTSIP KEFETPDVDK AVDEVKKDPN
 ITVVEKPAED LGNVSSKDLA AKEKEVDQLQ KEQAKKIAQQ AAELKAKNEK IAKENAEIAA
 KNKAERKEXX KEVAEYNKHK NENSYVNEAI SKNLVFDQSV VTKDTKISSI KGGKFIKATD
 FNKVNAGDSK DIFTKLKDKM GKKXTGNFQN SFVKEANLGS NGGYAVLLEK NKPVTVTYTG
 LNASYLGRKI TKAEFVYELQ SSPSQSGTLN AVFSNDPIIT AFIGTNRVNG KDVKTRLTIK
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 GKFYSPEDID YGTGPSGLKN SDWDAVGHNK AYFGSGVGLA NGRISFSFGM TTKGKSNVPV
 SSAQWFAPXT NLNAQSVKPI FNYGNPKEPE KATIEFNXYK ANVVPVLVPN KEVTDGQKNX
 NDLNVXRGDS LQYIVTGDIT ELAKVDPKTV TKQGIRDITD AEKVITIDLSK VKVYQADASL
 NXKDXKAVAA AINSXKAKDV TASYXLNLDQ NVTAMMKTN ADGSVVLAMG YKYLVLFPFV
 VKNVEGDFFEN TAVQLTXDGE TVTNTVINHV PGSNPSKDVK ADKNGTVGSV SLHDKDIPLQ
 TKIYYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTGKW HAITXYDLKV GXKTLKAGTD
 ISAYILLENK DNKDLTFTMN QALLAALNEG SNKVGKQAWS VYLEVERXKT GDVENTQTEN
 YNKELVRSNT VVTHTPDDPK PTKAVHNKKG EXIXHGKVAR GDVLSYEMTW DLKGYDKDFA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

FDTVDLATGV SFFDDYDETX VTPIKDLLRV KDSKGDITN QFTISWDDAK GTVTXSAKDP
 QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFGQR IKTNTVVNHI PKVXPBKDVV
 IKVGDQSQN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISDKLDVKH DKFSGQWSVF
 ANSNFVLADG TKVNGDDIS KLFTMTFEQG VVKITASQAF XDAMNLKENK NVAHSWKAFI
 GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPQTPP EKTIVPPTP KTPQAPVEPL
 VVEKASVPE LPQTGEKQNV LLTVAGSLAA MLGLAGLGFK RRKETK

EF064-3 (SEQ ID NO:243)

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 GTGACTGCTT CTTATGANCT CAATTTAGAT CAAAACACCG TCACAGCAAT GATGAAAACC
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 GTAGTGAAAA ATGTAGAAGG CGATTTTGAA AATACAGCTG TTCAGCTGAC AAANGATGGN
 GAAACGGTAA CAAATACAGT GATTAACCAT GTGCCAGGTA GTAATCCTTC CAAAGATGTA
 AAAGCAGATA AAAACGGTAC AGTTGGCAGT GTTTCTCTAC ATGATAAAGA TATTCCGTTA
 CAAACAAAAA TTTATTATGA AGTGAAATCT TCCGAACGTC CAGCNAACTA TGGCGGAATN
 ACNGAAGAAT GGGGCATGAA TGATGTCTTG GACACGACCC ATGATCGTTT CACAGGNAAA
 TGGCACGCTA TTACNAANTA TGACCTTAAA GTAGGGGANA AAACGTTAAA AGCAGGAACA
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 CCACAAGCCT TTATTCTAGC GNATGGTGGG CAAGAATTGC GTGTAACNCT CCTACAAAA
 GTCAAAGCCG ATGTTTCTGG NGATGTTTAT AATTTCAGCGG AACAAAATAC ATTTGGNCAA
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 TCGAAACTAT TCACGATGAC CTTTGAACAA GGGGTAGTGA AAATCACGGC CAGTCAAGCC
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EF064-4 (SEQ ID NO:244)

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 VKNVEGDFEN TAVQLTXDGE TVTNTVINHV PGSNPSKDV ADKNGTVGSV SLHDKDIPLO
 TKIYYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTGKW HAITXYDLKV GXKTLKAGTD
 ISAYILLKEN DNKDLFTTMN QALLAALNEG SNKVGKQAWS VYLEVERXKT GDVENTQTEN
 YNKELVRNST VVTHTPDDPK PTKAVHNKKG EXIXHGKVAR GDVLSYEMTW DLKGYDKDFA
 FDTVDLATGV SFFDDYDETX VTPIKDLLRV KDSKGDITN QFTISWDDAK GTVTXSAKDP
 QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFGQR IKTNTVVNHI PKVXPBKDVV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

IKVGDQSQN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISDKLDVKH DKFSGQWSVF
 ANSNFVLADG TKVNGDDIS KLFMTTFEQG VVKITASQAF XDAMNLKENK NVAHSWKAFI
 GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPQTPP EKTIVVPPTP KTPQAPVEPL
 VVEKASV

EF065-1 (SEQ ID NO:245)

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 CATTCACACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAACCTAAAC AACCGCTAAA ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCACCA
 ACGAACCCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TTCATTTACC AATGACTAAT
 ACAACAGTAA ATCCACTTTA CATGATCGCA GGTTAATTG TCCTTATAGT GGCTATTAGC
 TTTGGCATAA CAAAAAATAA AAAAAGAAAA AATTAG

EF065-2 (SEQ ID NO:246)

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 MLASYRGGKQ FMFPDGKTKI NSADYDMNVR VNTQLTYDKS QFVSGFGDVR TYGGTPTAPG
 LKLALDTYNQ THGDLTNRKT YFLLVTDGVA NTRLDGYLHK TNTNDSINEY PDPRHPLQVS
 VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGFPFVKQE
 LQQSSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
 NDVPVQINGQ TISATSTEGY VGNITIHIEV KENTAIDAAT LVSSGTMNQG TIAKEFPEAT
 IPKNDNAHAC DVTPEPTIT KDIENQEHLD LTNREDSFDW HVKTAFGNET STWTQASMVD
 DINKVLDIID VKVTDENGKD VTANGTVTQE NNKVTFEMNK QADSVDYLSG HTYTMTITTK
 IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHNSNKP VTPPPVDPNI AKDVEGQEH
 DLNTRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDT DVKVTDENGK DVTANGKVTQ
 ENNKVTFEMN XQADSVDYLS GHTYTMTITT KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHNSNKP TVTPPAPTPE DPTITKDIEG QEHLDLNTRD QEFKWNVKA FGNETSTWTQ
 ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
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EF065-3 (SEQ ID NO:247)

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 AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
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CAAGAAAATA ACAAAGTAAC TTTTGAAATG AACAANCAAG CNGACAGCTA TGAATATTTA
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GAATTAGCAC CTTATATTGA ACAAGGTGGC ATTCCCAACC AAGCCGACTT GAACTTTGGC
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CATTTCAACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCT
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EF065-4 (SEQ ID NO:248)

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EF066-1 (SEQ ID NO:249)

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TCAGTGGAAT ATAGTAATGA CTACCAAGGT GCAGCAGCAG AAGTTTTCAG GTTAAACCAA

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAAATTACTA ACCAAGGCTA TGAAATGATT AATGCGTATT GGGAAAGTGT TGAATCTTTA
 AGTTCAGTGA ATTCACTACTT TGATAAATAT AAAACAGAAG TGGGTCCCTTT TGTAACAA
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EF066-2 (SEQ ID NO:250)

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 VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPFVKQE
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 EGDVLHNSKP TVTPPAPTPE DPTITKDIEG QEHLDLTNRD QEFKWNVKA FGNETSTWTQ
 ASMVDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

PKQPLKPKKP LTPTNHQAPT NPVNFGKSAS KGIHLPMNT TVNPLYMIAG LIVLIVAISF
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EF066-3 (SEQ ID NO:251)

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AGTTCAGTGA ATTCATACCT TGATAAATAT AAAACAGAAG TGGGTCCCTT TGTAACAA
GAGTTGCAAC AAGGGTCTAG CACACCAGAA GATTTTATTA CAAGCCAATC TATTGATGAT
TTTACAACCC AATTAAAACA AATTGTCAAA GATCGTCTGG CGCAATCGAC ACCAGCAACA
GCTTCATTAA CGATTGCCAA TCAATTTGAT ATTCAATCTG CGACCGCTAC GGACGATGCT
GGAAATGATG TGCCTGTTCA AATTAACGGA CAAACCATT T CAGCAACTAG TACAGAAGGT
TACGTAGGAA ACATCACGAT TCACTACGAA GTCAAAGAAA ATACAGCGAT TGATGCAGCA
ACCCCTGTAA GTAGTGGGAC AATGAATCAA GGAACAATTG CTAAGGAATT TCCAGAAGCG
ACGATTCCTA AAAATGACAA TGCGCATGCG TGTGACGTGA CGCCAGAAGA TCCAACGATT
ACAAAAGATA TCGAAAATCA AGAACACTTA GATTTAACCA ATCGTGAAGA TAGTTTCGAT
TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCCAAGC CAGCATGGTG
GATGACATTA ATAAAGTGCT AGATATCATT GATGTGAAAG TCA

EF066-4 (SEQ ID NO:252)

AVKAGDTEGM TNTVKVKDDS
LADCKRILEG QATFPVQAGE TEPVDLVVVE DASGSFSDNF PHVRQAIDEV VQGLSDQDRV
MLASYRGGKQ FMFPDGKTKI NSADYDMNVR VNTQLTYDKS QFVSGFGDVR TYGGTPTAPG
LKLALDTYNQ THGDLTNRKT YFLLVTDGVA NTRLDGYLHK TMTNDSINEY PDPRHPLQVS
VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPFPVKQE
LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
NDVPVQINGQ TISATSTEGY VGNITIHIEV KENTAIDAAT LVSSGMTNQG TIAKEFPEAT
IPKNDNAHAC DVTPEPTIT KDIENTEHL D LTNREDSFDW HVKTAFGNET STWTQASMVD
DINKVLDIID VKVT

EF067-1 (SEQ ID NO:253)

TAGCGAAAGA AAATAGGGAG GATTAAAATG TTTAAGAAAG CAACGAAATT ATTATCGACA
ATGGTGATTG TCGCTGGAAC AGTTGTGGGA AATTTCAGTC CCACATTGGC TTTAGCTGAA
GAAGCGGTTA AAGCAGGAGA TACAGAAGGA ATGACCAATA CGGTGAAAGT GAAAGACGAC
AGTCTGGCTG ATTGTAAACG GATATTGGAA GGACAAGCTA CTTTCCCAGT TCAAGCGGGT
GAAACGGAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GTGGTAGTTT TTCAGATAAT
TTTCCACATG TAAGACAAGC GATTGATGAA GTGGTTCAAG GCTTATCTGA TCAAGACCGC
GTGATGCTGG CTTCATATCG CGGCGGAAAA CAATTTATGT TTCCTGATGG AAAGACAAAA
ATTAATTCAG CTGATTATGA TATGAATGTG CGCGTCAATA CGCAATTGAC TTATGATAAA
AGCCAATTTG TCTCTGGTTT TGGAGACGTT CGGACGTATG GTGGTACGCC AACCGCCCCA
GGATTGAAAC TCGCTTTAGA TACGTACAAT CAAACACACG GAGATTTAAC GAATCGAAAA
ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTTAGATGG TTACTTGCAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAGACCAATA CCAATGATTC AATCAATGAA TATCCAGATC CAAGACATCC TCTTCAAGTC
 TCAGTGGAAAT ATAGTAATGA CTACCAAGGT GCAGCAGCAG AAGTTTTAGC GTTAAACCAA
 GAAATTACTA ACCAAGGCTA TGAAATGATT AATGCGTATT GGGAAAGTGT TGAATCTTTA
 AGTTCAGTGA ATTCTACTTT TGATAAATAT AAAACAGAAG TGGGTCCTTT TGTAACACAA
 GAGTTGCAAC AAGGTCTAG CACACCAGAA GATTTTATTA CAAGCCAATC TATTGATGAT
 TTTACAACCC AATTAAAAACA AATTGTCAAAA GATCGTCTGG CGCAATCGAC ACCAGCAACA
 GCTTCATTAA CGATTGCCAA TCAATTTGAT ATTCAATCTG CGACCGCTAC GGACGATGCT
 GGAAATGATG TGCCTGTTCA AATTAACGGA CAAACCATT T CAGCAACTAG TACAGAAGGT
 TACGTAGGAA ACATACGAGT TCACTACGAA GTCAAAGAAA ATACAGCGAT TGATGCAGCA
 ACCCTTGTAA GTATGCGGAC AATGAATCAA GGAACAATTG CTAAGGAATT TCCAGAAGCG
 ACGATTCTTA AAAATGACAA TGCGCATGCG TGTGACGTGA CGCCAGAAGA TCCAACGATT
 ACAAAGATA TCGAAATCA AGAACACTTA GATTTAACCA ATCGTGAAGA TAGTTTCGAT
 TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCCAAGC CAGCATGGTG
 GATGACATTA ATAAAGTGCT AGATATCATT GATGTGAAAG TCACCGACGA AAATGGTAAA
 GATGTTACAG CTAACGGCAC AGTAACACAA GAAAATAACA AAGTAACCTT TGAAATGAAC
 AAACAAGCAG ACAGCTATGA CTATTTAAGT GGTCATACGT ATACAATGAC TATCACCCT
 AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT
 CCCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGACG TGTTACATTC CAACAAACCA
 ACCGTAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAGG ACAAGAACAT
 TTAGATTTAA CCAACCGCGA TCAAGAAATT AAATGGAACG TCAAAACAGC TTTCGGTAAAC
 GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
 ACTGATGTAA AAGTCACAGA TGAAAATGGT AAAGATGTTA CAGCTAACGG CAAAGTAACA
 CAAGAAAATA ACAAAGTAAC TTTTGAAATG AACAANCAAG CNGACAGCTA TGACTATTTA
 AGTGGTCATA CGTACACAAT GACCATTACT ACTAAAATCA AAGCTAGCGC AACGGACGAA
 GAATTAGCAC CTTATATTGA ACAAGGTGGC ATTCCCAACC AAGCCGACTT GAACTTTGGC
 AACGAAGGTG ACGTGTTCGA TTCCAACAAA CCAACCGTAA CACCACCTGC ACCAACGCCA
 GAAGATCCAA CGATTACAAA AGATATCGAA GGCCAAGAAC ATTTAGATTT AACCAACCGT
 GACCAAGAAT TTAAATGGAA CGTCAAAACA GCTTTCGGTA ACGAAACAAG CACATGGACC
 CAAGCCAGCA TGGTGGATGA CATTAAATAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
 GANGAAAATG GCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAA TAACAAAGTA
 ACTTTTACTA TGAACAAAAA AGATGACAGC TACTCTTACT TAGCTGGTCA TACATACACA
 ATGACTATTA CCACTAAAAT TAAACTGAC GCAACGGATG AAGAATTAGC GCCTTATATT
 GAACAAGGCG GGATTCCCAA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTTG
 CATTCCAACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCT
 GAACCTAAAC AACCGCTAAA ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCACCA
 ACGAACCCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TTCATTTACC AATGACTAAT
 ACAACAGTAA ATCCACTTTA CATGATCGCA GGTTTAATTG TCCTTATAGT GGCTATTAGC
 TTTGGCATAA CAAAAAATAA AAAAAGAAAA AATTAG

EF067-2 (SEQ ID NO:254)

MF KKATKLLSTM VIVAGTVVGN FSPTLALAE AVKAGDTEGM TNTVKVKDDS
 LADCKRILEG QATFPVQAGE TEPVDLVVE DASGSFSDNF PHVRQAIDEV VQGLSDQDRV
 MLASYRGKQ FMFPDGKTKI NSADYDMNR VNTQLTYDKS QFVSGFGDVR TYGGTPTAPG
 LKLALDTYNQ THGDLTNRKT YLLVTDGVA NTRLDGYLHK TNTNDSINEY PDPRHPLQVS
 VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPFPVKQE
 LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
 NDVPVQINGQ TISATSTEGY VGNITIHVEY KENTAIDAAT LVSSGTMNQ TIAKEFPEAT
 IPKNDNAHAC DVTPEPTIT KDIENTEHL LTNREDSFDW HVKTAFGNET STWTQASMVD
 DINKVLDIID VKVTDENGKD VTANGTVTQE NNKVTFEMNK QADSYDLSG HTYTMITTK
 IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHNSKPT VTPPPVDPNI AKDVEGQHL
 DLNTRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDIT DVKVTDENGK DVTANGKVTQ
 ENNKVTFEMN XQADSYDLS GHTYTMITTT KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHNSKP TVTPPAPTPE DPTITKDIEG QEHLDTNDR QEFKWNVKA FGNETSTWTQ

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLKPKKP LTPTNHQAPT NPVNF GKSSAS KGIHLPMTNT TVNPLYMIAG LIVLIVAISF
 GITKNKKRKN

EF067-3 (SEQ ID NO:255)

GCT AGATATCATT GATGTGAAAG TCACCGACGA AAATGGTAAA
 GATGTTACAG CTAACGCGAC AGTAACACAA GAAAAATAACA AAGTAACTTT TGAAATGAAC
 AAACAAGCAG ACAGCTATGA CTATTTAAGT GGTCATACGT ATACAATGAC TATCACCCT
 AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT
 CCCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGACG TGTTACATTC CAACAAACCA
 ACCGTAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAGG ACAAGAACAT
 TTAGATTTAA CCAACCGCGA TCAAGAAATTT AAATGGAACG TCAAAACAGC TTTTCGGTAAC
 GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
 ACTGATGTAA AAGTCACAGA TGAAAATGGT AAAGATGTTA CAGCTAACGG CAAAGTAACA
 CAAGAAAATA ACAAAGTAAC TTTTGAATG AACAANCAAG CNGACAGCTA TGACTATTTA
 AGTGGTCATA CGTACACAAT GACCATTACT ACTAAAATCA AAGCTAGCGC AACGGACGAA
 GAATTAGCAC CTTATATTGA ACAAGGTGGC ATTCCCAACC AAGCCGACTT GAACTTTGGC
 AACGAAGGTG ACGTGTTGCA TTCCAACAAA CCAACCGTAA CACCACCTGC ACCAACGCCA
 GAAGATCCAA CGATTACAAA AGATATCGAA GGCCAAGAAC ATTTAGATTT AACCAACCGT
 GACCAAGAAT TTAAATGGAA CGTCAAAACA GCTTTCGGTA ACGAAACAAG CACATGGACC
 CAAGCCAGCA TGGTGGATGA CATTAAATAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
 GANGAAATG GCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAAA TAACAAAGTA
 ACTTTTACTA TGAACAAAAA AGATGACAGC TACTCTTACT TAGCTGGTCA TACATACACA
 ATGACTATTA CCACTAAAAT TAAACTGAC GCAACGGATG AAGAATTAGC GCCTTATATT
 GAACAAGGCG GGATTCCTCA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTTG
 CATTCCAACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCT
 GAACCTAAAC AACCCTAAA ACCGAAAAA CCGTTGACGC CTACAAATCA TCAAGCACCA
 ACGAACCCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TT

EF067-4 (SEQ ID NO:256)

VLDIID VKVTDENGKD VTANGTVTQE NNKVTFEMNK QADSYDYLSG HTYMTITTK
 IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHNSNKPT VTPPPVDPNI AKDVEGQEH
 DLNTRDQEFK WNVKTAFGNE TSTWTQASV DDINKVLDIT DVKVTDENGK DVTANGKVTO
 ENNKVTFEMN XQADSYDYLS GHYTMITTT KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHNSNK TVTPPAPTPE DPTITKDIEG QEHLDLNTRD QEFKWNVKTA FGNSTSTWTQ
 ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLKPKKP LTPTNHQAPT NPVNF GKSSAS KGIH

EF068-1 (SEQ ID NO:257)

TAGGGGAAGC TAATGATCTT GGTATTTATC GTTTATTTTA AAGAAAAGAG GGACGATCAG
 ATGAAAAAGA AAATTGTTGA GGATTTTAAT CGGAAAAGTC AGCATAAAAA ATGGACAAAA
 CGCAAGATGC TTAATTTAGC AATATCAAGT GGTTTATTAT TTACGTCATT AGCAATCCCT
 GTAAGTATAG CTGTTACCTC TGGCACAATC AGTGCATCAG CAGCGGTCTT GGATATCGAA
 CTATTATCAA ATGTTACCTC AAATAATGAC AGTGGCATT CAACGAGTAA TCGTTGGACA
 GCCGCAAACC AAAATCAACC AGTTAATTTT ACGGTTTCTG GTGGCGCTTT AGCAGATGCT
 TCCGCTGTGT TTAGTGGACA AAAACAAGCG GTGTTAGTGG TTCCTCCTGA GTTAAGAGGA
 AATGTAGCTG CAGCAGGCAG CGCAGCAATC AATACCAATG TCACGATTGA TCTTTCAAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

| | | | | | |
|-------------|-------------|-------------|-------------|------------|-------------|
| GTTACTTTTT | TGACTGCCGT | TTTGAATGCA | GCCAATGATT | TAACCAATGT | GATTACTCAA |
| ATTACCAGTG | GGGCGTTAGG | GAATTTAACT | GGTGTGATA | TTGATTGAC | GGAAGTGAAT |
| CGTCAATTGG | AATTAGTTAA | TAACATTGAA | AACTTAGGTG | CTGCTTCATT | TACAGCTCCG |
| GAAACGTTAG | CAGCTGACGG | CTCATACATT | AGTGCACCGA | TTAGTGATGG | TTTAGGGTTA |
| GTTTTAGCCC | AAAATGTTTC | AAACATCTTA | CAAGATTTGA | ATGCCGCAGT | TCAAGCTTTG |
| GAGGCAAAAG | GTACCAGTAT | CCCAAGTAAT | CTTGTCGCCG | CAGCTATAAA | TGCAGCCTTG |
| CTTCCTGTCA | AAGGCACGGT | AAACGTGGCT | GTTTCAGGTG | CTTTGCCTTT | ATTAGCGGTT |
| GGTGGTTTCA | GCGTAAATGA | GTTAGTGGAT | GCTTCTTTAC | TAGGCACAAC | CACGGTTACT |
| TTACCAACTA | CCGTTTCAAC | ACCTCAAAAT | TTATCCAATA | ATTTAGATGC | TCGTTTGTGA |
| GGAACAGTCG | TTCAAACAGA | TCTTTTAGAC | GTTAATTTAT | TAGCAACAGC | AGACGGTGTA |
| TCCAACATTT | ATTTTGCTGC | AGGCACTACT | AGTGAAGTAA | CCGCACCAAC | AATCACAGGA |
| GTAACAGGTA | ATTCAACAGC | AGGTACGAA | GTTAAAGGAA | CTGCCGATGC | CAATGCCACG |
| GTTGAAATCC | GAAATGCAGG | AGGCACCGTA | ATAGGCACAG | GTACCGCTGA | TGGGACAGGA |
| GCGTTTACAG | TTACCGTTCC | CGCAGGTGAA | GCAGGCGCCA | ATGAAACGTT | AACCGCCGTA |
| GCGAAAAACG | CCAGCGGNAC | AGAAAGNACG | CCAACAACGT | TCCAAACNCC | AGCGGATGAA |
| GCAACCGTAA | CCGCACCAAC | AATCACAGGA | GTGACAGGTA | ATTCAACGGC | AGGTTACGAA |
| GTTAAAGGAA | CTGCCGATGC | CAATGCCACG | GTTGAAATCC | GAAATGCAGG | AGGCACCGTA |
| ATAGGCACAG | GTACCGCTGA | TGGGACAGGA | GCGTTTACAG | TTACCGTTCC | CGCAGGTGAA |
| GCAGGTGCCA | ATGAAACGTT | AACCGCCGTA | GCGAAAAACG | CCAGCGGCAC | AGAAAGTACG |
| CCAACAACGT | TCCAAACACC | AGCGGATGAA | GCAACCGTAA | CCGCACCAAC | AATCACAGGA |
| GTGACAGGTA | ATTCAACAGC | AGGTTACGAA | GTTAAAGGAA | CTGCCGATGC | CAATGCCACG |
| GTTGAGATCC | GAAATGCAGG | AGGTGCCGTG | ATAGGTACAG | GTACTGCTGA | TGGGACAGGG |
| GCATTTACAG | TTACCATTTCC | CGCAGGTGAA | GCAGGTGCGA | ATGAAACGTT | AACCGCCGTA |
| GCGAAAAACG | CCAGCGGTAC | AGAAAGTACG | CCAACAACGT | TCCAAACGCC | AGCGGATCCT |
| AATACGCCCG | TGGCGACGCC | AATTGTTGAG | ACTGTAACAG | GTAGTACAAC | AAAAGGCTAT |
| GAGGTCAAAG | GGACTGCTGA | AGTTGGCACC | ACCATTGAGG | TTCGCGATGC | AGCTGGCACC |
| GTCTTTGGTA | CTGCAACAAC | TGGAAC TGAC | GGAAAATATA | CAGTGACTTT | AGATTCAGGA |
| ACAGCAACAG | CAAAATCAAAC | GCTGAGCGTT | GTAGCGAAAA | ACGCTAGTGG | CACGGAAAGT |
| CAACAGCAAA | CGGCGACAAC | ACCAGCTGAT | GTCACTGCAC | CAACAGTTGA | TAACATCACAA |
| GGCAACTCTG | GTTCCGGTTA | TGAAATTACA | GGAACAGCAG | ACCCTAACAC | AACAATCGAA |
| GTTCTGTGATC | CATCTGGGGC | AGTCATTGGT | ACAGGTACCT | CTGATGCGAA | TGGTGATTTT |
| ACTGTAACGC | TACCAACGGG | AACGACCAAT | CCTGGGGATA | CGTTAACAGT | GATTGGAAAG |
| GATAACGCGG | GAAATGAAAG | TCAACCGACT | GAAGTCCTTG | TTCTGTCTGA | TGCCACGGTT |
| ACAGCACCAA | CTGTAACAGG | AGTAACAGGT | AATTCAGTTG | CTGGTTATCA | GGTGACAGGC |
| ACCGCTGATC | CGAATGCTAC | CATCGAAAAT | CGTGATGCAG | ATGGGAACGT | GATTGCAACA |
| GGGACTGCCG | ATGGGACTGG | TTCTTTTGCT | GTGAACCTTC | CAGCTGGGAC | GGCAATGCGG |
| AATGAAACAT | TGACAGCGTT | AGCCAAAGAT | CCTGCTGGCA | ATACAAGTAC | ACCGACAACC |
| TTCCAAACAC | CAGCAGATGA | AGTAGTGGCA | CCGCCAAGTG | TCGACAAAGT | TACTGGGAAT |
| ACAACACAAG | GATATCAAGT | GACAGGTACC | GCTGAAC TTG | GCACCACCAT | TGAAGTTTCGT |
| GCAACAGACG | GAACAGTTTT | AGGCACCGCA | ACAAC TGAC | CGACTGGCCA | ATATACTGTG |
| ACGTTAGCTT | CAGGAAAAGC | AACAGCTAAA | CAAACAGTGA | ATGTAGTTGC | TAAAAATGAT |
| ACTGGACTTG | AGAGTCAACC | AACTACAGCT | ATGACACCCG | CTGATGTTAC | CACACCAACA |
| ATTGGTGACA | TTACTGGAGA | TTCAACAAC T | GGTTATGAAA | TCACTGGGAC | GGCGGACCTT |
| AATACCACCA | TTGAAGTACG | GAACCCAGAT | GGAACAATTA | TTGGTACAAC | GACAACGGAT |
| GATCAAGGAA | ACTTTACTGT | GGACCTTCCA | GCGGGAGCCG | CTAATCCTGG | TGATACATTA |
| ACAGTTGTTG | GAAAAGACCG | TGACGGCAAT | GAAAGTCAAC | CAACGGAAGT | GACGGTCCCT |
| GAAGATGCAA | CCGTAGCAGC | ACCAACTGTG | ACGACTGTTA | CAGGAACAAC | TGCCACTGGG |
| TATCAAGTAA | CCGGCACGGC | AGAGCCAAAT | GTCACCAT TG | AGATTACAAA | TGAAGCAGGT |
| TTAGTTATTG | CTACGGGAAC | GACTGATGGT | GCTGGCGCAT | TTACAATCAC | TCTTCCGACG |
| GGCACAAGCA | CAGCTAACGA | AGCCTTAACT | GCCATTGCGA | AAGATGCTGC | TGGGAAAGAA |
| AGTAATCCGA | CTGCTTTTCAA | AACACCTGCT | GATCCAGATG | CACCAAGTCG | GACACCTACT |
| GTTGACAAAA | TCACTGGTAG | CACGACAAAC | GGCTATCAAG | TAGTAGGAGC | AGCAGAAGTT |
| GGTACAACAG | TTGAGGTGCG | TGACGCCGAT | GGCACAGTCC | TTGGCATGGC | AACTACTGGA |
| ACTGATGGCA | AATACACAGT | GACTTTAGAG | CCAGGGAAGG | CCTCAGCTAA | CGAAACAATA |

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

| | | | | | |
|------------|-------------|------------|------------|------------|-------------|
| ACTGTCGTAG | CGAAAAATGC | AACAGGAAAA | GAAAGTCAGC | CAGCTACAGC | AACTACACCA |
| GTCGACTTAG | CCACACCAAC | CATTGATTCT | ATTACCGGAA | ATTCTAGTAA | AGGTTACGAA |
| ATCACTGGAA | CGGCGGAGCC | AAAAACCACT | ATTGATGTCC | GTGACGCAGA | CGGAACCATC |
| ATTGCTGCTA | CAACTGCTAA | CGAAACCGGC | CAATATACGG | TGACTCTACC | AGCTGGCGTA |
| GTGACACCAG | GAGAAACGAT | TACGATTATT | AGCAAAGATG | GCGCAGGTAA | TGAAAGTCAA |
| CCAGCTACAG | CCGTTATTCC | AGCGGATGTT | GTTTTAGCGG | CGCCAACAT | TACGAAGGTT |
| GAAGGAAACA | AAGCCAATGG | CTATACAGTC | ACTGGAAGTG | CTGATCCAAA | TGTCACGGTT |
| CAATTTTACA | ATAGCAGTGA | ACAATTATTG | GCAAGTGGCA | ATACAACATC | TGGAGGTACC |
| TTCTCCGTTT | ATATTGCAGC | AGGGTTAGCA | ACAGAAAAAG | AAACGTTAAC | CGCACTAACC |
| ACAGATACAC | AAGGAAATGT | GAGTCCTAAA | ACCACATTTA | TGACGCCAGC | CGATATTACG |
| GGAGAACCAG | AGATTAAAT | TGCGGCACCA | ACTGTTTCTT | CAGTTTTAGG | AACGTCTAAA |
| GCCGGCTACC | TCATCAAAGG | AACAGCTGAA | CCAAACCGAA | TCATTCAAAT | TAGTAACCGA |
| CTATTAAGAA | TGTGTGATTGC | TGTAGGTGCC | ACCGATGCTG | AAGGCAACTT | CGCTATCCAA |
| TTAACAGCGG | GACAAGCGAC | TGCTCAACAA | AGTTTACTTG | CGACAGCTAC | CGATGGCGCA |
| GGACATTACA | GTACGGCTAC | AACCTTCATG | ACGCCAGCCG | ACCCAACGAA | TCCTGGAGGA |
| GGCAATGGTA | CACTGGCGG | AAATAACGGC | AATACAGCGC | GCAATACAGG | AAACAATGGC |
| GCAACTGGCG | GGAATAATGG | GAATGGTTCA | AACACAGGTT | CAAATCCAAA | TGGAGGTTCT |
| GTTTTAGGCA | CAACAGGTTT | TGGCTTAGGT | TCACTAGGCA | ATGGCCTCGG | TACAAATGGT |
| AGTGGCTACC | ACCCTAAACT | AAGTACCATC | AGTTATGGCA | CTGGAAATCA | CGGGAAAACA |
| GGCTACTTAC | CTAGCACAGG | TGAAAAAGAG | TCTTCAGCCG | TGACAACAAG | TTTGTGTTGGC |
| GCCTTTGTGC | CACTCCTTGC | GAGCATGGGA | ATCATCAAAC | GCAAACGTAA | AAACTAG |

EF068-2 (SEQ ID NO:258)

M KKKIVEDFNR KSQHKWTKR KMLNLAISSG LLFTSLAIPV
 SIAVTSGETIS ASAAVLDIEL LSNVTSNNDG GTSTSNRWTA ANQNQPVNFT VSGGALADAS
 AVFSGQKQAV LVVPELGRN VAAAGSAAIN TNNVTIDLSKV TFLTAVLNAA NDLTNVITQI
 TSGALGNLTG VDIIDLTEVNR QLELVNNIEN LGAASFTAPE TLAADGSYIS APISDGLGLV
 LAQNVSNILQ DLNAAVQALE AKGTSIPSNL VAAAINAALL PVKGTVNVAV SGALPLLAVG
 GSGVNELVDA SLLGTTTTVTL PTTVSTPQNL SNNLDARFVG TVVQTDLLDV NLLATADGVS
 NIYFAAGTTS EVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
 FTVTVPAGEA GANETLTAVA KNASGTEXTPT TTFQTPADEA TVTAPTITGV TGNSTAGYEV
 KGTADANATV EIRNAGGTVI GTGTADGTGA FTVTVPAGEA GANETLTAVA KNASGTESTP
 TTFQTPADEA TVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
 FTVTVPAGEA GANETLTAVA KNASGTESTP TTFQTPADPN TPVATPIVET VTGSTTKGYE
 VKGTAEVGTI IEVRDAAGTV LGTATTGTDG KYTVTLDSGT ATANQTLSTV AKNASGTESQ
 PATATTPADV TAPTVDNITG NSGSGYEITG TADPNITIEV RDPGSAVIGT GTSDANGDFT
 VTLPTGTTNP GDTLTVIGKD NAGNESQPTG VLVPADATVT APTVTGVTGN SVAGYQVITGT
 ADPNATIEIR DADGNVIATG TADGTGSFAV NLPAGTANAN ETLTALAKDP AGNTSTPTTF
 QTPADEVVPV PSVDKVTGNT TQGYQVTGTA ELGTTIEVRA TDGTVLGTAT TGPTGQYITVT
 LASGKATAKQ TVNVVAKNDT GLESQPTTAM TPADVTTPTI GDITGDSTTG YEITGTADPN
 TTIEVRNPDG TIIGTTTTDD QGNFTVDLPA GAANPGDTLT VVGKDGDNNE SQPTEVTVPE
 DATVAAPTIV TVTGTATTGY QVTGTAEPNV TIEIHNEAGL VIATGTTDGA GAFTITLPTG
 TATANEALTA IAKDAAGKES NPTAFKTPAD PDAPVATPTV DKITGSTTNG YQVVGAAEVG
 TTVVEVRDADG TVLGMATTGT DGKYTVTLEP GKASANETIT VVAKNATGKE SQPATATTPV
 DLATPTIDSI TGNSSKGYEI TGTAEPKTTI DVRDADGTII AATTANETGQ YTVTLPAQVV
 TPGETITIIIS KDGAGNESQP ATAVIPADV LAAPTITKVE GNKANGYTVT GTADPNVTVQ
 FYNSSSEQLLA SGNNTTGGTF SVHIAAGLAT EKETLTALTT DTQGNVSPKT TFMTFPADITG
 EPEIKIAAQS VSSVLGTSKA GYLIKGTAEF NRRIQISNRL LRSVIAVGAT DAEGNFQIQL
 TAGQATAQPS LLATATDAGG HYSTATFMT PADPTNPGGG NGNTGGNNGN TGGNTGNNGA
 TGGNNGNGSN TGSNPNNGSG LGTTGSGLS LGNGLGTNGS GYHPKLTSTIS YGTGNHKGKTG
 YLPSTGEKES SAVTTSFLGA FVALLASMI IKRKRKN

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF068-3 (SEQ ID NO:259)

CTC TGGCACAATC AGTGCATCAG CAGCGGTCTT GGATATCGAA
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EF068-4 (SEQ ID NO:260)

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 TSGALGNLTG DLIDLTEVNR QLELVNNIEN LGAASFTAPE TLAADGSYIS APISDGLGLV
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 GSGVNELVDA SLLGTTTTVTL PTTVSTPQNL SNNLDARFVG TVVQTDLLDV NLLATADGVS
 NIYFAAGTTS EVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
 FTVTVPAGEA GANETLTAVA KNASGTEXP TTFQTP

EF069-1 (SEQ ID NO:261)

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 TCCGCTGTGT TTAGTGGACA AAAACAAGCG GTGTTAGTGG TTCTCCTGA GTTAAGAGGA
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 GTTACTTTTT TGACTGCCGT TTTGAATGCA GCCAATGATT TAACCAATGT GATTACTCAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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ATTACCAAGTG GGGCGTTAGG GAATTTAACT GGTGTTGATA TTGATTTGAC GGAAGTGAAT
CGTCAATTGG AATTAGTTAA TAACATTGAA AACTTAGGTG CTGCTTCATT TACAGCTCCG
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GTTTTAGCCC AAAATGTTTC AAACATCTTA CAAGATTTGA ATGCGGCAGT TCAAGCTTTG
GAGGCAAAAG GTACCAGTAT CCCAAGTAAT CTTGTGCGCCG CAGCTATAAA TGCAGCCTTG
CTTCCTGTCA AAGGCACGGT AAACGTGGCT GTTTCAGGTG CTTTGCCCTT ATTAGCGGTT
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AGTAATCCGA CTGCTTTCAA AACACCTGCT GATCCAGATG CACCAGTCGC GACACCTACT
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GGTACAAACG TTGAGGTGCG TGACGCCGAT GGCACAGTCC TTGGCATGGC AACTACTGGA
ACTGATGGCA AATACACAGT GACTTTTAGAG CCAGGGAAGG CCTCAGCTAA CGAAACAATA
ACTGTCGTAG CGAAAAATGC AACAGGAAAA GAAAGTCAGC CAGCTACAGC AACTACACCA

```

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 ATCACTGGAA CGGCGGAGCC AAAAACCACCT ATTGATGTCC GTGACGCAGA CGGAACCATC
 ATTGCTGCTA CAACTGCTAA CGAAACCGGC CAATATACGG TGA CTCTACC AGCTGGCGTA
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 CCAGCTACAG CCGTTATTCC AGCGGATGTT GTTTTAGCGG CGCCAACCTAT TACGAAGGTT
 GAAGGAAACA AAGCCAATGG CTATACAGTC ACTGGAACCTG CTGATCCAAA TGTACCGGTT
 CAATTTTACA ATAGCAGTGA ACAATTATTG GCAAGTGGCA ATACAACTAC TGGAGGTACC
 TTCTCCGTTT ATATTGCAGC AGGGTTAGCA ACAGAAAAAG AAACGTTAAC CGCACTAACC
 ACAGATACAC AAGGAAATGT GAGTCCTAAA ACCACATTTA TGACGCCAGC CGATATTACG
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 GCCGGCTACC TCATCAAAGG AACAGCTGAA CCAAACCGAA TCATTCAAAT TAGTAACCGA
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 GGTTTAGGCA CAACAGGTTT TGGCTTAGGT TCACTAGGCA ATGGCCTCGG TACAAATGGT
 AGTGGCTACC ACCCTAAACT AAGTACCATC AGTTATGGCA CTGGAAATCA CGGGAAAACA
 GGCTACTTAC CTAGCACAGG TGAAAAAGAG TCTTCAGCCG TGACAACAAG TTTGTTTGGC
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EF069-2 (SEQ ID NO:262)

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 AVFSGQKQAV LVVPPPELRGN VAAAGSAAIN TNVTIDLSKV TFLTAFLNAA NDLTNVITQI
 TSGALGNLTG VDIDLTEVNR QLELVNNIEN LGAASFTAPE TLAADGSYIS APISDGLGLV
 LAQNVSNILQ DLNAAVQALE AKGTSIPSNL VAAAINAALL PVKGTVNVAV SCALPLLAAG
 GSGVNELVDA SLGTTTTLV PTTVSTPQNL SNNLDARFVG TVVQTDLLDV NLLATADGVS
 NIYFAAGTTS EVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
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 KGTADANATV EIRNAGGTVI GTGTADGTGA FTVTVPAGEA GANETLTAVA KNASGTESTP
 TTFQTPADEA TVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGAVI GTGTADGTGA
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 TAGQATAQQS LLATATDGAG HYSTATTFTM PADPTNPGGG NGNTGGNNGN TGGNTGNNGA
 TGGNNGNGSN TGSNPNCGSG LGTTGSLGGS LGNGLGTNGS GYHPKLSTIS YGTGNHGKGT
 YLPSTGEKES SAVTTSLFGA FVALLASMG I KRKRKN

EF069-3 (SEQ ID NO:263)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 GAGGTCAAAG GGAAGTCTGA AGTTGGCACC ACCATTGAGG TTCGCGATGC AGCTGGCACC
 GTCCTTGCTA CTGCAACAAC TGGAACTGAC GGAAAAATATA CAGTGACTTT AGATTTCAGGA
 ACAGCAACAG CAAATCAAAC GCTGAGCGTT GTAGCGAAAA ACGCTAGTGG CACGGAAAGT
 CAACCAGCAA CGGCGACAAC ACCAGCTGAT GTCAGTGCAC CAACAGTTGA TAACATCACA
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EF069-4 (SEQ ID NO:264)

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 PATATTADV TAPTVDNITG NSGSGYEITG TADPNTTIEV RDPGSAVIGT GTSANGDFT
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 LASGKATAKQ TVNVVAKNDT GLESOPTTAM TPADVTTPTI GDITGDSTTG YEITGTADPN
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EF070-1 (SEQ ID NO:265)

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 ATTACCAGTG GGGCGTTAGG GAATTTAACT GGTGTTGATA TTGATTTGAC GGAAGTGAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

| | | | | | |
|-------------|-------------|------------|-------------|-------------|-------------|
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| GTTTTAGCCC | AAAATGTTTC | AAACATCTTA | CAAGATTGGA | ATGCGGCAGT | TCAAGCTTTG |
| GAGGCAAAAG | GTACCAGTAT | CCCAAGTAAT | CTTGTCGCCG | CAGCTATAAA | TGCAGCCTTG |
| CTTCCTGTCA | AAGGCACGGT | AAACGTGGCT | GTTTCAGGTG | CTTTGCCTTT | ATTAGCGGTT |
| GGTGGTTCAG | GCGTAAATGA | GTTAGTGGAT | GCTTCCTTAC | TAGGCACAAC | CACGGTTACT |
| TTACCAACTA | CCGTTTCAAC | ACCTCAAAAT | TTATCCAATA | ATTTAGATGC | TCGTTTTGTA |
| GGAACAGTCG | TTCAAACAGA | TCTTTTAGAC | GTTAATTTAT | TAGCAACAGC | AGACGGTGTA |
| TCCAACATTT | ATTTTGCTGC | AGGCACTACT | AGTGAAGTAA | CCGCACCAAC | AATCACAGGA |
| GTAACAGGTA | ATTCAACAGC | AGGTTACGAA | GTTAAAGGAA | CTGCCGATGC | CAATGCCACG |
| GTTGAAATCC | GAAATGCAGG | AGGCACCGTA | ATAGGCACAG | GTACCGCTGA | TGGGACAGGA |
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| CCAACAACGT | TCCAAACACC | AGCGGATGAA | GCAACCGTAA | CCGCACCAAC | AATCACAGGA |
| GTGACAGGTA | ATTCAACAGC | AGGTTACGAA | GTTAAAGGAA | CTGCCGATGC | CAATGCCACG |
| GTTGAGATCC | GAAATGCAGG | AGGTGCCGTG | ATAGGTACAG | GTACTGCTGA | TGGGACAGGG |
| GCATTTACAG | TTACCATTC | CGCAGGTGAA | GCAGGTGCCA | ATGAAACGTT | AACCGCCGTA |
| GCGAAAAACG | CCAGCGGTAC | AGAAAGTACG | CCAACAACGT | TCCAAACGCC | AGCGGATCCT |
| AATACGCCCG | TGGCGACGCC | AATTGTTGAG | ACTGTAACAG | GTAGTACAAC | AAAAGGCTAT |
| GAGGTCAAAG | GGACTGCTGA | AGTTGGCACC | ACCATTGAGG | TTCCGCGATGC | AGCTGGCACC |
| GTCCTTGCTA | CTGCAACAAC | TGGAACGTAC | GGAAAAATATA | CAGTGACTTT | AGATTACAGGA |
| ACAGCAACAG | CAAATCAAAC | GCTGAGCGTT | GTAGCGAAAA | ACGCTAGTGG | CACGGAAAGT |
| CAACCAGCAA | CGGCGACAAC | ACCAGCTGAT | GTCACGTGCAC | CAACAGTTGA | TAACATCACA |
| GGCAACTCTG | GTTCTGGGTTA | TGAAATTACA | GGAACAGCAG | ACCCTAACAC | AACAATCGAA |
| GTTCTGTGATC | CATCTGGGGC | AGTCATTGGT | ACAGGTACCT | CTGATGCGAA | TGGTGATTTT |
| ACTGTAACGC | TACCAACGGG | AACGACCAAT | CCTGGGGATA | CGTTAACAGT | GATTGGAAAG |
| GATAACGCGG | GAAATGAAAG | TCAACCGACT | GAAGTCCTTG | TTCTTGCTGA | TGCCACGGTT |
| ACAGCACCAA | CTGTAACAGG | AGTAACAGGT | AATTCAGTTG | CTGGTTATCA | GGTGACAGGC |
| ACCGCTGATC | CGAATGCTAC | CATCGAAATT | CGTGATGCAG | ATGGGAACGT | GATTGCAACA |
| GGGACTGCCG | ATGGGACTGG | TTCTTTTGCT | GTGAACCTTC | CAGCTGGGAC | GGCAAATGCC |
| AATGAAACAT | TGACAGCGTT | AGCCAAAGAT | CCTGCTGGCA | ATACAAGTAC | ACCGACAACC |
| TTCCAAACAC | CAGCAGATGA | AGTAGTGGCA | CCGCCAAGTG | TCGACAAAGT | TACTGGGAAT |
| ACAACACAAG | GATATCAAGT | GACAGGTACC | GCTGAACTTG | GCACCACCAT | TGAAGTTCGT |
| GCAACAGACG | GAACAGTTTT | AGGCACCGCA | ACAACCTGGAC | CGACTGGCCA | ATATACTGTG |
| ACGTTAGCTT | CAGGAAAAGC | AACAGCTAAA | CAAACAGTGA | ATGTAGTTGC | TAAAAATGAT |
| ACTGGACTTG | AGAGTCAACC | AACTACAGCT | ATGACACCCG | CTGATGTTAC | CACACCAACA |
| ATTGGTGACA | TTACTGGAGA | TTCAACAAC | GGTTATGAAA | TCCTGGGAC | GGCGGACCC |
| AATACCACCA | TTGAAGTACG | GAACCCAGAT | GGAACAATTA | TTGGTACAAC | GACAACGGAT |
| GATCAAGGAA | ACTTTACTGT | GGACCTTCCA | GCGGGAGCCG | CTAATCCTGG | TGATACATTA |
| ACAGTTGTTG | GAAAAGACGG | TGACGGCAAT | GAAAGTCAAC | CAACGGAAGT | GACGGTCCCT |
| GAAGATGCAA | CCGTAGCAGC | ACCAACTGTG | ACGACTGTTA | CAGGAACAAC | TGCCACTGGG |
| TATCAAGTAA | CCGGCACGGC | AGAGCCAAAT | GTCACCATTG | AGATTACAAA | TGAAGCAGGT |
| TTAGTTATTG | CTACGGGAAC | GACTGATGGT | GCTGGCGCAT | TTACAATCAC | TCTTCCGACG |
| GGCACAGCAA | CAGCTAACGA | AGCCTTAAC | GCCATTGCGA | AAGATGCTGC | TGGGAAAGAA |
| AGTAATCCGA | TCGCTTTCAA | AACACCTGCT | GATCCAGATG | CACCAGTCGC | GACACCTACT |
| GTTGACAAAA | TCACTGGTAG | CACGACAAAC | GGCTATCAAG | TAGTAGGAGC | AGCAGAAGTT |
| GGTACAACAG | TTGAGGTGCG | TGACGCCGAT | GGCACAGTCC | TTGGCATGGC | AACTACTGGA |
| ACTGATGGCA | AATACACAGT | GACTTTAGAG | CCAGGGAAGG | CCTCAGCTAA | CGAAACAATA |
| ACTGTCTGTG | CGAAAAATGC | AACAGGAAAA | GAAAGTCAGC | CAGCTACAGC | AACTACACCA |
| GTCGACTTAG | CCACACCAAC | CATTGATTCT | ATTACCGGAA | ATTCTAGTAA | AGGTTACGAA |

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATCACTGGAA CGGCGGAGCC AAAAACCCT ATTGATGTCC GTGACGCAGA CGGAACCATC
 ATTGCTGCTA CAACTGCTAA CGAAACCGGC CAATATACGG TGACTCTACC AGCTGGCGTA
 GTGACACCAG GAGAAACGAT TACGATTATT AGCAAAGATG GCGCAGGTAA TGAAAGTCAA
 CCAGCTACAG CCGTTATTCC AGCGGATGTT GTTTTAGCGG CGCCAACTAT TACGAAGGTT
 GAAGGAAACA AAGCCAATGG CTATACAGTC ACTGGAAGTG CTGATCCAAA TGTCACGGTT
 CAATTTTACA ATAGCACTGA ACAATTATTG GCAAGTGGCA ATACAACCTAC TGGAGGTACC
 TTCTCCGTTT ATATTGCAGC AGGGTTAGCA ACAGAAAAAG AAACGTTAAC CGCACTAAC
 ACAGATACAC AAGGAAATGT GAGTCCTAAA ACCACATTTA TGACGCCAGC CGATATTACG
 GGAGAACCAG AGATTAAAAAT TGCGGCACCA ACTGTTTCTT CAGTTTTAGG AACGTCTAAA
 GCCGGCTACC TCATCAAAGG AACAGCTGAA CCAAACCGAA TCATTCAAAT TAGTAACCGA
 CTATTAAGAA GTGTGATTGC TGTAGGTGCC ACCGATGCTG AAGGCAACTT CGCTATCCAA
 TTAACAGCGG GACAAGCGAC TGCTCAACAA AGTTTACTTG CGACAGCTAC CGATGGCGCA
 GGACATTACA GTACGGCTAC AACCTTCATG ACGCCAGCCG ACCCAACGAA TCCTGGAGGA
 GGCAATGGTA AACTTGCGCG AAATAACGGC AATACAGCGG GCAATACAGG AAACAATGGC
 GCAACTGGCG GGAATAATGG GAATGGTTCA AACACAGGTT CAAATCCAAA TGGAGGTTCT
 GGTTTAGGCA CAACAGGTTT TGGCTTAGGT TCACTAGGCA ATGGCCTCGG TACAAATGGT
 AGTGGCTACC ACCCTAACT AAGTACCATC AGTTATGGCA CTGGAAATCA CGGGAAAAACA
 GGCTACTTAC CTAGCACAGG TGAAAAAGAG TCTTCAGCCG TGACAAACAAG TTTGTTTGGC
 GCCTTTGTCT CACTCCTTGC GAGCATGGGA ATCATCAAAC GCAAACGTAA AAACCTAG

EF070-2 (SEQ ID NO:266)

M KKKIVEDFNR KSQHKWTKR KMLNLAISSG LLFTSLAIPV
 SIAVTSGTIS ASAAVLDEL LSNVTSNNDG GTSTSNRWTA ANQNQPVNFT VSGGALADAS
 AVFSGQKQAV LVVPPELRGN VAAAGSAIN TNVTIDLSKV TFLTAVLNAA NDLTNVITQI
 TSGALGNLTG VDIDLTEVNR QLELVNNIEN LGAASFTAPE TLAADGSYIS APISDGLGLV
 LAQNVSNILQ DLNAAVQALE AKGTSIPSNL VAAAINAALL PVKGTVNVAV SGALPLLAAG
 GSGVNELVDA PLLGTTTFTL PTTVSTPQNL SNNLDAREVG TVVQTDLLDV NLLATADGVS
 NIYFAAGTTS EVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
 FTVTVPAGEA GANETLTAVA KNASGTESTP TTFQTPADEA TVTAPTITGV TGNSTAGYEV
 KGTADANATV EIRNAGGTVI GTGTADGTGA FTVTVPAGEA GANETLTAVA KNASGTESTP
 TTFQTPADEA TVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGAVI GTGTADGTGA
 FTVTVPAGEA GANETLTAVA KNASGTESTP TTFQTPADPN TPVATPIVET VTGSTTKGYE
 VKGTAEVGTT IEVRDAAGTV LGTATTGTDG KYTVTLDSGT ATANQTLSTV AKNASGTESQ
 PATATTPADV TAPTVDNITG NSGSGYEITG TADPNTTIEV RDPGAVIGT GTSDANGDFT
 VTLPTGTTNP GDTLTVIGKD NAGNESQPTL VLVPADATVT APTVTGVTGN SVAGYQVTGT
 ADPNATIEIR DADGNVIATG TADGTGSFAV NLPAGTANAN ETLTALAKDP AGNTSTPTTF
 QTPADEVVAP PSVDKVTGNT TQGYQVTGTA ELGTTIEVRA TDGTVLGTAT TGPTGQYTVT
 LASGKATAKQ TVNVVAKNDT GLESTPTTAM TPADVTTPTI GDITGDSTTG YEITGTADPN
 TTIEVRNPDG TIIGTTTDD QGNFTVDLPA GAANPGDTLT VVGKDGDCNE SQPTEVTVPE
 DATVAAPTIV TVTGTATGY QVTGTAEPNV TIEIHNEAGL VIATGTTDGA GAFTITLPTG
 TATANEALTA IAKDAAGKES NPTAFKTPAD PDAPVATPTV DKITGSTTNG YQVVGAAEVG
 TTVEVRDADG TVLGMATTGT DGKYTVTLEP GKASANETIT VVAKNATGKE SQPATATTPV
 DLATPTIDSI TGNSSKGYEI TGTAEPKTTI DVRDADGTII AATTANETGQ YTVTLPAVV
 TPGETITIS KDGAGNESQP ATAVIPADV LAAPTITKVE GNKANGYTVT GTADPNVTVQ
 FYNSSQQLLA SGNTTGGTF SVHIAAGLAT EKETLTALT DTQGNVSPKT TFMTPADITG
 EPEIKIAAPT VSSVLGTSKA GYLIKGTAE NRIIQISNRL LRSVIAVGAT DAEGNFIAQL
 TAGQATAQQS LLATATDGAG HYSTATTFMT PADPTNPGG NGNTGGNNGN TGGNTGNNGA
 TGGNNGNGSN TGSNPNNGSG LGTTGSLGS LGNGLGTNGS GYHPKLSTIS YGTGNHGKTG
 YLPSTGEKES SAVTTSLEGA FVALLASMI IKRKRKN

EF070-3 (SEQ ID NO:267)

CGG TGACGGCAAT GAAAGTCAAC CAACGGAAGT GACGGTCCCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAAGATGCAA CCGTAGCAGC ACCAACTGTG ACGACTGTTA CAGGAACAAC TGCCACTGGG
TATCAAGTAA CCGGCACGGC AGAGCCAAAT GTCACCATTG AGATTACAA TGAAGCAGGT
TTAGTTATTG CTACGGGAAC GACTGATGGT GCTGGCGCAT TTACAATCAC TCTTCCGACG
GGCACAGCAA CAGCTAACGA AGCCTTAACT GCCATTGCGA AAGATGCTGC TGGGAAAGAA
AGTAATCCGA CTGCTTTTCAA AACACCTGCT GATCCAGATG CACCAGTCGC GACACCTACT
GTTGACAAAA TCACTGGTAG CACGACAAAC GGCTATCAAG TAGTAGGAGC AGCAGAAAGTT
GGTACAACAG TTGAGGTGCG TGACGCCGAT GGCACAGTCC TTGGCATGGC AACTACTGGA
ACTGATGGCA AATACACAGT GACTTTAGAG CCAGGGAAGG CCTCAGCTAA CGAAACAATA
ACTGTCTGTAG CGAAAAATGC AACAGGAAAA GAAAGTCAGC CAGCTACAGC AACTACACCA
GTCGACTTAG CCACACCAAC CATTGATTCT ATTACCGGAA ATTCTAGTAA AGGTTACGAA
ATCACTGGAA CGGCGGAGCC AAAAACCCTT ATTGATGTCC GTGACGCAGA CGGAACCATC
ATTGCTGCTA CAACTGCTAA CGAAACCGGC CAATATACGG TGA CTCTACC AGCTGGCGTA
GTGACACCAG GAGAAACGAT TACGATTATT AGCAAAGATG GCGCAGGTAA TGAAGTCAA
CCAGCTACAG CCGTTATTCC AGCGGATGTT GTTTTAGCGG CGCCAAC TAT TACGAAGGTT
GAAGGAAACA AAGCCAATGG CTATACAGTC ACTGGAAC TGATCCAAA TGTCACGGTT
CAATTTTACA ATAGCAGTGA ACAATTATTG GCAAGTGGCA ATACAAC TAC TGGAGGTACC
TTCTCCGTTT ATATTGCAGC AGGGTTAGCA ACAGAAAAAG AAACGTTAAC CGCACTAACC
ACAGATACAC AAGGAAATGT GAGTCCTAAA ACCACATTTA TGACGCCAGC CGATATTACG
GGAGAACCAG AGATTAAAAAT TGCGGCACCA ACTGTTTCTT CAGTTTTAGG AACGCTAAA
GCCGGCTACC TCATCAAAGG AACAGCTGAA CCAAACCGAA TCATTCAAAT TAGTAACCGA
CTATTAAGAA GTGTGATTGC TGTAGGTGCC ACCGATGCTG AAGGCAACTT CGCTATCCAA
TTAACAGCGG GACAAGCGAC TGCTCAACAA AGTTTACTTG CGACAGCTAC CGATGGCGCA
GGACATTACA GTACGGCTAC AACCTTCATG ACGCCAGCCG ACCCAACGAA TCCTGGAGGA
GGCAATGGTA ACACTGGCGG AAATAACGGC AATACAGGCG GCAATACAGG AAACAATGGC
GCAACTGGCG GGAATAATGG GAATGGTTCA AACACAGGTT CAAATCCAAA TGGAGGTTCT
GGTTTAGGCA CAACAGGTTT TGGCTTAGGT TCACTAGGCA ATGGCCTCGG TACAAATGGT
AGTGGCTACC ACCCTAACT AAGTACCATC AGTTATGGCA CTGGAATCA CGGGAAAACA
GGCTACT

EF70-4 (SEQ ID NO:268)

DGDGNE SQPTEVTVPE

DATVAAPT VT TVTGTTATGY QVTGTAEPNV TIEIHNEAGL VIATGTTDGA GAFTITLPTG
TATANEALTA IAKDAAGKES NPTAFKTPAD PDAPVATPTV DKITGSTTNG YQVVGAAEVG
TTVEVRDADG TVLGMATTGT DGKYTVTLEP GKASANETIT VVAKNATGKE SQPATATTPV
DLATPTIDSI TGNSSKGYEI TGTAEPKTTI DVRDADGTII AATTANETGQ YTVTLPAVVV
TPGETITIIIS KDGAGNESQP ATAVIPADV LAAPTITKVE GNKANGYTVT GTADPNVTVQ
FYNSSQQLLA SGNTTTGGTF SVHIAAGLAT EKETLTALTT DTQGNVSPKT TFMTPADITG
EPEIKIAAPT VSSVLGTSKA GYLIKGTAEF NRIQISNRL LRSVIAVGAT DAEGNFAIQL
TAGQATAQQS LLATATDGAG HYSTATTFMT PADPTNPGGG NGNTGGNNGN TGGNTGNNGA
TGGNNGNGSN TGSNPNGGSG LGTTGSGLGS LGNGLGTNGS GYHPKLSTIS YGTGNHGKTG
YL

EF071-1 (SEQ ID NO:269)

TAAGTAGAAG TGGTCGGGAC AAACGTAGAA CTTTCGCTGA TTGCCGAAGA AATTACTTCT
GTCCCGCCAT TTATCTGCAG GTTTAAGCCG TGGAAGGGAA GTTATTTTGA CTTTCCTTTC
ATGGCTTTTT TAAGAAAGGA GCATGCTATG TTTAAAAAT TAATGATTCA ACTTGCTTTA
GTGATTGGTT TAAGTTTAAC GATTCCGATG ACGGCTTNCG CTTACACCAT CGAAGCGGAT
CCAATCAACT TTA CTATTATTT TCCCGGCTCT GCAAGCAATG AATTAATTGT TTTACATGAA
TCTGGAAACG AGCGGAACCT AGGACCACAC AGTTTAGACA ATGAAGTGGC CTATATGAAA
CGAAATTGGT CAAATGCTTA TGTCTCATAT TTTGTCCGAT CTGGTGGACG AGTGAAACAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTAGCTCCTG CTGGCCAAAT TCAATATGGC GCAGGTTCTT TAGCTAATCA AAAAGCCTAT
 GCGCAAATCG AATTGGCTCG AACGAATAAT GCGGCGACAT TTAAAAAAGA TTATGCTGCC
 TATGTTAATT TGGCCCGTGA TTTGGCTCAG AACATTGGTG CTGATTTTTC TCTGGACGAT
 GGAACAGGTT ATGGCATAGT CACTCATGAT TGGATTACAA AAAATTGGTG GGGAGATCAT
 ACAGATCCTT ATGGTTATTT AGCGCGTGGG GGATTAGTAA AGCGCATTGG CACNAGATTT
 ACAACGGGCG TTTTCNGNAAC AGGTGAGACT GGTCAATTATT CAGCCAGGTA A

EF071-2 (SEQ ID NO:270)

MF KKLMIQLALV

IGLSLTIPMT AXAYTIEADP INFYTFPGSA SNELIVLHES GNERNLGPHS LDNEVAYMKR
 NWSNAYVSYF VSGGGRVKQL APAGQIQYGA GSLANQKAYA QIELARTNNA ATFKKDYAAY
 VNLARDLAQN IGADFSLDDG TGYGIVTHDW ITKNWWGDHT DPYGYLARGG LVKRIGTRFT
 TGVSXTGETG HYSAR

EF071-3 (SEQ ID NO:271)

G TTTAAAAAAT TAATGATTCA ACTTGCTTTA

GTGATTGGTT TAAGTTTAAC GATTCCGATG ACGGCTTNCG CTTACACCAT CGAAGCGGAT
 CCAATCAACT TTAATTATTT TCCCGGCTCT GCAAGCAATG AATTAATTGT TTTACATGAA
 TCTGGAAACG AGCGGAACCT AGGACCACAC AGTTTAGACA ATGAAGTGGC CTATATGAAA
 CGAAATTGGT CAAATGCTTA TGTCTCATAT TTTGTCCGAT CTGGTGGACG AGTGAAACAA
 TTAGCTCCTG CTGGCCAAAT TCAATATGGC GCAGGTTCTT TAGCTAATCA AAAAGCCTAT
 GCGCAAATCG AATTGGCTCG AACGAATAAT GCGGCGACAT TTAAAAAAGA TTATGCTGCC
 TATGTTAATT TGGCCCGTGA TTTGGCTCAG AACATTGGTG CTGATTTTTC TCTGGACGAT
 GGAACAGGTT ATGGCATAGT CACTCATGAT TGGATTACAA AAAATTGGTG GGGAGATCAT
 ACAGATCCTT ATGGTTATTT AGCGCGTGGG GGATTAGTAA AGCGCATTGG CACNAGATTT
 ACAACGGGCG TTTTCNGNAAC AGGTGAGACT GGTCAATTATT CAGCCAGGT

EF071-4 (SEQ ID NO:272)

F KKLMIQLALV

IGLSLTIPMT AXAYTIEADP INFYTFPGSA SNELIVLHES GNERNLGPHS LDNEVAYMKR
 NWSNAYVSYF VSGGGRVKQL APAGQIQYGA GSLANQKAYA QIELARTNNA ATFKKDYAAY
 VNLARDLAQN IGADFSLDDG TGYGIVTHDW ITKNWWGDHT DPYGYLARGG LVKRIGTRFT
 TGVSXTGETG HYSAR

EF072-1 (SEQ ID NO:273)

TAATCAATGA AAAACGCACG TTGGTTAAGT ATTTGCGTCA TGCTACTCGC TCTTTTCGGG
 TTTTCACAGC AAGCATTAGC AGAGGCATCG CAAGCAAGCG TTCAAGTTAC GTTGACAAA
 TTATTGTTCC CTGATGGTCA ATTACCAGAA CAGCAGCAA ACACAGGGGA AGAGGGAACG
 CTGCTTCAAA ATTATCGGGG CTTAAATGAC GTCACCTATC AAGTCTATGA TGTGACGGAT
 CCGTTTTATC AGCTTCGTTT TGAAGGAAAA ACGGTCCAAG AGGCACAGCG TCAATTAGCA
 GAAACCGGTG CAACAAATAG AAAACCGATC GCAGAAGATA AAACACAGAC AATAAATGGA
 GAAGATGGAG TGGTTTCTTT TTCATTAGCT AGCAAAGATT CGCAGCAACG AGATAAAGCC
 TATTTATTTG TTGAAGCGGA AGCACCAGAA GTGGTAAAGG AAAAAGCTAG CAACCTAGTA
 GTGATTTTGC CTGTTCAAGA TCCACAAGGG CAATCGTTAA CGCATATTCA TTTATATCCA
 AAAAATGAAG AAAATGCCTA TGACTTACCA CCACTTGAAA AAACGGTACT CGATAAGCAA
 CAAGGCTTTA ATCAAGGAGA GCACATTAAC TATCAGTTAA CGACTCAGAT TCCAGCGAAT
 ATTTTAGGAT ATCAGGAATT CCGTTTGTCA GATAAGGCGG ATACAACGTT GACACTTTTA
 CCAGAATCAA TTGAGGTAAA AGTGGCTGGA AAAACAGTTA CTACAGGTTA CACACTGACG
 ACGCAAAAGC ATGGATTTAC GCTTGATTTT TCAATTAAAG ACTTACAAA CTTTGCAAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAAACAATGA CTGTGTCGTA TCAAATGCGT TTAGAAAAGA CCGCTGAACC TGACACTGCG
 ATTAACAACG AAGGACAATT AGTCACGGAC AAACATACCT TGACTAAAAG AGCCACAGTT
 CGTACAGGCG GCAAGTCTTT TGTCAAAGTT GATAGTGAAA ATGCGAAAAT CACCTTGCCA
 GAGGCTGTTT TTATCGTCAA AAATCAAGCG GGGGAATACC TCAATGAAAC AGCAAACGGG
 TATCGTTGGC AAAAAGAAAA AGCATTAGCT AAAAAATTCA CGTCTAATCA AGCCGGTGAA
 TTTTCAGTTA AAGGNNTTAA AAGATGGCCA GTACTTCTTG GAAGAAATCT CTGCACCAAA
 AGGTTATCTT CTGAATCAAA CAGAAATTCC TTTTACGGTG GGAAAAAATT CTTATGCAAC
 GAACGGACAA CGAACAGCAC CGTTACATGT AATCAATAA

EF072-2 (SEQ ID NO:274)

MKNARWLSI CVMLLALFGF SQQALAEASQ ASVQVTLHLK LFPDQQLPEQ QQNTGEEGTL
 LQNYRGLNDV TYQVYDVTDV FYQLRSEGKT VQEAQRQLAE TGATNRKPIA EDKTQTINGE
 DGVVSFSLAS KDSQQRDKAY LFVEAEAEV VKEKASNLVV ILPVQDPQGG SLTHIHLYPK
 NEENAYDLPP LEKTVLDDKQQ GFNQGEHINY QLTTQIPANI LGYQEFRLSD KADTTLTLLP
 ESIEVKVAGK TVTTGYTLTT QKHGFTLDFS IKDLQNFANQ TMTVSYQMRL EKTAEPDTAI
 NNEGQLVTDK HTLTKRATVR TGGKSFVKVD SENAKITLPE AVFIVKNQAG EYLNETANGY
 RWQKEKALAK KFTSNQAGEF SVKGXKRWPV LLGRNLCTKR LSSESNRNSF YGGKKFLCNE
 RTTNSTVTCTN Q

EF072-3 (SEQ ID NO:275)

ATTACCAGAA CAGCAGCAAA ACACAGGGGA AGAGGGAACG
 CTGCTTCAAAA ATTATCGGGG CTAAATGAC GTCACCTATC AAGTCTATGA TGTGACGGAT
 CCGTTTTATC AGCTTCGTTT TGAAGGAAAA ACGGTCCAAG AGGCACAGCG TCAATTAGCA
 GAAACCGGTG CAACAAATAG AAAACCGATC GCAGAAGATA AAACACAGAC AATAAATGGA
 GAAGATGGAG TGGTTTCTTT TTCATTAGCT AGCAAAGATT CGCAGCAACG AGATAAAGCC
 TATTTATTTG TTGAACCGGA AGCACCAGAA GTGGTAAAGG AAAAAGCTAG CAACCTAGTA
 GTGATTTTGC CTGTTCAAGA TCCACAAGGG CAATCGTTAA CGCATATTCA TTTATATCCA
 AAAAATGAAG AAAATGCCTA TGACTTACCA CCACTTGAAA AAACGGTACT CGATAAGCAA
 CAAGGCTTTA ATCAAGGAGA GCACATTAAC TATCAGTTAA CGACTCAGAT TCCAGCGAAT
 ATTTTAGGAT ATCAGGAATT CCGTTTGTCA GATAAGGCGG ATACAACGTT GACACTTTTA
 CCAGAATCAA TTGAGGTAAG AGTGGCTGGA AAAACAGTTA CTACAGGTTA CACTGTACG
 ACGCAAAAGC ATGGATTTAC GCTTGATTTT TCAATTAAAG ACTTACAAAA CTTTGCAAAT
 CAAACAATGA CTGTGTCGTA TCAAATGCGT TTAGAAAAGA CCGCTGAACC TGACACTGCG
 ATTAACAACG AAGGACAATT AGTCACGGAC AAACATACCT TGACTAAAAG AGCCACAGTT
 CGTACAGGCG GCAAGTCTTT TGTCAAAGTT GATAGTGAAA ATGCGAAAAT CACCTTGCCA
 GAGGCTGTTT TTATCGTCAA AAATCAAGCG GGGGAATACC TCAATGAAAC AGCAAACGGG
 TATCGTTGGC AAAAAGAAAA AGCATTAGCT AAAAAATTCA CGTCTAATCA AGCCGGTGAA
 TTTTCAGTTA AAGGNNTTAA AAGATGGCCA GTACTTCTTG GAAGAAATCT CTGCACCAAA
 AGGTTATCTT CTGAATCAAA CAGAAATTCC TTTTACGGTG GGAAAAAATT CTTATGCAAC
 GAACGGACAA CGAACAGCAC CGTTACATGT A

EF072-4 (SEQ ID NO:276)

QLPEQ QQNTGEEGTL
 LQNYRGLNDV TYQVYDVTDV FYQLRSEGKT VQEAQRQLAE TGATNRKPIA EDKTQTINGE
 DGVVSFSLAS KDSQQRDKAY LFVEAEAEV VKEKASNLVV ILPVQDPQGG SLTHIHLYPK
 NEENAYDLPP LEKTVLDDKQQ GFNQGEHINY QLTTQIPANI LGYQEFRLSD KADTTLTLLP
 ESIEVKVAGK TVTTGYTLTT QKHGFTLDFS IKDLQNFANQ TMTVSYQMRL EKTAEPDTAI
 NNEGQLVTDK HTLTKRATVR TGGKSFVKVD SENAKITLPE AVFIVKNQAG EYLNETANGY
 RWQKEKALAK KFTSNQAGEF SVKGXKRWPV LLGRNLCTKR LSSESNRNSF YGGKKFLCNE
 RTTNSTVTCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF073-1 (SEQ ID NO:277)

TAAATGAACA AATTAAATAC AAAATTACTG ATTGGCTATA TTCTTTTAGG AGCCTTAATC
 ATTGCTGTCG CTAGAGAATA TGGCTTCTTC GCTTTTGTGA TTCTGGTAGG CTTTTTAGTA
 TTCGTTCTCT ATCGAAAAA GAAAAATGCC GCCGACAAA GCGATCAAAT GCCTTACTTA
 ACGAAAGATA AAGAAGCCCA TTATCGTGAG TTGGGGTTAT CTCCACAAGA AATTGATTTT
 TTCAGAAGTA CAATGAGCAC AGCCAAAAA CAAATCATA AATTGCAAGA AAACATGAAT
 CGTTCAACTA AATTACGGGC GATTGACTTA CGTAATGATA CTACGAAGGT TTCTAAAGCT
 CTGTTTAAAG AGTTAGTGAA AGAACCTAAA AAGTTACACT TAGCCAATCA CTTTCTCTAT
 ACACATTTAC CAAATATCGT TGACTTAACA AGTAAACATT TAGAAATCGA ACAACACGAA
 GTAAAAACA AACAAACGTA TGAAAAATTA GAAGAAAGCG CACAAATCAT TGACCAATTG
 TCAAAATTAG TTAAAAATGA TTATGAGGAA ATCGTTTCCG ATGACTTAGA CGATTTAGAT
 GTCGAAATGT CGATCGCTAA AAGCAGCTTG TCGCAAAAAG CTGCAACTGA GGAATCACCT
 CAAGTAAACG AAGACCAGCA ATAA

EF073-2 (SEQ ID NO:278)

MNKLNTKLLI GYILLGALII AVAREYGFFA FVILVGFLVF VLYRKKKNAA DKSDQMPYLT
 KDKEAHYREL GLSPQEIDFF RSTMSTAKKQ IIQLQENMNR STKLRAIDLR NDTTKVSKAL
 FKELVKEPKK LHLANHFLYT HLPNIVDLTS KHLEIEQHEV KNKQTYEKL ESEAIIIDQLS
 KLVKNDYEEI VSDDLDDLDV EMSIAKSSLS QKAATEESPQ VNEDQQ

EF073-3 (SEQ ID NO:279)

CT ATCGAAAAA GAAAAATGCC GCCGACAAA GCGATCAAAT GCCTTACTTA
 ACGAAAGATA AAGAAGCCCA TTATCGTGAG TTGGGGTTAT CTCCACAAGA AATTGATTTT
 TTCAGAAGTA CAATGAGCAC AGCCAAAAA CAAATCATA AATTGCAAGA AAACATGAAT
 CGTTCAACTA AATTACGGGC GATTGACTTA CGTAATGATA CTACGAAGGT TTCTAAAGCT
 CTGTTTAAAG AGTTAGTGAA AGAACCTAAA AAGTTACACT TAGCCAATCA CTTTCTCTAT
 ACACATTTAC CAAATATCGT TGACTTAACA AGTAAACATT TAGAAATCGA ACAACACGAA
 GTAAAAACA AACAAACGTA TGAAAAATTA GAAGAAAGCG CACAAATCAT TGACCAATTG
 TCAAAATTAG TTAAAAATGA TTATGAGGAA ATCGTTTCCG ATGACTTAGA CGATTTAGAT
 GTCGAAATGT CGATCGCTAA AAGCAGCTTG TCGCAAAAAG CTGCAACTGA GGAATCACCT
 CAAGTAAACG AAGACCAGCA AT

EF073-4 (SEQ ID NO:280)

YRKKKNAA DKSDQMPYLT
 KDKEAHYREL GLSPQEIDFF RSTMSTAKKQ IIQLQENMNR STKLRAIDLR NDTTKVSKAL
 FKELVKEPKK LHLANHFLYT HLPNIVDLTS KHLEIEQHEV KNKQTYEKL ESEAIIIDQLS
 KLVKNDYEEI VSDDLDDLDV EMSIAKSSLS QKAATEESPQ VNEDQQ

EF074-1 (SEQ ID NO:281)

TAAAGGAGTT CTCAAAAAAT GAAGCTAAAA AAAATAATTC CTGCTTTTCC CCTTCTTTCA
 ACCGTTGCAG TTGGCTTGTG GTTAACGCCT ACTCAAGCTT CTGCAGATGC TGCGGATACG
 ATGGTAGATA TCTCTGGCAA AAAAGTGTG GTTGGATATT GGCATAACTG GGCTCAAAA
 GGACGCGATG GTTACAAACA AGGAACATCA GCATCACTAA ACCTTTCAGA AGTAAATCAA
 GCCTACAATG TCGTACCGGT TTCCTTCATG AAAAGCGATG GCACGACACG GATTCCTACG
 TTCAAGCCTT ATAACCAAAC GGACACTGCC TTCCGACAAG AAGTCGCACA ATTAAATAGT
 CAAGGTCCGC CAGTTTATT GGCACCTGGT GGAGCAGATG CACATATTCA ATTAGTCAAA
 GGCGATGAAC AAGCCTTTGC GAATGAAATC ATTCTGCAAG TGGAAACATA CGGCTTTGAT
 GGTTTAGACA TCGACTTAGA GCAATTGGCG ATTACTGCTG GCGACAACCA AACCGTCATC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCTGCTACGT TGAAAATAGT CAAAGACCAT TATCGAGCAC AAGGAAAAAA TTTCATCATT
 ACGATGGCAC CAGAATTCCC TTATTTAAAA CCTGGTGCCG CTTATGAAAC ATACATTACT
 TCCCTAAATG GTTATTATGA TTACATTGCC CCACAATTAT ATAACCAAGG CGGCGACGGT
 GTCTGGGTTG ATGAAGTTAT GACTTGGGTT GCTCAAAGCA ACGATGCTCT AAAATACGAG
 TTCCTCTATN ATATT

EF074-2 (SEQ ID NO:282)

MKLKK IIPAFPLLST VAVGLWLTPT QASADAADTM VDISGKKVLV GYWHNWASKG
 RDGYKQGTSA SLNLSEVNQA YNVVPVSFMK SDGTTRIPTF KPYNQTDATF RQEVQQLNSQ
 GRAVLLALGG ADAHIQLVKG DEQAFANEII RQVETYGFDG LDIDLEQLAI TAGDNQTVIP
 ATLKIVKDHY RAQGKNFIIT MAPEFPYLKP GAAYETYITS LNGYYDYIAP QLYNQGGDGV
 WVDEVMTWVA QSNDAKLYEF LYXI

EF074-3 (SEQ ID NO:283)

TGC TGCGGATACG
 ATGGTAGATA TCTCTGGCAA AAAAGTGTG GTTGGATATT GGCATAACTG GGCCTCAAAA
 GGACGCGATG GTTACAAACA AGGAACATCA GCATCACTAA ACCTTTCAGA AGTAAATCAA
 GCCTACAATG TCGTACCGGT TTCCTTCATG AAAAGCGATG GCACGACACG GATTCTTACG
 TTCAAGCCTT ATAACCAAAC GGACACTGCC TTCCGACAAG AAGTCGCACA ATTAAATAGT
 CAAGGTCGCG CAGTTTTATT GGCAC'TGGT GGAGCAGATG CACATATTCA ATTAGTCAAA
 GCGGATGAAC AAGCCTTTGC GAATGAAATC ATTTCGTCAAG TGGAAACATA CGGCTTTGAT
 GGT'TTAGACA TCGACTTAGA GCAATTGGCG ATTACTGCTG GCGACAACCA AACCGTCATC
 CCTGCTACGT TGAAAATAGT CAAAGACCAT TATCGAGCAC AAGGAAAAAA TTTCATCATT
 ACGATGGCAC CAGAATTCCC TTATTTAAAA CCTGGTGCCG CTTATGAAAC ATACATTACT
 TCCCTAAATG GTTATTATGA TTACATTGCC CCACAATTAT ATAACCAAGG CGGCGACGGT
 GTCTGGGTTG ATGAAGTTAT GACTTGGGTT GCTCAAAGCA ACGATGCTCT AAAATACGAG
 TTCCTCT

EF074-4 (SEQ ID NO:284)

AADTM VDISGKKVLV GYWHNWASKG
 RDGYKQGTSA SLNLSEVNQA YNVVPVSFMK SDGTTRIPTF KPYNQTDATF RQEVQQLNSQ
 GRAVLLALGG ADAHIQLVKG DEQAFANEII RQVETYGFDG LDIDLEQLAI TAGDNQTVIP
 ATLKIVKDHY RAQGKNFIIT MAPEFPYLKP GAAYETYITS LNGYYDYIAP QLYNQGGDGV
 WVDEVMTWVA QSNDAKLYEF LY

EF075-1 (SEQ ID NO:285)

TAACCTATAA GAAAAAAATC ACAACCTGTG ATAAATTATT GGAGGNAAAA TATGTCAAAA
 GGGAAGAAAA TTTTGGCCAT TATCNTTGGG ATTATCTTGG NTCTATTTCT TGCAGTTGTT
 GGAATGGGAG CAAAAC'TTTA TTGGGATGTT TCTAAATCAA TGGATAAAAC CTATGAAACA
 GTAGAACGAT CTAACAAAAAG TCAGGTCAAT TTAAACAATA AGGAGCCTTT TTCTGTTTTA
 TTATTAGGGA TTGATACAGG CGATGATGGG CGTGTGAGC AAGGTCGTTC GGATACAACA
 ATTGTTGCAA CAGTTAATCC TCGTGACAAG CAAACAACCT TAGTCAGTCT TGCTCGCGAT
 ACCTATGTTG ATATTCCAGG TCAAGGAAAA CAAGATAAAT TGAATCACGC CTATGCTTTT
 GGTGGCGCAT CTTTAGCAAT GGACACAGTT GAAAAC'TATT TAAACATACC TATTAATCAT
 TATGTTTCAA TTAATATGGC TGGTTTAAAA GAATTAGTCA ACGCGGTTGG CGGAATCGAA
 GTGAACAATA ATCTGACTTT TTCTCAAGAC GGATATGATT TTACGATTGG TAAAATTICA
 TTGGATGGTG AACAAGCACT CTCCTATTCA AGAATGCGTT ACGAAGACCC TAATGGTGAC
 TACGGCCGCC AAGAACGTCA AAGAAAAGTG ATTGAAGGCA TCGTCCAAAA AGTCTTAAGT
 CTTAACAGCG TAAGCAACTA TCAAGAAATT TTAACAGCTG TTTCTGATAA TATGAAGACA
 GATTTAAGTT TTGATGACAT GAAAAAAATT GCCTTAGATT ATCGCAGTGC CTTTGGTAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTGAAACAAG ACCAACTTCA AGGTACTGGT TTTATGCAAG ATGGTGTTC CTATCAACGT
 GTGGATGAAC AAGAATTAAC TCGTGTCCAA CAAGAGTTGA AAAATCAATT GAATACAAA
 TAA

EF075-2 (SEQ ID NO:286)

MSKG KKIFAIIXGI ILXLFLAVVG MGAKLYWDVS KSMDKTYETV
 ERSKKSQVNL NNKEPFSVLL LGIDTGDDGR VEQGRSDTTI VATVNPRDKQ TTLVSLARDT
 YVDIPGQKQ DKLNHAYAFG GASLAMDTVE NYLNIPINHY VSINMAGLKE LVNAVGGIEV
 NNNLTFSQDG YDFTIGKISL DGEQALSYSR MRYEDPNGDY GRQERQRKVI EGIVQKVLSL
 NSVSNYQEIL TAVSDNMKTD LSFDDMKKIA LDYRSAFGKV KQDQLQGTGF MQDGVSYQRV
 DEQELTRVQQ ELKNQLNTK

EF075-3 (SEQ ID NO:287)

ACTTTA TTGGGATGTT TCTAAATCAA TGGATAAAAC CTATGAAACA
 GTAGAACGAT CTAAAAAAG TCAGGTCAAT TTAACAATA AGGAGCCTTT TTCTGTTTTA
 TTATTAGGGA TTGATACAGG CGATGATGGG CGTGTGAGC AAGGTCGTTT GGATACAACA
 ATTGTTGCAA CAGTTAATCC TCGTGACAAG CAAACAACCT TAGTCAGTCT TGCTCGCGAT
 ACCTATGTTG ATATTCCAGG TCAAGGAAAA CAAGATAAAT TGAATCACGC CTATGCTTTT
 GGTGGCGCAT CTTTAGCAAT GGACACAGTT GAAAACTATT TAAACATACC TATTAATCAT
 TATGTTTCAA TTAATATGGC TGGTTTAAAA GAATTAGTCA ACGCGGTTGG CGGAATCGAA
 GTGAACAATA ATCTGACTTT TTCTCAAGAC GGATATGATT TTACGATTGG TAAAATTTCA
 TTGGATGGTG AACAAGCACT CTCCTATTCA AGAATGCGTT ACGAAGACCC TAATGGTGAC
 TACGGCCGCC AAGAAGCTCA AAGAAAAGTG ATTGAAGGCA TCGTCCAAA AGTCTTAAGT
 CTTAACAGCG TAAGCAACTA TCAAGAAATT TTAACAGCTG TTTCTGATAA TATGAAGACA
 GATTTAAGTT TTGATGACAT GAAAAAATT GCCTTAGATT ATCGCAGTGC CTTTGGTAAA
 GTGAAACAAG ACCAACTTCA AGGTACTGGT TTTATGCAAG ATGGTGTTC CTATCAACGT
 GTGGATGAAC AAGAATTAAC TCGTGTCCAA CAAGAGTTGA AAAATCAATT GAATACAAA

EF075-4 (SEQ ID NO:288)

KLYWDVS KSMDKTYETV
 ERSKKSQVNL NNKEPFSVLL LGIDTGDDGR VEQGRSDTTI VATVNPRDKQ TTLVSLARDT
 YVDIPGQKQ DKLNHAYAFG GASLAMDTVE NYLNIPINHY VSINMAGLKE LVNAVGGIEV
 NNNLTFSQDG YDFTIGKISL DGEQALSYSR MRYEDPNGDY GRQERQRKVI EGIVQKVLSL
 NSVSNYQEIL TAVSDNMKTD LSFDDMKKIA LDYRSAFGKV KQDQLQGTGF MQDGVSYQRV
 DEQELTRVQQ ELKNQLNTK

EF076-1 (SEQ ID NO:289)

TAGAAAATAA CAGAGGAGCT GAAGGAAATG AAAGCATCAA CAAAAATTGG TATCGGTTTA
 AGCATTGCTG CAGTTGCAAG TGTCTCTGTT GCAGTCATCG CTTCTGAAAA AATTATTAG
 AAGGTATCTC ATGTTTCCAA TCGTTATAAA GTTAAAAAGT TTGTAGACGA TAAATTTGAT
 GGAAACCAA AATTATTATC GATTGTCGAT GATTTATCCG ATGATGAATT AGATTCTGTT
 TTTAATGTTG TGGATCGTGT GAAAGATGGC GGTTCAAAAT TAGCTGAATA TGGCGAAAAA
 GTTAAAGACA ATACAGATTG TTTAAAAGAA CGCTTTTTCAT CATTATTGA AGATGCAATG
 AAGTTAAAAA AGTGGCCTAG GCCATCTTTT TTTTATAAAA ATAATTCTTT TGTTCACAA
 TAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF076-2 (SEQ ID NO:290)

MK ASTKIGIGLS IAAVASVSV A VIASEKIIKK VSHVSNRYKV KKFVDDKFDG
 NQKLLSIVDD LSDDELDSVL NVVDRVKDGG SKLAEYGEKV KDNTDSLKER FFTFIEDAMK
 LKKWPRPSFF YKNSFVST

EF076-3 (SEQ ID NO:291)

CATCG CTTCTGAAAA AATTATTAAG
 AAGGTATCTC ATGTTTCCAA TCGTTATAAA GTTAAAAAGT TTGTAGACGA TAAATTTGAT
 GGAAACCAAA AATTATTATC GATTGTCGAT GATTATATCCG ATGATGAATT AGATTCTGTT
 TTAAATGTTG TGGATCGTGT GAAAGATGGC GGTTCAAAAT TAGCTGAATA TGGCGAAAAA
 GTTAAAGACA ATACAGATTC TTTAAAAGAA CGCTTTTCA CATTATTGA AGATGCAATG
 AAGTTAAAAA AGTGGCCTAG GCCATCTTTT TTTTATAAAA ATAATTCTT

EF076-4 (SEQ ID NO:292)

VIASEKIIKK VSHVSNRYKV KKFVDDKFDG
 NQKLLSIVDD LSDDELDSVL NVVDRVKDGG SKLAEYGEKV KDNTDSLKER FFTFIEDAMK
 LKKWPRPSFF YKNS

EF077-1 (SEQ ID NO:293)

TAATGTAAAG TGAATGATGG GAGAGAAAAA GAGATGAAGC ATGTAACAAA ATTGGGGATT
 ACAATTATAA CAGGAGTTTT GGCATTATTA TTTGAATTTA TTTTACATCA GCCGAATTGG
 GCGTATGGCA TTATTTTAAT AACAGGTTCT GTAATGGCGT TAATGATGTT CTGGGAAATG
 ATTCAAACCT TACGTGAAGG AAAATATGGT GTCGATATTT TAGCGATTAC CGCTATCGTT
 GCAACCTTAG CTGTGGGAGA ATACTGGGCC AGTTTGATGA TTTTAATTAT GTTGACTGGT
 GGTGATTCAT TAGAAGACTA TGCCGCTGGA AAAGCTAACC AAGAGCTGAA GTCATTATTG
 GATAACTCGC CACAAAAAGC TCATCGCTTG AATGGCGAAA ATTTAGAAGA TGTTTCTGTT
 GAGGAAATCA ATGTTGGCGA TGAATTAGTA GTAAACCAG GGGAACTAGT TCCAGTTGAT
 GGCTTGGTAA AAACCGGGAC ATCAACAGTC GATGAATCTT CATTAAACAGG AGAATCAAAA
 CCAATTGAAA AAAATCCTGG GGATGAATTA ATGTCGGGTT CCGTGAATGG TGACGGCTCT
 TTGAAAATGG TTGCTGAAAA AACTGTAGCA GACAGTCAAT ATCAACAAT TGTTGAACTTA
 GTGAAAGAAT CTGCGGCGCG TCCAGCTCAT TTTGTACGTT TAGCAGATCG CTATGCGGTA
 CCTTTTACAC TAGTTGCCCTA CCTAATTGCA GGTGTTGCTT GGTGTTGTTT CAAAAAGTCCG
 ACACGTTTTG CGGAAGTCTT AGTTGTTGCT TCGCCGTGTC CTTTAATTCT ATCTGCCCCA
 ATTGCTTTAG TGGCAGGGAT GGGTCGTTCA AGTCGTCATG GGGTCGTTAT TAAATCGGGA
 ACGATGGTCG AAAAATTAGC TTCTGCAAAA ACGATTGCGT TTGATAAAAC AGGCACGATT
 ACGCAAGGAC AACTTTCTGT TGATCAAGTC CAACCAATCA ATGCTGGAAT AACTGCTGCT
 GAATTAGTGG GATTGGCAGC AAGCGTGGAA CAAGAATCAA GTCATATTTT AGCTAGATCA
 ATTGTTGCTT ATGCCAGAAA GCAAGATGTC CCATTAAAAA ATATTACAGA TCTAGCGGAA
 GTTTCTGGTG CTGGCGTGAA GGCATTTGTG GATGGTGCTG AGATACGGGT AGGTAAAAAG
 AATTTTGTGA CACAAGAGTC TCAAGAAACT GAAAAAATTG ATAAAACGAC TATTCATATT
 TCACGTAATG GCACATATTT AGGCCGAATT ACTTTTACAG AACTGTACG CCCAGAAGCA
 AAAGAGACTA TGGAAAAATT ACACCAATTA CATCTTCAAC GAATTTTAAT GCTGACGGGG
 GATCAAGAAAT CCGTTGCAGA AACGATTGCT GCAGAAGTAG GAATTACCGA AGTACATGGG
 GAATGTTTAC CACAAGATAA ATTAACATATT CTAAAAGAAT TGCCTAAAAGA AAATCATCCA
 GTCATCATGG TAGGAGATGG TGTAATGAT GCACCTTCGC TTGCTGCTGC AGACGTAGGT
 ATTGCTATGG GTGCTCATGG AGCTACTGCG GCTAGTGAAG CTGCTGACGT TGTATTTTTA
 AAAGATGACT TAAGTAAAGT CAGCCAAGCG GTCGAAATTG CCCAAGATAC CATGAAAAAT
 GCCAAACAAT CTGTATTAAT CGGAATTTTT ATCTGCGTTT TACTAATGTT AATTGCTAGT
 ACCGGGATCA TTCCGGCGCT AATCGGGGCT ATGCTACAAG AAGTCGTGGA CACTGTGTCA
 ATCTTATCTG CTTTGCCTGC TCGTCAATT GGCCAGTAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF077-2 (SEQ ID NO:294)

MKHVTKLGIT IITGVLALLF EFILHQPNEW YGIILITGSV MALMMFWEMI
 QTLREGKYGV DILAITAIVA TLAVGEYWAS LMILIMLTGG DSLEDYAAGK ANQELKSLLD
 NSPQKAHRLN GENLEDVSVE EINVGDELVV KPGELVPVDG LVKTGTSTVD ESSLTGESKP
 IEKNPGDELM SGSVNGDGS LKMAEKTVD SQYQTIVNLV KESAARPAHF VRLADRYAVP
 FTLVAYLIAG VAWFVSKSPT RFAEVLVVAS PCPLILSAPI ALVAGMGRSS RHGVVKSQT
 MVEKLASAKT IAFDKTGTIT QGQLSVDQVQ PINAGITAAE LVGLAASVEQ ESSHILARSI
 VAYARKQDVP LKNITDLAEV SGAGVKAFVD GAEIRVGKKN FVTQESQETE KIDKTTIHIS
 RNGTYLGRIT FTDTVRPEAK ETMEKLHQLH LQRILMLTGD QESVAETIAA EVGITEVHGE
 CLPQDKLTIL KELPKENHPV IMVGDGVNDA PSLAAADVGI AMGAHGATAA SETADVILK
 DDLKSVSQAV EIAQDTMKIA KQSVLIGIFI CVLLMLIAST GIIPALIGAM LQEVVDTVSI
 LSLARRRIG Q

EF077-3 (SEQ ID NO:295)

TCA GCCGAATTGG
 GCGTATGCCA TTATTTTAAT AACAGGTTCT GTAATGGCGT TAATGATGTT CTGGGAAATG
 ATTCAAACCT TACGTGAAGG AAAATATGGT GTCGATATTT TAGCGATTAC CGCTATCGTT
 GCAACCTTAG CTGTGGGAGA ATACTGGGCC AGTTTGATGA TTTTAATTAT GTTGACTGGT
 GGTGATTCAT TAGAAGACTA TGCCGCTGGA AAAGCTAACC AAGAGCTGAA GTCATTATG
 GATAACTCGC CACAAAAAGC TCATCGCTTG AATGGCGAAA ATTTAGAAGA TGTTTCTGTT
 GAGGAAATCA ATGTTGGCGA TGAATTAGTA GTAAAACCAG GGGAACTAGT TCCAGTTGAT
 GGCTTGGTAA AAACCGGGAC ATCAACAGTC GATGAATCTT CATTACAGG AGAATCAAAA
 CCAATTGAAA AAAATCCTGG GGATGAATTA ATGTCGGGTT CCGTGAATGG TGACGGCTCT
 TTGAAATGG TTGCTGAAA AACTGTAGCA GACAGTCAAT ATCAAACAAT TGTGAACCTA
 GTGAAAGAA CTGCGGCGCG TCCAGCTCAT TTTGTACGTT TAGCAGATCG CTATGCGGTA
 CCTTTTACAC TAGTTGCCA CTAATTGCA GGTGTTGCTT GGTGTTGTTT AAAAAGTCCG
 ACACGTTTTG CGGAAGTCTT AGTTGTTGCT TCGCCGTGTC CTTTAATTCT ATCTGCCCCA
 ATTGCTTTAG TGGCAGGGAT GGGTCGTTCA AGTCGTCATG GGGTCGTTAT TAAATCGGGA
 ACGATGGTCG AAAAATTAGC TTCTGCAAAA ACGATTGCGT TTGATAAAAC AGGCACGATT
 ACGCAAGGAC AACTTTCTGT TGATCAAGTC CAACCAATCA ATGCTGGAAT AACTGCTGCT
 GAATTAGTGG GATTGGCAGC AAGCGTGGAA CAAGAATCAA GTCATATTTT AGCTAGATCA
 ATTGTTGCTT ATGCCAGAAA GCAAGATGTC CCATTAAAAA ATATTACAGA TCTAGCGGAA
 GTTTCTGGTG CTGGCGTGAA GGCATTTGTG GATGGTGCTG AGATACGGGT AGGTAAAAAG
 AATTTTGTA CACAAGAGTC TCAAGAACT GAAAAAATG ATAAAACGAC TATTATATTT
 TCACGTAATG GCACATATTT AGGCCGAATT ACTTTTACAG ACACGTGACG CCCAGAAGCA
 AAAGAGACTA TGGAAAAATT ACACCAATTA CATCTTCAAC GAATTTTAAT GCTGACGGGG
 GATCAAGAAT CCGTTGCAGA AACGATTGCT GCAGAAGTAG GAATTACCGA AGTACATGGG
 GAATGTTTAC CACAAGATAA ATTAATATT CTAAAAGAA TGCCTAAAGA AAATCATCCA
 GTCATCATGG TAGGAGATGG TGTAATGAT GCACCTTCGC TTGCTGCTGC AGACGTAGGT
 ATTGCTATGG GTGCTCATGG AGCTACTGCG GCTAGTGAAA CTGCTGACGT TGTTATTTTA
 AAAGATGACT TAAGTAAAGT CAGCCAAGCG GTCGAAATTG CCCAAGATAC CATGAAAATT
 GCCAAACAAT CTGTATTAAT CGGAATTTTT ATCTGCGTTT TACTAATGTT AATTGCTAGT
 ACCGGGATCA TTCCGGCGCT AATCGGGGCT ATGCTACAAG AAGTCGTGGA CACTGTGTCA
 ATCTTATCTG CTTTGCCTGC TCGTCGAATT GGCC

EF077-4 (SEQ ID NO:296)

QPNWA YGIILITGSV MALMMFWEMI
 QTLREGKYGV DILAITAIVA TLAVGEYWAS LMILIMLTGG DSLEDYAAGK ANQELKSLLD
 NSPQKAHRLN GENLEDVSVE EINVGDELVV KPGELVPVDG LVKTGTSTVD ESSLTGESKP
 IEKNPGDELM SGSVNGDGS LKMAEKTVD SQYQTIVNLV KESAARPAHF VRLADRYAVP

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

FTLVAYLIAG VAWFVSKSPT RFAEVLVVAS PCPLILSAPI ALVAGMGRSS RHGVVKSQT
MVEKLASAKT IAFDKTGTIT QGQLSVDQVQ PINAGITAAE LVGLAASVEQ ESSHILARSI
VAYARKQDVP LKNITDLAEV SGAGVKAFVD GAEIRVGKKN FVTQESQETE KIDKTTIHIS
RNGTYLGRIT FTDTVRPEAK ETMEKLHQLH LQRILMLTGD QESVAETIAA EVGITEVHGE
CLPQDKLTIL KELPKENHPV IMVGDGVNDA PSLAAADVGI AMGAHGATAA SETADVILK
DDLKSVSQAV EIAQDTMKIA KQSVLIGIFI CVLLMLIAST GIIPALIGAM LQEVVDTVSI
LSALRRARRIG

EF079-1 (SEQ ID NO:297)

TAATTTCTAG CATCACCGAA GAAATTTTTTA GAAAAACAAA GAGCCTGGGC CAATCACTGT
CCCAGGCTCT CATGCTTTAT TTTTAAGGAG GAAGCAATGA AGTCAAAAAA GAAACGTCGT
ATCATTGATG GTTTTATGAT TCTTTTACTG ATTATTGGAA TAGGTGCATT TCGGTATCCT
TTTGTTAGCG ATGCATTAAA TAACTATCTG GATCAACAAA TTATCGCTCA TTATCAAGCA
AAAGCAAGCC AAGAAAAACAC CAAAGAAATG GCTGAACCTC AAGAAAAAAT GGAAAAAGAA
AACCAAGAAT TAGCGAAAAA AGGCAGCAAT CCTGGATTAG ATCCTTTTTTC TGAAACGCAA
AAAACAACGA AAAAACCCAGA CAAATCCTAT TTTGAAAGTC ATACGATTGG TGTTTTAACC
ATTCCAAAAA TAAATGTCCG TTTACCAATT TTTGATAAAA CGAATGCATT GCTATTGGAA
AAAGGAAGCT CCTTGTTAGA AGGAACCTCC TATCCTACAG GTGGTACGAA TACACATGCG
GTCATTTTCAG GCCATCGTGG TCTCCCTCAA GCCAAATTAT TTACAGATTT GCCAGAATTA
AAAAAAGGCG ATGAATTTTTA TATCGAAGTC AATGGGAAGA CGCTTGCTTA TCAAGTAGAT
CAAATAAAAA CCGTTGAACC AACTGATACA AAAGATTAC ACATTGAGTC TGGCCAAGAT
CTCGTCACTT TATTAACCTG CACACCGTAT ATGATAAACA GTCATCGGTT ATTAGTTCGA
GGACATCGTA TCCCATATCA ACCAGAAAAA GCAGCAGCGG GGATGAAAAA AGTGGCACAA
CAACAAAATT TACTATTATG GACATTACTT TTAATTGCCT GTGCGTTAAT TATTAGCGGC
TTCATTATCT GGTACAAGCG ACGGAAAAAG ACGACCAGAA AACCAAAGTA G

EF079-2 (SEQ ID NO:298)

MKSKKKRRI IDGFMILLI IGIGAFAYPF
VSDALNNYLD QIIIAHYQAK ASQENTKEMA ELQEKMEKKN QELAKKGSNP GLDPFSETQK
TTKKPKDSYF ESHITGVLT PKINVRLPIF DKTNALLLEK GSSLLEGTSY PTGGTNTHAV
ISGHRGLPQA KLFTDLPELK KGDEFYIEVN GKTLAYQVDQ IKTVEPTDTK DLHIESGQDL
VTLTCTPYM INSHRLLVRG HRIPTYQPEKA AAGMKKVAQQ QNLLLWTLLE IACALIISGF
IIWYKRRKKT TRKPK

EF079-3 (SEQ ID NO:299)

TCCT
TTTGTTAGCG ATGCATTAAA TAACTATCTG GATCAACAAA TTATCGCTCA TTATCAAGCA
AAAGCAAGCC AAGAAAAACAC CAAAGAAATG GCTGAACCTC AAGAAAAAAT GGAAAAAGAA
AACCAAGAAT TAGCGAAAAA AGGCAGCAAT CCTGGATTAG ATCCTTTTTTC TGAAACGCAA
AAAACAACGA AAAAACCCAGA CAAATCCTAT TTTGAAAGTC ATACGATTGG TGTTTTAACC
ATTCCAAAAA TAAATGTCCG TTTACCAATT TTTGATAAAA CGAATGCATT GCTATTGGAA
AAAGGAAGCT CCTTGTTAGA AGGAACCTCC TATCCTACAG GTGGTACGAA TACACATGCG
GTCATTTTCAG GCCATCGTGG TCTCCCTCAA GCCAAATTAT TTACAGATTT GCCAGAATTA
AAAAAAGGCG ATGAATTTTTA TATCGAAGTC AATGGGAAGA CGCTTGCTTA TCAAGTAGAT
CAAATAAAAA CCGTTGAACC AACTGATACA AAAGATTAC ACATTGAGTC TGGCCAAGAT
CTCGTCACTT TATTAACCTG CACACCGTAT ATGATAAACA GTCATCGGTT ATTAGTTCGA
GGACATCGTA TCCCATATCA ACCAGAAAAA GCAGCAGCGG GGATGAAAAA AGTGGCACAA
CAACAAAATT TACTATTATG GACATTACTT TTAATTGCCT GTGCGTTAAT TATTAGCGGC
TTCATTATCT GGTACAAGCG ACGGAAAAAG ACGACCAGAA AACCAA

EF079-4 (SEQ ID NO:300)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

PF

VSDALNNYLD QQIIAHYQAK ASQENTKEMA ELQEKMEKKN QELAKKGSNP GLDPFSETQK
 TTKKPKDSYF ESHITIGVLT I PKINVRLPIF DKTNALLLEK GSSLLEGTSY PTGGTNTHAV
 ISGHRGLPQA KLFTDLPELK KGDEFYIEVN GKTLAYQVDQ IKTVEPTDTK DLHIESGQDL
 VTLLTCTPYM INSHRLLV RG HRIPYQPEKA AAGMKKVAQQ QNLLLWTL LL IACALIISGF
 IIWYKRRKKT TRKP

EF080-1 (SEQ ID NO:301)

TAGTTACACT CGTTTAGGGC TAGCAACGTT AGGCATTTTC GCTGGACTCT TAGCACTCTT
 TTTATTAGGA GGTTATTTC TATGAAAAAA CGACTTTTAC CTATTTT TTT CCTAATACTT
 CTTACCTTTG GCCTTGCCCT ACCCGTTTCG GCGGCTGAAA ATTCAATTGA TGATGGCGCA
 CAATTACTGA CACCTGATCA AATCAACCAA CTAAAGCAAG AGATACAACC TTTAGAAGAA
 AAAACAAAAG CCTCTGTCTT TATTGTAACC ACAAATAATA ATACCTATGG CGATGAACAA
 GAATATGCAG ATCATTATCT TTTAAATAAA GTTGGCAAGG ACCAAAATGC GATTCTTTT
 CTCATTGATA TGGACTTACG GAAAATCTAC ATCTCTACTT CTGGAAACAT GATTGATTAT
 ATGACAGATG CACGAATTGA TGATACCTTA GATAAAATAT GGGATAATAT GAGTCAAGGA
 AATTATTTTCG CGGCTGCTCA AACCTTTGTT CAGGAAACTC AAGCATTTGT TAATAAAGGG
 GTTCCTGGGG GGCCTATCG TGTGGACAGC GAAACAGGTA AAATCACTCG TTATAAAGTC
 ATTACCCCGC TGGAAATGGT AATTGCTTTT GCTGCTGCGC TGATACTCAG TTTGGTCTTC
 TTAGGCATTA ATATTTCTAA ATATCAATTA AAATTTTCAA GTTATCAATA TCCCTTTAGG
 GAAAAAACAA CTTTAAACTT AACCTCCCGC ACAGATCAGT TAACCAACTC TTTTCATCACT
 ACGCGTCGTA TTCCTAAAA CAATGGCGGC AGTGGCGGAA TGGGCGGTGG TGGTAGCACC
 ACCCACTCAA CTGGCGGCGG CACATTCGGT GCGGCGGTC GAAGTTTTTA G

EF080-2 (SEQ ID NO:302)

MKKR LLPIFFLILL TFGLALPVS AENSIDDGAQ
 LLTPDQINQL KQEIQPLEEK TKASVFIVTT NNNTYGDEQE YADHYLLNKV GKDQNAIFL
 IDMDLRKIYI STSGNMIDYM TDARIDDTLD KIWDNMSQGN YFAAAQTFVQ ETQAFVNKGV
 PGGHYRVDSE TGI TRYKVI TPLEMVI AALILSLVFL GINISKYQLK FSSYQYPFRE
 KTTLNLTSTRT DQLTNSFIT RRIPKNNGGS GGMGGGGSTT HSTGGGTGG GGRSF

EF080-3 (SEQ ID NO:303)

GGCTGAAA ATTCAATTGA TGATGGCGCA
 CAATTACTGA CACCTGATCA AATCAACCAA CTAAAGCAAG AGATACAACC TTTAGAAGAA
 AAAACAAAAG CCTCTGTCTT TATTGTAACC ACAAATAATA ATACCTATGG CGATGAACAA
 GAATATGCAG ATCATTATCT TTTAAATAAA GTTGGCAAGG ACCAAAATGC GATTCTTTT
 CTCATTGATA TGGACTTACG GAAAATCTAC ATCTCTACTT CTGGAAACAT GATTGATTAT
 ATGACAGATG CACGAATTGA TGATACCTTA GATAAAATAT GGGATAATAT GAGTCAAGGA
 AATTATTTTCG CGGCTGCTCA AACCTTTGTT CAGGAAACTC AAGCATTTGT TAATAAAGGG
 GTTCCTGGGG GGCCTATCG TGTGGACAGC GAAACAGGTA AAATCACTCG TTATAAAGTC
 ATTACCCCGC TGGAAATGGT AATTGCTTTT GCTGCTGCGC TGATACTCAG TTTGGTCTTC
 TTAGGCATTA ATATTTCTAA ATATCAATTA AAATTTTCAA GTTATCAATA TCCCTTTAGG
 GAAAAAACAA CTTTAAACTT AACCTCCCGC ACAGATCAGT TAACCAACTC TTTTCATCACT
 ACGCGTCGTA TTCCTAAAA CAATGGCGGC AGTGGCGGAA TGGGCGGTGG TGGTAGCACC
 ACCCACTCAA CTGGCGGCGG CACATTCGGT GCGGCGGTC GAAGT

EF080-4 (SEQ ID NO:304)

AENSIDDGAQ
 LLTPDQINQL KQEIQPLEEK TKASVFIVTT NNNTYGDEQE YADHYLLNKV GKDQNAIFL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

IDMDLRKIYI STSGNMIDYM TDARIDDTLD KIWDNMSQGN YFAAAQTFVQ ETQAFVNKGV
 PGGHYRVDSE TKGITRYKVI TPLEMVIAFA AALILSLVFL GINISKYQLK FSSYQYPFRE
 KTTLNLSRT DQLTNSFIIT RRIPKNNGGS GGMGGGGSTT HSTGGGTFGG GGRS

EF081-1 (SEQ ID NO:305)

TGAATGGAAC GAAGCAATCG TAATAAAAAA TCTTCAAAAA AACCACCTTAT TCTTGGTGT
 TCTGCCCTTGG TTCTAATCGC TGCTGCCGGT GCGGGGTATT ATGCTTATAG TCAATGGCAA
 GCCAAACAAG AATTAGCCGA AGCGAAGAAA ACAGCTACTA CATTTTTTAAA CGTATTGTCA
 AAACAGGAAT TTGATAAGTT ACCGTCCGTT GTTCAAGAAG CTAGCTTAAA GAAAAATGGC
 TATGATACTA AATCTGTTGT TGAAAAATAC CAAGCAATTT ATTCAGGGAT TCAAGCAGAA
 GGAGTCAAAG CTAGTGATGT TCAAGTCAAA AAGGCGAAAG ACAATCAATA CACATTTACC
 TATAAATTAT CGATGAGCAC GCCTTTAGGC GAAATGAAAG ATTTGTCTTA TCAATCAAGT
 ATCGCCAAAA AAGGCGATAC CTACCAAATC GCTTGAAGC CATCTTTAAT TTTTCCAGAT
 ATGTCAGGAA ATGATAAAAT TTGATTCAA GTAGATAATG CCAAACGTGG AGAAATTGTC
 GATCGTAATG GTAGTGGGCT AGCAATTAAC AAAGTGTGTTG ACGAAGTGGG CGTAGTGCCT
 GGCAAACTCG GTTCTGGCGC AGAAAAACA GCCAATATCA AAGCTTTTAG TGATAAATTC
 GCGGTTTCTG TTGATGAAAT CAATCAAAAG TTAAGCCAAG GATGGGTCCA AGCAGACTCC
 TTTGTACCAA TCACAGTCGC TTCTGAACCA GTGACAGAAT TACCAACAGG GGCTGCGACA
 AAAGATACAG AGTCACGTTA TTATCCGCTG GGGGAAGCAN TCGCAATTA A

EF081-2 (SEQ ID NO:306)

MERSNRNKKK SKKPLILGVS ALVLIAAAGG GYYAYSQWQA KQELAEAKKT ATTFNLVLSK
 QEFDKLPSVV QEASLKKNKY DTKSVVEKYQ AIYSGIQAEG VKASDVQVKK AKDNQYTFTY
 KLSMSTPLGE MKDLSYQSSI AKKGDYQIA WKPSLIFPDM SGNDKISIQV DNAKRGEIVD
 RNSGLAINK VFDEGVVPG KLGSGAEKTA NIKAFSDKFG VSVDEINQKL SQGWVQADSF
 VPITVASEPV TELPTGAATK DTESRYPLG EAXRN

EF081-3 (SEQ ID NO:307)

T GCGGGGTATT ATGCTTATAG TCAATGGCAA
 GCCAAACAAG AATTAGCCGA AGCGAAGAAA ACAGCTACTA CATTTTTTAAA CGTATTGTCA
 AAACAGGAAT TTGATAAGTT ACCGTCCGTT GTTCAAGAAG CTAGCTTAAA GAAAAATGGC
 TATGATACTA AATCTGTTGT TGAAAAATAC CAAGCAATTT ATTCAGGGAT TCAAGCAGAA
 GGAGTCAAAG CTAGTGATGT TCAAGTCAAA AAGGCGAAAG ACAATCAATA CACATTTACC
 TATAAATTAT CGATGAGCAC GCCTTTAGGC GAAATGAAAG ATTTGTCTTA TCAATCAAGT
 ATCGCCAAAA AAGGCGATAC CTACCAAATC GCTTGAAGC CATCTTTAAT TTTTCCAGAT
 ATGTCAGGAA ATGATAAAAT TTGATTCAA GTAGATAATG CCAAACGTGG AGAAATTGTC
 GATCGTAATG GTAGTGGGCT AGCAATTAAC AAAGTGTGTTG ACGAAGTGGG CGTAGTGCCT
 GGCAAACTCG GTTCTGGCGC AGAAAAACA GCCAATATCA AAGCTTTTAG TGATAAATTC
 GCGGTTTCTG TTGATGAAAT CAATCAAAAG TTAAGCCAAG GATGGGTCCA AGCAGACTCC
 TTTGTACCAA TCACAGTCGC TTCTGAACCA GTGACAGAAT TACCAACAGG GGCTGCGACA
 AAAGATACAG AGTCACGTTA TTATCCGCTG GGGG

EF081-4 (SEQ ID NO:308)

G GYYAYSQWQA KQELAEAKKT ATTFNLVLSK
 QEFDKLPSVV QEASLKKNKY DTKSVVEKYQ AIYSGIQAEG VKASDVQVKK AKDNQYTFTY
 KLSMSTPLGE MKDLSYQSSI AKKGDYQIA WKPSLIFPDM SGNDKISIQV DNAKRGEIVD
 RNSGLAINK VFDEGVVPG KLGSGAEKTA NIKAFSDKFG VSVDEINQKL SQGWVQADSF
 VPITVASEPV TELPTGAATK DTESRYPLG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF082-1 (SEQ ID NO:309)

TAAAAAATGA AAAAGATCGT GCGCATTTC A GCATTTTGT TCGTTGCTAC GCCTCTTATG
 CTTTTAAATA GTTCAAAAGT TGAAGCAGCT CAAGTCGCTT CTATTCAATC CAACGCTGAT
 ATTACGTTTG CTCTTGATAA TACTGTCACG CCACCTGTCA ACCCGACGAA CCCTTCTCAG
 CCTGTGACAC CTAATCCTGC TGATCCTCAT CAACCTGGTA CAGCCGGACC CCTTAGTATT
 GACTATGTTT CAAATATCCA TTTTGGATCA AAACAAATTC AAGCCGGAAC AGCGATCTAT
 TCGGCACAAC TGGATCAAGT GCAAAATAGT ACTGGCGATT TAATTAGCGT GCCAAACTAT
 GTTCAAGTAA CTGACAAACG TGGTCTAAAT CTGGCTGGA AATTATCAGT TAAACAGAGT
 GCGCAATTTG CTACAAGTGA TTCAACACCC GCTGTTTTGG ATAATGCATC CTTGACCTTT
 TTAGCAGCAA CACCCAATTC AACACAGTTA CTTTCTTTGG CGCCATTAAC GGTCCCAGTA
 ACCTTGGATC CAACTGGTGC CGCCACTTCT CCTGTGGCGA CTGCCGCTCT TTCAACAGGA
 ATGGGCACTT GGACATTAGC TTTTGGTAGC GGANCGACCG CTGCTCAAGG CATTCAATTA
 ACTGTTCTCTG CGACAACGAA AAAAGTTGCA GCTAAACAAT ATAAAACAAC GCTTACTTGG
 ATTTTGGATG ATACACCACT TTAA

EF082-2 (SEQ ID NO:310)

MKKIVRISS ILFVATPLML LNSSKVEAAQ VASIQSNADI TFALDNTVTP PVNPTNPSQP
 VTPNPADPHQ PGTAGPLSID YVSNHFGSK QIQAGTAIYS AQLDQVQNST GDLISVPNYV
 QVTDKRG LNL GWKLSVKQSA QFATSDSTPA VLDNASLTFL AATPNSTQLL SLAPLTPVPT
 LDPTGAATSP VATAALSTGM GTWTLAFSG XTA AQGIQLT VPATTKKVAA KQYKTTLTWI
 LDDTPL

EF082-3 (SEQ ID NO:311)

AGCT CAAGTCGCTT CTATTCAATC CAACGCTGAT
 ATTACGTTTG CTCTTGATAA TACTGTCACG CCACCTGTCA ACCCGACGAA CCCTTCTCAG
 CCTGTGACAC CTAATCCTGC TGATCCTCAT CAACCTGGTA CAGCCGGACC CCTTAGTATT
 GACTATGTTT CAAATATCCA TTTTGGATCA AAACAAATTC AAGCCGGAAC AGCGATCTAT
 TCGGCACAAC TGGATCAAGT GCAAAATAGT ACTGGCGATT TAATTAGCGT GCCAAACTAT
 GTTCAAGTAA CTGACAAACG TGGTCTAAAT CTGGCTGGA AATTATCAGT TAAACAGAGT
 GCGCAATTTG CTACAAGTGA TTCAACACCC GCTGTTTTGG ATAATGCATC CTTGACCTTT
 TTAGCAGCAA CACCCAATTC AACACAGTTA CTTTCTTTGG CGCCATTAAC GGTCCCAGTA
 ACCTTGGATC CAACTGGTGC CGCCACTTCT CCTGTGGCGA CTGCCGCTCT TTCAACAGGA
 ATGGGCACTT GGACATTAGC TTTTGGTAGC GGANCGACCG CTGCTCAAGG CATTCAATTA
 ACTGTTCTCTG CGACAACGAA AAAAGTTGCA GCTAAACAAT ATAAAACAAC GCTTACTTGG
 ATTTTGGATG ATACACCACT

EF082-4 (SEQ ID NO:312)

AQ VASIQSNADI TFALDNTVTP PVNPTNPSQP
 VTPNPADPHQ PGTAGPLSID YVSNHFGSK QIQAGTAIYS AQLDQVQNST GDLISVPNYV
 QVTDKRG LNL GWKLSVKQSA QFATSDSTPA VLDNASLTFL AATPNSTQLL SLAPLTPVPT
 LDPTGAATSP VATAALSTGM GTWTLAFSG XTA AQGIQLT VPATTKKVAA KQYKTTLTWI
 LDDTP

EF083-1 (SEQ ID NO:313)

TAATTTAAAA GACAAGGAGA AATAAAAATG AAAAAGAAAA TTTTAGCAGG AGCGCTTGTC
 GCTCTGTTTT TTATGCCTAC AGCTATGTTT GCCGCAAAAG GAGACCAAGG TGTGGATTGG
 GCGATTTATC AAGGTGAACA AGGTCGCTTT GGCTATGCAC ATGATAAATT CGCTATTGCC
 CAGATTGGAG GCTACAATGC TAGCGGTATT TATGAACAAT ACACATATAA AACGCAAGTG
 GCAAGTGCTA TTGCCCAAGG TAAACGTGCG CATACTATA TTTGGTATGA CACTTGGGGA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AACATGGACA TTGCGAAAAC AACAAATGGAT TACTTTTTCG CACGTATTCA AACGCCTAAA
 AATTCCATCG TTGCATTAGA TTTTGAACAT GGAGCGTTGG CTAGTGTTC AGATGGATAT
 GGAGGATATG TAAGTTCAGA TGCCGAAAAA GCAGCAAATA CAGAGACAAT TTTGTACGGT
 ATGCGCAGAA TCAAACAGGC TGGCTATACT CCAATGTATT ACAGCTATAA GCCATTTACA
 CTAAATCATG TAAACTATCA ACAAATCATC AAAGAGTTTC CTAACCTTTT ATGGATTGCT
 GCGTATCCTA TCGATGGTGT GTCACCATAT CCATTGTATG CTTATTTCCC AAGCATGGAT
 GGTATTGGTA TTTGGCAATT CACATCCGCT TATATTGCAG GTGGTTTAGA TGGTAACGTA
 GATTTAACAG GAATTACGGA TAGTGGTTAT ACAGATACCA ATAAACCAGA AACGGATACG
 CCAGCAACAG ATGCAGGCGA AGAAATTGAA AAAATACCTA ATTCTGATGT TAAAGTTGGC
 GATACCGTCA AAGTGAAATT TAATGTAGAT GCTTGGGCAA CTGGGGAAGC TATTCCGCAA
 TGGGTAAAAG GAAACAGCTA CAAAGTGCAA GAAGTAACTG GAAGCAGAGT ATTGCTTGAA
 GGTATCTTGT CATGGATTAG CAAAGGTGAT ATTGAATTAT TGCCAGACGC AACAGTCGTC
 CCTGATAAGC AACCAGAAGC GACTCATGTG GTACAATACG GAGAAACATT ATCAAGTATT
 GCTTATCAAT ATGGAACAGA CTATCAAACG TTGGCGGCAT TAAATGGATT GGCTAATCCA
 AATCTTATTT ATCCTGGTCA AGTTTGTAAA GTCAATGGAT CGGCAACAAG TAATGTCTAC
 ACGGTTAAAT ACGGCGATAA TTTATCTAGT ATTGCAGCAA AACTTGGCAC TACTTATCAA
 GCTTAGCTG CATTAAACGG ATTAGCAAAT CCTAACTTGA TTTATCCAGG TCAAACATTG
 AATTATTAA

EF083-2 (SEQ ID NO:314)

MK KKILAGALVA LFFMPTAMFA AKGDQGVDDWA IYQGEQGRFG YAHDKFAIAQ
 IGGYNASGIY EQYTYKTQVA SAIAQKRAH TYIWDYDWN MDIAKTMDY FLPRIQTPKN
 SIVALDFEHG ALASVPDGYG GYVSSDAEKA ANTETILYGM RRIKQAGYTP MYYSYKPFLL
 NHVNYQQIIK EFPNSLWIAA YPIDGVSPYP LYAYFSPMDG IGIWQFTSAY IAGGLDGNVD
 LTGITDSGYT DTNKPETDTP ATDAGEEIEK IPNSDVKVG D TVKVKNVDA WATGEAIPQW
 VKGNSYKVQE VTGSRVLLEG ILSWISKGDI ELLPDATVVP DKQPEATHVV QYGETLSSIA
 YQYGTDYQTL AALNGLANPN LIYPGQVLKV NGSATSNVYT VKYGDNLSSI AAKLGTITYQA
 LAALNGLANP NLIYPGQTLN Y

EF083-3 (SEQ ID NO:315)

AAAAG GAGACCAAGG TGTGGATTGG
 GCGATTTATC AAGGTGAACA AGGTCGCTTT GGCTATGCAC ATGATAAATT CGCTATTGCC
 CAGATTGGAG GCTACAATGC TAGCGGTATT TATGAACAAT ACACATATAA AACGCAAGTG
 GCAAGTGCTA TTGCCCAAGG TAAACGTGCG CATACTATA TTTGGTATGA CACTTGGGGA
 AACATGGACA TTGCGAAAAC AACAAATGGAT TACTTTTTCG CACGTATTCA AACGCCTAAA
 AATTCCATCG TTGCATTAGA TTTTGAACAT GGAGCGTTGG CTAGTGTTC AGATGGATAT
 GGAGGATATG TAAGTTCAGA TGCCGAAAAA GCAGCAAATA CAGAGACAAT TTTGTACGGT
 ATGCGCAGAA TCAAACAGGC TGGCTATACT CCAATGTATT ACAGCTATAA GCCATTTACA
 CTAAATCATG TAAACTATCA ACAAATCATC AAAGAGTTTC CTAACCTTTT ATGGATTGCT
 GCGTATCCTA TCGATGGTGT GTCACCATAT CCATTGTATG CTTATTTCCC AAGCATGGAT
 GGTATTGGTA TTTGGCAATT CACATCCGCT TATATTGCAG GTGGTTTAGA TGGTAACGTA
 GATTTAACAG GAATTACGGA TAGTGGTTAT ACAGATACCA ATAAACCAGA AACGGATACG
 CCAGCAACAG ATGCAGGCGA AGAAATTGAA AAAATACCTA ATTCTGATGT TAAAGTTGGC
 GATACCGTCA AAGTGAAATT TAATGTAGAT GCTTGGGCAA CTGGGGAAGC TATTCCGCAA
 TGGGTAAAAG GAAACAGCTA CAAAGTGCAA GAAGTAACTG GAAGCAGAGT ATTGCTTGAA
 GGTATCTTGT CATGGATTAG CAAAGGTGAT ATTGAATTAT TGCCAGACGC AACAGTCGTC
 CCTGATAAGC AACCAGAAGC GACTCATGTG GTACAATACG GAGAAACATT ATCAAGTATT
 GCTTATCAAT ATGGAACAGA CTATCAAACG TTGGCGGCAT TAAATGGATT GGCTAATCCA
 AATCTTATTT ATCCTGGTCA AGTTTGTAAA GTCAATGGAT CGGCAACAAG TAATGTCTAC
 ACGGTTAAAT ACGGCGATAA TTTATCTAGT ATTGCAGCAA AACTTGGCAC TACTTATCAA
 GCTTTAGCTG CATTAAACGG ATTAGCAAAT CCTAACTTGA TTTATCCAGG TCAAACATTG
 AAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF083-4 (SEQ ID NO:316)

KGDQGVDDWA IYQGEQGRFG YAHDKFAIAQ
 IGGYNASGIY EQYTYKTQVA SAIAQKRAH TYIWYDTWGN MDIAKTMDY FLPRIQTPKN
 SIVALDFEHG ALASVPDGYG GYVSSDAEKA ANTETILYGM RRIQAGYTP MYYSYKPFLL
 NHVNYQIIK EFPNSLWIAA YPIDGVSPYP LYAYFPSMDG IGIWQFTSAY IAGGLDGNVD
 LTGITDSGYT DTNKPETDTP ATDAGEEIEK IPNSDVKVG D TVKVKFNVD A WATGEAIPQW
 VKGNSYKVGQ VTGSRVLEGL ILSWISKGDI ELLPDATVVP DKQPEATHVV QYGETLSSIA
 YQYGTDTYQTL AALNGLANPN LIYPGQVLKV. NGSATSNVYT VKYGDNLSSI AAKLGTYYQA
 LAALNGLANP NLIYPGQTLN

EF084-1 (SEQ ID NO:317)

TAGTCAAACG TTTATTTTTT CCTTAAATCC AGAAAAATC CCGTAATTAT GGTACACTAC
 CTATTGAATT GGAGGAGAAC TATGAAGAAA TTTGATGTAA TTATTGTCGG TGCTGGGACG
 AGCGGTATGA TGGCCACGAT TCGGCGCGCC GAAGCAGGCG CTCAAGTATT ATTGATTGAA
 AAAAATCGCC GTGTTGGGAA AAAATTATTA ATGACTGGTG GCGGCCGCTG TAATGTAACC
 AATAATCGGC CCGCAGAAGA AATCATTTCA TTTATTCCTG GGAATGGAAA ATTTTATAC
 AGCGCATTTT CACAATTTGA TAACTATGAT ATCATGAACT TTTTGAATC CAATGGTATT
 CACTTAAAAG AAGAAGATCA CGGACGCATG TTCCCTGTGA CAGATAAATC GAAGTCAATT
 GTTGATGCGC TATTTAACCG CATTAACGAA TTAGGAGTCA CTGTTTTTAC AAAACACAG
 GTCACAAAAT TACTACGAAA AGACGATCAA ATAATTGGCG TTGAAACCGA ACTGGAAAAA
 ATTTATGCAC CGTGTGTTGT ATTAACAACT GCGCGCCGCA CTTATCCTTC CACAGGAGCA
 ACTGTGTATG GCTATAAACT AGCCAAAAAA ATGGGGCATA CCATCAGCCC GCTCTACCTT
 ACCGAATCAC CTATTATTTT TGAAGAACCT TTTATCCTGG ATAAACGTT GCAAGGTCTC
 TCTTTACAAG ATGTTAATTT AACTGTTTGT AACCAAAAAG GAAAACCTTT AGTTAATCAT
 CAAATGGATA TGCTGTTTAC ACATTTTGGC ATTTTCAGGAC CTGCCGCGCT CCGCTGTCTT
 AGTTTTTATTA ACCAAGAATT AACTCGCAAC GGTAATCAAC CTGTCACGGT AGCCTTGGAT
 GTGTTTCCGA CAAAATCTTT TGAAGAAGTG CCTGCCAAAC AACTAACAGA AAAGCAACGN
 CTTTCCTTTG TGGAACACT GAAAGACTTT CAGTTCACTG TTACGAAAAC ATTGCCTTTG
 GAAAAATCTT TTGTCACAGG CCGTGGGATT TCCCTCAAAG AAGTGACCCC TAAAACAATG
 GAGAGCAAAT TAGTCAATGG TTTATTTTTT GCTGGTGAAC TTTTAGATAT TAATGGCTAT
 ACTGGAGGCT ACAATGTTAC AGCTGCATTT GTCACCTGGAC ATGTTGCTGG CTCCCATGCC
 GCAGAAATTG CAGAATACAC CTATTTACCA ATTGAAGAAG TCTAA

EF084-2 (SEQ ID NO:318)

MKKF DVIIVGAGTS GMMATIAAAE AGAQVLLIEK
 NRRVGKKLLM TGGGRCNVTN NRPAEEIISF IPGNGKFLYS AFSQFDNYDI MNFFESNGIH
 LKEEDHGRMF PVTDKSKSIV DALFNRLINEL GVTVFTKTQV TKLLRKDDQI IGVETELEKI
 YAPCVVLTG GRYPSTGAT GDGYKLAKKM GHTISPLYPT ESPIISEEPF ILDKTLQGLS
 LQDVNLTVLN QKGKPLVNHQ MDMLFTHFGI SGPAALRCSS FINQELTRNG NQPVTVALDV
 FPTKSFEEVP AKQLTEKQRL SFVELLKDFQ FTVTKTLPLE KSFVTGGGIS LKEVTPKTIME
 SKLVNGLFFA GELLDINGYT GGYNVTAADFV TGHVAGSHAA EIAEYTYLPI EEV

EF084-3 (SEQ ID NO:319)

C GAAGCAGGCG CTCAAGTATT ATTGATTGAA
 AAAAATCGCC GTGTTGGGAA AAAATTATTA ATGACTGGTG GCGGCCGCTG TAATGTAACC
 AATAATCGGC CCGCAGAAGA AATCATTTCA TTTATTCCTG GGAATGGAAA ATTTTATAC
 AGCGCATTTT CACAATTTGA TAACTATGAT ATCATGAACT TTTTGAATC CAATGGTATT
 CACTTAAAAG AAGAAGATCA CGGACGCATG TTCCCTGTGA CAGATAAATC GAAGTCAATT
 GTTGATGCGC TATTTAACCG CATTAACGAA TTAGGAGTCA CTGTTTTTAC AAAACACAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTCACAAAAT TACTACGAAA AGACGATCAA ATAATTGGCG TTGAAACCGA ACTGGAAAAA
 ATTTATGCAC CGTGTGTTGT ATTAACAACCT GGCGGCCGCA CTTATCCTTC CACAGGAGCA
 ACTGGTGATG GCTATAAACT AGCCAAAAAA ATGGGGCATA CCATCAGCCC GCTCTACCCCT
 ACCGAATCAC CTATTATTTT TGAAGAACCT TTTATCCTGG ATAAAACGTT GCAAGGTCTC
 TCTTTACAAG ATGTTAATTT AACTGTTTTG AACCAAAAAG GAAAACCTTT AGTTAATCAT
 CAAATGGATA TGCTGTTTAC ACATTTTGGC ATTTTCAGGAC CTGCCGCGCT CCGCTGTTCT
 AGTTTTATTA ACCAAGAATT AACTCGCAAC GGTAAATCAAC CTGTCACGGT AGCCTTGGAT
 GTGTTTCCGA CAAAATCTTT TGAAGAAGTG CCTGCCAAAC AACTAACAGA AAAGCAACGN
 CTTTCCTTTG TGGAACTACT GAAAGACTTT CAGTTCAC TGTTACGAAAAC ATTGCCTTTG
 GAAAAATCTT TTGTACAGG CGGTGGGATT TCCCTCAAAG AAGTGACCCC TAAAACAATG
 GAGAGCAAAT TAGTCAATGG TTTATTTTTT GCTGGTGAAC TTTTAGATAT TAATGGCTAT
 ACTGGAGGCT ACAATGTTAC AGCTGCATTT GTCACGGAC ATGTTGCTGG CTCCCATGCC
 GCAGAAATTG CAGAATACAC CTATTTACCA ATTGAAGAAG TC

EF084-4 (SEQ ID NO:320)

E AGAQLVLLIEK

NRVRGKLLM TGGGRCNVN NRPAEEIISF IPGNGKFLYS AFSQFDNYDI MNFFESNGIH
 LKEEDHGRMF PVTDKSKSIV DALFNRI NEL GVTVFTKTQV TKLLRKDDQI IGVETELEKI
 YAPCVVLTG GRTPSTGAT GDGYKLAKKM GHTISPLYPT ESPIISEEPF ILDKTLQGLS
 LQDVNLTVLN QKGKPLVNHQ MDMLFTHFGI SGPAALRCSS FINQELTRNG NQPVTVALDV
 FPTKSFEVFP AKQLTEKQRL SFVELLKDFQ FTVTKTLPLE KSFVTGGGIS LKEVTPKIME
 SKLVNGLFFA GELLDINGYT GGYNVTA AFV TGHVAGSHAA EIAEYTYLPI EEV

EF085-1 (SEQ ID NO:321)

TAACCCATGA AATCATTTTG TCCCGCATAT GGGGATATGA CTTTGACGGT GATGGCAGCA
 CAGTCCACAC TCATATCAAA AATCTGCGGG CGAACTGCCG GAAAATATCA TCAAAACCAT
 CCGCGGTGTA GGTACCGAT TGGAGGAATC ATTATAATGG AAAGAAAAGG GATTTTCATT
 AAGGTTTTTT CCTATACGAT CATTGTCTTG TTACTGCTTG TCGGTGTAAC GGCAACACTG
 TTTGCACAGC AATTTGTGTC TTATTTTACA GCGATGGAAG CACAGCAAAC AGTAAATCC
 TATCAGCCAT TGGTGGAACT GATTCAGAAT AGCGATAGGC TTGATATGCA AGAGGTGGCA
 GGGCTGTTTC ACTACAATAA CCAATCCTTT GAGTTTTATA TTGAAGATAA AGAGGGAAGC
 GTACTCTATG CCACACCGAA TGCCGATACA TCAAATAGTG TTAGGCCCGA CTTTCTTTAT
 GTGGTACATA GAGATGATAA TATTTTCGATT GTTGCTCAAA GCAAGGCAGG TGTGGGATTG
 CTTTATCAAG GGCTGACAAT TCGGGGAATT GTTATGATTG CGATAATGGT TGTATTACAGC
 CTTTTATGCG CGTATATCTT TGCGCGGCAA ATGACAACGC CGATCAAAGC CTTAGCGGAC
 AGTGCGAATA AAATGGCAA CCGTAAAGAA GTACCGCCGC CGCTGGAGCG AAAGGATGAG
 CTTGGCGCAC TGGCTCACGA CATGCATTCC ATGTATATCA GGCTGAAAGA AACCATCGCA
 AGGCTGGAGG ATGAAATCGC AAGGGAACAT GAGTTGGAGG AAACACAGCG ATATTTCTTT
 GCGGCAGCCT CTCATGAGTT AAAAAACGCC ATCGCGGCTG TAAGCGTTCT GTTGGAGGGA
 ATGCTTGAAA ATATCGGTGA CTACAAAGAC CATTCTAAGT ATCTGCGCGA ATGCATCAAA
 ATGATGGACA GGCAGGGCAA AACCATTTCG GAAATACTGG AGCTTGTCAG CCTGAACGAT
 GGGAGAATCG TACCCATAGC CGAACCGCTG GACATAGGCG GCACGGTTGC CGAGCTGCTA
 CCCGATTTTC AAACCTTGGC AGAGGCAAAC AACCAGCGGT TCGTCACAGA TATTCCAGCC
 GGACAAATTG TCCTGTCCGA TCCGAAGCTG ATCCAAAAGG CGCTATCCAA TGTCATATTG
 AATGCGGTTT AGAACACGCC CCAGGGAGGT GAGGTACGGA TATGGAGTGA GCCTGGGGCT
 GAAAAATACC GTCTTTCCGT TTTGAACATG GGCGTTCACA TTGATGATAC TGCACCTTTCA
 AAGCTGTTCA TCCCATTTCTA TCGCATTGAT CAGGCGCGAA GCAGCAAAAA GTGGGCGAAG
 CGGTTTGGGG CTTGCCATCG TACAAAAAAC GCTGGATGCC ATGAGCCTCC AATATGCGCT
 GGAAAAACACC TCAGATGGCG TTTTGTCTG GCTGGATTTA CCGCCACAT CAACACTATA
 AATATTTAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF085-2 (SEQ ID NO:322)

MERKGIK

VFSYTIIVLL LLVGVTTATLF AQQFVSYFRA MEAQQTIVKSY QPLVELIQNS DRLDMQEVAG
 LFHYNQSFY FYIEDKEGSV LYATPNADTS NSVRPDLVY VHRDDNISIV AQSAGVGLL
 YQGLTIRGIV MIAIMVVFSL LCAYIFARQM TPIKALADS ANKMANLKEV PPPLERKDEL
 GALAHDMHSM YIRLKETIAR LEDEIAREHE LEETQRYFFA AASHELKTP I AAVSVLLEGM
 LENIGDYKDH SKYLRECIKM MDRQKKTISE ILELVSLNDG RIVPIAEPLD IGRTVAELLP
 DFQTLAEANN QRFVTDIPAG QIVLSDPKLI QKALSNVILN AVQNTPOGGE VRIWSEPGAE
 KYRLSVLNMG VHIDDTALSK LFIPFYRIDQ ARSSKKWAKR FGACHRTKNA GCHEPPICAG
 KHLRWRFLA GFTAHINTIN I

EF085-3 (SEQ ID NO:323)

GC AATTTGTGTC TTATTTTCAGA GCGATGGAAG CACAGCAAAC AGTAAAATCC
 TATCAGCCAT TGGTGGAACT GATTCAGAAT AGCGATAGGC TTGATATGCA AGAGGTGGCA
 GGGCTGTTTC ACTACAATAA CCAATCCTTT GAGTTTTATA TTGAAGATAA AGAGGGAAGC
 GTACTCTATG CCACACCGAA TGCCGATACA TCAAATAGTG TTAGGCCCCA CTTTCTTTAT
 GTGGTACATA GAGATGATAA TATTTTCGATT GTTGCTCAA GCAAGGCAGG TGTGGGATTG
 CTTTATCAAG GGCTGACAAT TCGGGGAATT GTTATGATTG CGATAATGGT TGTATTCAGC
 CTTTATGCG CGTATATCTT TGCGCGGCAA ATGACAACGC CGATCAAAGC CTTAGCGGAC
 AGTGCGAATA AAATGGCAA CCTGAAAGAA GTACCGCCGC CGCTGGAGCG AAAGGATGAG
 CTTGGCGCAC TGGCTCACGA CATGCATTC ATGTATATCA GGCTGAAAGA AACCATCGCA
 AGGCTGGAGG ATGAAATCGC AAGGGAACAT GAGTTGGAGG AAACACAGCG ATATTTCTTT
 GCGGCAGCCT CTCATGAGTT AAAAACGCC CTACAAAGAC CATTCTAAGT ATCTGCGCGA ATGCATCAA
 ATGCTTGAAA ATATCGGTGA CTACAAAGAC CATTCTAAGT ATCTGCGCGA ATGCATCAA
 ATGATGGACA GGCAGGGCAA AACCATTTCC GAAATACTGG AGCTTGTCAG CCTGAACGAT
 GGGAGAATCG TACCCATAGC CGAACCGCTG GACATAGGGC GCACGGTTGC CGAGCTGCTA
 CCCGATTTTC AAACCTTGGC AGAGGCAAAC AACCAGCGGT TCGTCACAGA TATTCAGCC
 GGACAAATTG TCCTGTCCGA TCCGAAGCTG ATCCAAAAGG CGCTATCCAA TGTCATATTG
 AATGCGGTTT AGAACACGCC CCAGGGAGGT GAGGTACGGA TATGGAGTGA GCCTGGGGCT
 GAAAAATACC GTCTTTCCGT TTGAACATG GCGCTTCACA TTGATGATAC TGCACTTTCA
 AAGCTGTTCA TCCCATTTCTA TCGCATTGAT CAGGCGCGAA GCAGCAAAA GTGGGCGAAG
 CGGTTTGGGG CTTGCCATCG TACAAAAAAC GCTGGATGCC ATGAGCCTCC AATATGCGCT
 GGAAACACC TCAGATGGCG TTTTGTCTTG GCTGGATTTA CCGCCACAT CAACACTATA
 AATATTT

EF085-4 (SEQ ID NO:324)

QFVSYFRA MEAQQTIVKSY QPLVELIQNS DRLDMQEVAG
 LFHYNQSFY FYIEDKEGSV LYATPNADTS NSVRPDLVY VHRDDNISIV AQSAGVGLL
 YQGLTIRGIV MIAIMVVFSL LCAYIFARQM TPIKALADS ANKMANLKEV PPPLERKDEL
 GALAHDMHSM YIRLKETIAR LEDEIAREHE LEETQRYFFA AASHELKTP I AAVSVLLEGM
 LENIGDYKDH SKYLRECIKM MDRQKKTISE ILELVSLNDG RIVPIAEPLD IGRTVAELLP
 DFQTLAEANN QRFVTDIPAG QIVLSDPKLI QKALSNVILN AVQNTPOGGE VRIWSEPGAE
 KYRLSVLNMG VHIDDTALSK LFIPFYRIDQ ARSSKKWAKR FGACHRTKNA GCHEPPICAG
 KHLRWRFLA GFTAHINTIN I

EF086-1 (SEQ ID NO:325)

TAACTGGTGG GATTGGCAA TTGGTTCCGC GCAGCGCTAA CAGATACATT GATTTTATTA
 CATGATGACC TATTGAATAC AGATGCAGAA AAATTAAATA AATTTACTGC TCCGCTGATG
 CTGTATGCAA AAGATCCAAA CATACAATGG CCAATTTATC GTGCAACAGG AGCTAACTTA
 ACAGATATTT CAATCACCGT TTTAGGTACT GGACTTTTGT TAGAAGATAA TCAACGCCTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTACAAGTAC AAGAAGCTGT TCCGTCCGTT TTAAAAAGTG TTTCTCTGCG TGATGGCTTA
 TATCCTGATG GTTCCTTGAT TCAACATGGT TATTTTCCGT ACAACGGCAG TTACGGGAAT
 GAGTTGCTAA AAGGGTTTGG ACGAATTCAG ACTATTTTAC AAGGTTCCGA CTGGGAGATG
 AATGACCTTA ACATTAGTAA TTTATTTAAT GTTGTGGATA AAGGTTACTT ACAATTGATG
 GTAAATGGAA AAATGCCATC GATGGTTTCT GGTAGAAGTA TTTCCAGAGC GCCAGAAACG
 AATCCTTTTA CTACAGAGTT TGAATCGGGT AAAGAAACAA TAGCTAATTT AACCTTAATT
 GCAAAATTTG CACCAGAAAA TTTAAGAAAT GACATTTATA CATCTATCCA AACGTGGCTT
 CAACAAAGTG GGTCACTACTA TCATTTCTTT AAAAAACCA GAGATTTTGA AGCGTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGCGTCA CCTGCCCAAG CGACACCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCCTA CAGAAAAATA ACGAATATGC GGTGGGGATC
 AGTATGTATT CACAACGTGT CGGAAACTAT GAATTTGGGA ATACGGAAAA TAAAAAGGC
 TGGCATAACAG CAGACGGCAT GCTTTATTTA TACAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACCAGGAA CGACAGTTGA CACAAGAGAA
 TTGGCAAATG GTGCTTATAC AGGGAAACGC AGTCCCCAGT CATGGGTAGG TGGCTCAAAT
 AATGGACAGG TTGCCTCTAT AGGAATGTTT TTAGATAAAA GTAATGAAGG AATGAACTTA
 GTTGCTAAAA AATCTTGGTT CTTATTAGAT GGTCAAATCA TTAATTTGGG AAGTGGCATT
 ACTGGTACGA CAGATGCTTC GATTGAAACA ATCCTCGATA ATCGGATGAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATTCTT GGATTAGTTT AAGCGCAGCG
 ANTCCATTGA ATAACATTGG CTATGTTTTT CCTAATTCNA TGAATACGCT TGATGTTCAA
 ATAGAAGAAC GCTCTGGTCG CTACGGAGAT ATTAACGAAT ACTTTGTTAA TGATAAAACC
 TATACAAATA CATTTGCTAA AATTAGTAAA AATTATGGCA AGACTGTTGA AAATGGTACT
 TACGAAATATT TAACAGTGCT TGGGAAAACG AATGAAGAAA TCGCAGCTCT TTCTAAAAAC
 AAAGGCTATA CTGTTCTAGA AAATACAGCA AACTTACAAG CCATTGAAGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATTGCAG GACTGTATGC GTATGATCCA
 ATGTCGGTTA TTTTCAGAAA AATTGATAAC GGTGTTTATC GCTTAACTCT TGCGAATCCT
 TTACAAAATA ATGCATCCGT TTCTATTGAA TTTGATAAGG GCATTCTTGA AGTAGTCGCA
 GCGGACCCAG AAATTTCTGT TGACCAAAAT ATTATCACTT TAAATAGTGC GGGGTTAAAT
 GGCAGCTCGC GTTCAATCAT TGTTAAAACA ACTCCTGAAG TAACGAAAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT ACACCGCAAG CAGCTGGAAA
 GTCTACAGCG AAGCATTGAA ACAAGCACAA ACTGTGGCAG ATCAAACAAC AGCAACGCAA
 GCAAGAGTAG ACCAAGCAGA AACAGAGTTA CGTTCGGCAG TGAAGCAATT GGTAAGAGTG
 CCAACTAAAG AAGTAGATAA AACCAACTTG TTGAAAATCA TCAAAGAAAA CGAGAAACAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA GTGAAGCATT GAAGCAAGCG
 CAACTGTGG CAGATCAAAC AACAGCAACG CAAGCAGAAG TAGACCAAGC AGAAGCAAAA
 CTACGTTCCG CAGTGAAGCG ATTAACATTG AAAAATAGTG GGGAAAATAA AAAGGAGCAA
 AAAAATGGGG GGAATAATGG ACACCTAAAT ACTAGTACAG GAGTTGATCA AACTGGTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCAGAAAAG CTAGCCAATT TTTACCGAGC
 ACAGGAGAAA AGAAATCGAT CGCGCTTGTG ATTATTGGTC TTCTAGTTAT CGCCAGTGGG
 TGTCTTTTAC TTTTTCGTAA AAGTAAATCG AAGAAGTAA

EF086-2 (SEQ ID NO:326)

LVGLANWFRA ALDTLILLH DDLLNTDAEK LNKFTAPLML YAKDPNIQWP IYRATGANLT
 DISITVLGTG LLEDNQRLV QVQEA VPSVL KSVSSGDGLY PDGSLIQHGY FPYNGSYGNE
 LLKGFGRQIT ILQGS DWEMN DPNISNLFNV VDKGYLQLMV NGKMPSMVSG RSISRAPETN
 PFTTEFESGK ETIANLTLIA KFA PENLRND IYTSIQTWLQ QSGSYHFFK KPRDFEALID
 LKNVVNSASP AQATPMQSLN VYGSM DRV LQ KNNEYAVGIS MYSQVRVNGYE FGNTENKKGW
 HTADGMLYLY NQDFAQFDEG YWATIDPYRL PGTTVDREL ANGAYTGKRS PQSWVGGSSNN
 GQVASIGMFL DKSNEGMNLV AKKSWFLLDG QIINLGS GIT GTTDASIETI LDNRMIHPQE
 VKLNQGS DKD NSWISLSAAX PLNNIGYVFP NSMNTLDVQI EERSGRYGD I NEYFVNDKTY
 TNTFAKISK N YGKTVENGTY EYLT VVGKT N EEI AALSKNK GTVLENTAN LQAIEAGNYV
 MMNTVNDQNE IAGLYAYDPM SVISEKIDNG VYRLTLANPL QNNASVSIEF DKGILEVVAA
 DPEISVDQNI ITLNSAGLNG SSRSIIKTT PEVTKEALEK LIQE QKEHQE KDYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVKVP TKEVDKTNLL KIIKENEKHO

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EKDYTASSWK VYSEALKQAO TVADQTTATQ AEVDQAEAKL RSAVKRLTLK NSGENKKEQK
 NGGNNGHLNT STGVDQTGTK QVKPSSQGGF RKASQFLPST GEKKSIALVI IGLLVIASGC
 LLVFRKSKSK K

EF086-3 (SEQ ID NO:327)

ACCAGAAAA TTTAAGAAAT GACATTTATA CATCTATCCA AACGTGGCTT
 CAACAAAGTG GGTCATACTA TCATTTCTTT AAAAAACCAA GAGATTTTGA AGCGTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGCGTCA CCTGCCCAAG CGACACCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCCTA CAGAAAAATA ACGAATATGC GGTGGGGATC
 AGTATGTATT CACAACGTGT CGGAAACTAT GAATTTGGGA ATACGGAAAA TAAAAAGGC
 TGGCATAACAG CAGACGGCAT GCTTTATTTA TACAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACCAGGAA CGACAGTTGA CACAAGAGAA
 TTGGCAAATG GTGCTTATAC AGGGAAACGC AGTCCCCAGT CATGGGTAGG TGGCTCAAAT
 AAT

EF086-4 (SEQ ID NO:328)

PENLRND IYTSIQTWLQ QSGSYHFFK KPRDFEALID
 LKNVNSASP AQATPMQSLN VYGSMDRVLQ KNNEYAVGIS MYSQVRVNGYE FGNTENKKGW
 HTADGMLYLY NQDFAQFDEG YWATIDPYRL PGTTVDITREL ANGAYTKRS PQSWVGGSNN

EF087-1 (SEQ ID NO:329)

TAACTGGTGG GATTGGCAAA TTGGTTCCGC GCAGCGCTAA CAGATACATT GATTTTATTA
 CATGATGACC TATTGAATAC AGATGCAGAA AAATTAAATA AATTTACTGC TCCGCTGATG
 CTGTATGCAA AAGATCCAAA CATACAATGG CCAATTTATC GTGCAACAGG AGCTAACCTA
 ACAGATATTT CAATCACCCT TTTAGGTACT GGACTTTTGT TAGAAGATAA TCAACGCCTA
 GTACAAGTAC AAGAAGCTGT TCCGTCCGTT TTAAGAGTG TTTCTCTGG TGATGGCTTA
 TATCCTGATG GTTCCTTGAT TCAACATGGT TATTTTCCGT ACAACGGCAG TTACGGGAAT
 GAGTTGCTAA AAGGGTTTGG ACGAATTCAG ACTATTTTAC AAGGTTCCGA CTGGGAGATG
 AATGACCCTA ACATTAGTAA TTTATTTAAT GTTGTGGATA AAGGTTACTT ACAATTGATG
 GTAAATGGAA AAATGCCATC GATGGTTTCT GGTAGAAGTA TTTCCAGAGC GCCAGAAACG
 AATCCTTTTA CTACAGAGTT TGAATCGGGT AAAGAAACAA TAGCTAATTT AACCTTAATT
 GCAAAATTTG CACCAGAAAA TTTAAGAAAT GACATTTATA CATCTATCCA AACGTGGCTT
 CAACAAAGTG GGTCATACTA TCATTTCTTT AAAAAACCAA GAGATTTTGA AGCGTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGCGTCA CCTGCCCAAG CGACACCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCCTA CAGAAAAATA ACGAATATGC GGTGGGGATC
 AGTATGTATT CACAACGTGT CGGAAACTAT GAATTTGGGA ATACGGAAAA TAAAAAGGC
 TGGCATAACAG CAGACGGCAT GCTTTATTTA TACAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACCAGGAA CGACAGTTGA CACAAGAGAA
 TTGGCAAATG GTGCTTATAC AGGGAAACGC AGTCCCCAGT CATGGGTAGG TGGCTCAAAT
 AATGGACAGG TTGCCTCTAT AGGAATGTTT TTAGATAAAA GTAATGAAGG AATGAACCTA
 GTTGCTAAAA AATCTTGGTT CTTATTAGAT GGTCAAATCA TTAATTTGGG AAGTGGCATT
 ACTGGTACGA CAGATGCTTC GATTGAAACA ATCCTCGATA ATCGGATGAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATCTTT GGATTAGTTT AAGCGCAGCG
 ANTCCATTGA ATAACATTGG CTATGTTTTT CTAATTCNA TGAATACGCT TGATGTTCAA
 ATAGAAGAAC GCTCTGGTCG CTACGGAGAT ATTAACGAAT ACTTTGTTAA TGATAAAACC
 TATACAAATA CATTTGCTAA AATTAGTAAA AATTATGGCA AGACTGTTGA AAATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATGAAGAAA TCGCAGCTCT TTCTAAAAAC
 AAAGGCTATA CTGTTCTAGA AAATACAGCA AACTTACAAG CCATTGAAGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATTCAG GACTGTATGC GTATGATCCA
 ATGTCCGGTTA TTTCAGAAAA AATTGATAAC GGTGTTTATC GCTTAACTCT TCGGAATCCT
 TTACAAAATA ATGCATCCGT TTCTATTGAA TTTGATAAGG GCATTCTTGA AGTAGTCGCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCGGACCCAG AAATTTCTGT TGACCAAAAT ATTATCACTT TAAATAGTGC GGGGTAAAT
 GGCAGCTCGC GTTCAATCAT TGTTAAAACA ACTCCTGAAG TAACGAAAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT ACACCGCAAG CAGCTGGAAA
 GTCTACAGCG AAGCATTGAA ACAAGCACAA ACTGTGGCAG ATCAAACAAC AGCAACGCAA
 GCAGAAAGTAG ACCAAGCAGA AACAGAGTTA CGTTCGGCAG TGAAGCAATT GGTAAGAGTG
 CCAACTAAAG AAGTAGATAA AACCAACTTG TTGAAAATCA TCAAAGAAAA CGAGAAACAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA GTGAAGCATT GAAGCAAGCG
 CAAACTGTGG CAGATCAAAC AACAGCAACG CAAGCAGAAG TAGACCAAGC AGAAGCAAAA
 CTACGTTCCG CAGTGAAGCG ATTAACATTG AAAAATAGTG GGGAAAATAA AAAGGAGCAA
 AAAAATGGGG GGAATAATGG ACACTTAAAT ACTAGTACAG GAGTTGATCA AACTGGTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCAGAAAAG CTAGCCAATT TTTACCGAGC
 ACAGGAGAAA AGAAATCGAT CGCGCTTGTG ATTATTGGTC TTCTAGTTAT CGCCAGTGGG
 TGTCTTTTAG TTTTTCGTAA AAGTAAATCG AAGAAGTAA

EF087-2 (SEQ ID NO:330)

LVGLANWFRA ALTDTLILLH DDLNNTDAEK LNKFTAPLML YAKDPNIQWP IYRATGANLT
 DISITVLGTG LLEDNQRLV QVQEA VPSVL KSVSSGDGLY PDGSLIQHGY FPNYSYGNE
 LLKGFGRIQT ILQGSWEMN DPNISNLFNV VDKGYLQLMV NGKMPSMVSG RSISRAPETN
 PFTTEFESGK ETIANLTLIA KFAPENLRND IYTSIQTWLQ QSGSYHFFK KPRDFEALID
 LKNVNSASP AQATPMQSLN VYGSMDRVLQ KNNEYAVGIS MYSQVRVNGYE FGNTENKKGW
 HTADGMLYLY NQDFAQFDEG YWATIDPYRL PGTTVDREL ANGAYTGKRS PQSWVGGSNN
 GQVASIGMFL DKSNEGMNLV AKKSWFLLDG QIINLGSGIT GTTDASIETI LDNRMIHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMNTLDVQI EERSGRYDI NEYFVNDKTY
 TNTFAKISK N YGKTVENGTY EYLTUVGKTN EEIAALSKNK GYTVLENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYRLTLANPL QNNASVSIEF DKGILEVVAA
 DPEISVDQNI ITLNSAGLNG SSRSIIVKTT PEVTKEALEK LIQEKEHQE KDYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAE TELR SAVKQLVKVP TKEVDKTNLL KIIKENEKHQ
 EKDYTASSWK VYSEALKQAQ TVADQTTATQ AEVDQAEAKL RSAVKRLTLK NSGENKKEQK
 NGGNNGHLNT STGVDQTGTK QVKPSSQGGF RKASQFLPST GEKKSIALVI IGLLVIASGC
 LLVFRKSKSK K

EF087-3 (SEQ ID NO:331)

A ATCGGATGAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATTCTT GGATTAGTTT AAGCGCAGCG
 ANTCCATTGA ATAACATTGG CTATGTTTTT CCTAATTCNA TGAATACGCT TGATGTTCAA
 ATAGAAGAAC GCTCTGGTCG CTACGGAGAT ATTAACGAAT ACTTTGTTAA TGATAAAACC
 TATACAAATA CATTTGCTAA AATTAGTAAA AATTATGGCA AGACTGTTGA AAATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATGAAGAAA TCGCAGCTCT TTCTAAAAAC
 AAAGGTATA CTGTTCTAGA AAATACAGCA AACTTACAAG CCATTGAAGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATTGCAG GACTGTATGC GTATGATCCA
 ATGTCGGTTA TTTCAGAAAA AATTGATAAC GGTGTTTATC GCTTAACTCT TGCGAATCCT
 TTACAAAATA ATGCATCC

EF087-4 (SEQ ID NO:332)

NRMHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMNTLDVQI EERSGRYDI NEYFVNDKTY
 TNTFAKISK N YGKTVENGTY EYLTUVGKTN EEIAALSKNK GYTVLENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYRLTLANPL QNNAS

EF088-1 (SEQ ID NO:333)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TAACTGGTGG GATTGGCAAA TTGGTTCCGC GCAGCGCTAA CAGATACATT GATTTTATTA
 CATGATGACC TATTGAATAC AGATGCAGAA AAATTAAATA AATTTACTGC TCCGCTGATG
 CTGTATGCAA AAGATCCAAA CATACAATGG CCAATTTATC GTGCAACAGG AGCTAACCTA
 ACAGATATTT CAATCACCGT TTTAGGTACT GGACTTTTGT TAGAAGATAA TCAACGCCTA
 GTACAAGTAC AAGAAGCTGT TCCGTCCGTT TTAAAAAGTG TTTCCTCTGG TGATGGCTTA
 TATCCTGATG GTTCCTTGAT TCAACATGGT TATTTTCCGT ACAACGGCAG TTACGGGAAT
 GAGTTGCTAA AAGGGTTTGG ACGAATTCAG ACTATTTTAC AAGGTTCCGA CTGGGAGATG
 AATGACCCTA ACATTAGTAA TTTATTTAAT GTTGTGGATA AAGGTTACTT ACAATTGATG
 GTAAATGGAA AAATGCCATC GATGGTTTCT GGTAGAAGTA TTTCCAGAGC GCCAGAAACG
 AATCCTTTTA CTACGAGTT TGAATCGGGT AAAGAAACAA TAGCTAATTT AACCTTAATT
 GCAAAATTTG CACCAGAAAA TTTAAGAAAT GACATTTATA CATCTATCCA AACGTGGCTT
 CAACAAAGTG GGTCATACTA TCATTTCTTT AAAAAACCAA GAGATTTTGA AGCGTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGCCTCA CCTGCCCCAAG CGACACCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCCTA CAGAAAAATA ACGAATATGC GGTGGGGATC
 AGTATGTATT CACAACGTGT CGGAAACTAT GAATTTGGGA ATACGGAAAA TAAAAAAGGC
 TGGCATACAG CAGACGGCAT GCTTTATTTA TACAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACCAGGAA CGACAGTTGA CACAAGAGAA
 TTGGCAAAATG GTGCTTATAC AGGGAAACGC AGTCCCCAGT CATGGGTAGG TGGCTCAAAT
 AATGGACAGG TTGCCTCTAT AGGAATGTTT TTAGATAAAA GTAATGAAGG AATGAACCTA
 GTTGCTAAAA AATCTTGGTT CTTATTAGAT GGTCAAATCA TTAATTTGGG AAGTGGCATT
 ACTGGTACGA CAGATGCTTC GATTGAAACA ATCCTCGATA ATCGGATGAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATTCTT GGATTAGTTT AAGCGCAGCG
 ANTCCATTGA ATAACATTGG CTATGTTTTT CCTAATTCNA TGAATACGCT TGATGTTCAA
 ATAGAAGAAC GCTCTGGTCTG CTACGGAGAT ATTAACGAAT ACTTTGTTAA TGATAAAACC
 TATACAAATA CATTTGCTAA AATTAGTAAA AATTATGGCA AGACTGTTGA AAATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATGAAGAAA TCGCAGCTCT TTCTAAAAAC
 AAAGCTATA CTGTTCTAGA AAATACAGCA AACTTACAAG CCATTGAAGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATTGCAG GACTGTATGC GTATGATCCA
 ATGTCGGTTA TTTCAGAAAA AATTGATAAC GGTGTTTATC GCTTAACCTT TCGGAATCCT
 TTACAAAAATA ATGCATCCGT TTCTATTGAA TTTGATAAGG GCATTCTTGA AGTAGTCGCA
 GCGGACCCAG AAATTTCTGT TGACCAAAAT ATTTCACTT TAAATAGTGC GGGGTTAAAT
 GGCAGCTCGC GTTCAATCAT TGTAAAAACA ACTCCTGAAG TAACGAAAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT ACACCGCAAG CAGCTGGAAA
 GTCTACAGCG AAGCATTGAA ACAAGCACAA ACTGTGGCAG ATCAAACAAC AGCAACGCAA
 GCAGAAGTAG ACCAAGCAGA AACAGAGTTA CGTTCGGCAG TGAAGCAATT GGTAAGAGTG
 CCAACTAAAG AAGTAGATAA AACCACCTTG TTGAAAATCA TCAAAGAAAA CGAGAAACAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGCTACA GTGAAGCATT GAAGCAAGCG
 CAACTGTGG CAGATCAAAAC AACAGCAACG CAAGCAGAAG TAGACCAAGC AGAAGCAAAA
 CTACGTTCCG CAGTGAAGCG ATTAACATTG AAAAATAGTG GGGAAAATAA AAAGGAGCAA
 AAAAATGGGG GGAATAATGG AACTTAAAT ACTAGTACAG GAGTTGATCA AACTGGTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCAGAAAAG CTAGCCAATT TTTACCGAGC
 ACAGGAGAAA AGAAATCGAT CGCGCTTGTG ATTATTGGTC TTCTAGTTAT CGCCAGTGGG
 TGTCTTTTAG TTTTTCGTAA AAGTAAATCG AAGAAGTAA

EF088-2 (SEQ ID NO:334)

LVGLANWFRA ALTDLILLH DLLLNTDAEK LNKFTAPML YAKDPNIQWP IYRATGANLT
 DISITVLGTG LLEDNQRLV QVQEA VPSVL KSVSSGDGLY PDGSLIQHGY FPYNGSYGNE
 LLKGFGRIGT ILQGSDEMWN DPNISNLFNV VDKGYLQLMV NGKMPSMVSG RSISRAPETN
 PFTTEFESGK ETIANLTIA KFAPENLRND IYTSIQTLWQ QSGSYHYHFK KPRDFEALID
 LKNVNSASP AQATPMQSLN VYGSMDRVLQ KNNEYAVGIS MYSQRVGNYE FGNTENKKGW
 HTADGMLYLY NQDFPMQDEG YWATIDPYRL PGTTVDREL ANGAYTGKRS PQSWVGGSNN
 GQVASIGMFL DKSNEGMNLV AKKSWFLLDG QIINLGSGIT GTTDASIETI LDNRMIHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMNTLDVQI EERSGRYDI NEYFVNDKTY

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TNTFAKISK N YGKTVENGTY EYLTVVGKTN EEIAALSKNK GYTVLENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYRLTLANPL QNNASVSIEF DKGILEVVAA
 DPEISVDQNI ITLNSAGLNG SSRSIIVKTT PEVTKEALEK LIQEQQEHQE KDYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVKVP TKEVDKTNLL KIIKENEKHQ
 EKDYTASSWK VYSEALKQAQ TVADQTTATQ AEVDQAEAKL RSAVKRLTLK NSGENKKEQK
 NGGNNGHLNT STGVDQTGTK QVKPSSQGGF RKASQFLPST GEKKSIALVI IGLLVIASGC
 LLVFRKSKSK K

EF088-3 (SEQ ID NO:335)

A ACTCCTGAAG TAACGAAAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT ACACCGCAAG CAGCTGGAAA
 GTCTACAGCG AAGCATTGAA ACAAGCACAA ACTGTGGCAG ATCAAACAAC AGCAACGCAA
 GCAGAAGTAG ACCAAGCAGA AACAGAGTTA CGTTCGGCAG TGAAGCAATT GGTAAAAGTG
 CCAACTAAAG AAGTAGATAA AACCACCTTG TTGAAATCA TCAAAGAAAA CGAGAAACAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA GTGAAGCATT GAAGCAAGCG
 CAACTGTGG CAGATCAAAC AACAGCAACG CAAGCAGAAG TAGACCAAGC AGAAGCAAAA
 CTACGTTCCG CAGTGAAGCG ATTAACATTG AAAAATAGTG GGGAAAAATAA AAAGGAGCAA
 AAAAATGGGG GGAATAATGG AACTTAAAT ACTAGTACAG GAGTTGATCA AACTGCTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCAGAAAAG CTAGCCAATT TTTACCGAGC
 ACAGGAGAAA AGAAA

EF088-4 (SEQ ID NO:336)

T PEVTKEALEK LIQEQQEHQE KDYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVKVP TKEVDKTNLL KIIKENEKHQ
 EKDYTASSWK VYSEALKQAQ TVADQTTATQ AEVDQAEAKL RSAVKRLTLK NSGENKKEQK
 NGGNNGHLNT STGVDQTGTK QVKPSSQGGF RKASQFLPST GEKK

EF089-1 (SEQ ID NO:337)

TGACAGATAC ACCTGCTAAC ACAGGAAACT AAGAACGACA GCATACACGC AAGATCGGGA
 TATAGGTCAA AAATTTTTTG GCTTATCTTT CGGTCTTTTG GTGCTTATAA TACAACAAAG
 AATGACAGAC ATAGGAGAAT GAATATGAAC AGATGGAAG TATATGCAAC GGTAATCGCT
 TGTATGTTAT TTGGCTGGAT TGGCGTGGAG GCGCACGCTT CTGAATTTAA TTTTGGCGTC
 ACACCAACAA TTCCCGAAAA TCAAGTGGAT AAATCAAAAA CCTACTTTGA CTTAAAAATG
 GCGCCTGGTG CCAACCAAAC CGTAGAAATT CAGTTACGCA ATGATACAGA TGAAGACATT
 ACCATTGAAA ATACGGTGAA CTCAGCGACA ACAAATTTAA ATGGCGTAGT AGAATATGGC
 CAAAACGGGA TCAACCTGA CAAAACCTTA CGTTTTAACT TAAAAGATTA TGTGGAAGCA
 CCGAAAGAAA TCATCTTGCC GAAGCATTC CAAAAGACCT TACCTTTAAC CATTACGATG
 CCTAAAGATT CTTTTGATGG CGTGATGGCT GCGGTATATA CACTCAAAGA GAAAAAGAAA
 GAAACAACGA CTTCTGCGGA TCAATCAAAA GGGTTAGCTA TTAATAATGA ATACTCCTAT
 GTTGTGGCTA TTATCTTCA GCAAAATGAG ACAAAGGTTT AACCAGATTT AAAATTACTG
 GGGGTTAAAC CAGGCCAAGT CAACGCGCGA AACGTCATCA ATGTTTCTTT ACAAACCCA
 CAAGCGGCCT ATTTAAACCA ATTACATTTA ATCAACACTG TTTCAAAAGG AGGCGAAACG
 CTTTACCAAT CCGTACTGTA GGATATGCAA GTGGCGCCAA ACTCTAACTT TAGTTACCCA
 ATTTCTTTAA AAGGGGAACG ATTAACGCCA GGAAATATG TCTTGAAATC AACGGCCTAT
 GGTGTAAGG ATGAAAAGG CACCTATCAA GTCAAAGGCG CCAATGGTGA AGAACGGTAC
 CTGTACAAAT GGAATTTAC AAAAGAATTT ACTATTCTG GGGACGTCG TAAAGAATTA
 AATGAAAAAG ACGTAACCAT TAAAGGAACC AATTGGTGGT TGTATCTACT GATTGCATTA
 ATCATCTAG CGTGCTCTT ATTGATTTT TCTTGTATC GTAAAAAGAA AAAAGAGGAA
 GAACAACAAT CTGAGCAATA A

EF089-2 (SEQ ID NO:338)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

MNR WKVYATVIAC

MLFGWIGVEA HASEFNFAVT PTIPENQVDK SKTYFDLKMA PGAKQTVEIQ LRNDTDEDIT
 IENTVNSATT NLNGVVEYGQ NGIKPDKTLR FNLKDYVEAP KEIILPKHSQ KTLPLTITMP
 KDSFDGVMAG GITLKEKKKE TTTSADQSKG LAINNEYSYV VAILLQONET KVQPDLLKLG
 VKPGQVNARN VINVSLQNPQ AAYLNQLHLI NTVSKGGETL YQSDTEDMQV APNSNFSYPI
 SLKGERLTPG KYVLKSTAYG VKDEKGTQV KCANGEERYL YKWEFTKEFT ISGDVAKELN
 EKDVITIKGTN WWLYLLIALI ILALLLLIFF LYRKKKKEEE QQSEQ

EF089-3 (SEQ ID NO:339)

T CTGAATTTAA TTTTGCGGTC

ACACCAACAA TTCCCGAAAA TCAAGTGGAT AAATCAAAAA CCTACTTTGA CTTAAAAATG
 GCGCCTGGTG CCAAACAAAC CGTAGAAATT CAGTTACGCA ATGATACAGA TGAAGACATT
 ACCATTGAAA ATACGGTGAA CTCAGCGACA ACAAATTTAA ATGGCGTAGT AGAATATGGC
 CAAAACGGGA TCAAACCTGA CAAAACCTTA CGTTTTAACT TAAAAGATTA TGTGGAAGCA
 CCGAAAGAAA TCATCTTGCC GAAGCATTCC CAAAAGACCT TACCTTTAAC CATTACGATG
 CCTAAAGATT CTTTTGATGG CGTGATGGCT GCGGGTATAA CACTCAAAGA GAAAAAGAAA
 GAAACAACGA CTCTGCGGA TCAATCAAAA GGGTTAGCTA TTAATAATGA ATACTCCTAT
 GTTGTGGCTA TTATTCTTCA GCAAAATGAG ACAAAGGTTT AACCAGATTT AAAATTACTG
 GGGGTAAAC CAGGCCAAGT CAACGCGCGA AACGTCATCA ATGTTTCTTT ACAAACCCA
 CAAGCGGCCT ATTTAAACCA ATTACATTTA ATCAACACTG TTTCAAAGG AGCGGAAACG
 CTTTACCAAT CCGATACTGA GGATATGCAA GTGGCGCAA ACTCTAACTT TAGTTACCCA
 ATTTCTTTAA AAGGGAACG AT

EF089-4 (SEQ ID NO:340)

SEFNFAVT PTIPENQVDK SKTYFDLKMA PGAKQTVEIQ LRNDTDEDIT

IENTVNSATT NLNGVVEYGQ NGIKPDKTLR FNLKDYVEAP KEIILPKHSQ KTLPLTITMP
 KDSFDGVMAG GITLKEKKKE TTTSADQSKG LAINNEYSYV VAILLQONET KVQPDLLKLG
 VKPGQVNARN VINVSLQNPQ AAYLNQLHLI NTVSKGGETL YQSDTEDMQV APNSNFSYPI
 SLKGER

EF090-1 (SEQ ID NO:341)

TAGTCTCTAA GAAATAAACC TAAATTTATT GATATAAAGG ATGAACAAAT GAAAAAGAA
 GAAATGCAAA TCGTAATAC ACGTCGTCAA AAATCAGGAA AAAATAATAA AAAGAAAGTA
 ATTATTACTT CTTTGGTTGG ACTAGCTCTG GTTGCTGGGG GCAGTTATGT TTATTTTCAA
 AGTCACTTTT TNCCAACCAC AAAAGTAAAT GGAGTTTCTG TAGGCTGGTT AAATGTAAAT
 GCTGCAGAAG AAAAATTAGC GCAAGTTAAT CAAACCGAAG AAGTTGTGGT TCAAACGGGG
 ACAAAGAAG AAAAAATTCA ACTTCTTAAA AAATACCAAT TGGATCAAAA ATTTTAAAAA
 GACCATTAC ACAGTAGCAA GGTGAAGCTA CCGTTAAACG AGGCATTCAA AAAAGAACTA
 GAAGCCAAAT TAGCAACTTT GAGTTTCCA GAGGGGAAAC CAAGCAAAAA TGCGAGTATC
 CGTCGAGGCA ATGGCACTTT TGAAATTGTT CCCGAAGAAC AAGGCACAGT AGTGGACACA
 CAGCGCTTAA ACCAGCAGAT TATTGCGGAT GTTGAAGCGG GAAAAGGCAA CTATCAATAT
 AATGCCAAAG ATTTTATATA AGCCCTGAA ATTACAAAAG AGGATCAAAC GTTAAAGGCA
 ACATTGACAA CGCTCAATAA CAAGTTAAAT AAAACAATTA CAGTTGATAT TAATGGTGAA
 AAAGTAGCCT TTGATAAAAC ACAAATTCAA AACGTGCTGA ATGATGATGG CACAATCAAC
 AAAGAAAAAC TAACTACTTG GGTGACACAA TTAGAAACAA CATATGGTTC TGCTAATCAA
 CCAGTTTAT TTACAGATGT TCACGGCAGC ACACGTCGTT TAAAAACAA CGGAAGTTAT
 GGCTGGTCGA TTGATGGGGC CAAAACGCAA GAACTACTAG TAAACGCGCT GAATAGCCAA
 GAACAAACGA ATGCAATCAC TGCTCCGTTG GTTGGTGATA CCAAAGAAAA TAGTAAAAAT
 GCCAATAATT ACATTGAAAT TGATTTAAAA GATCAAAAAA TGTATTGTTT CATTGATGGC
 AAAAAATAG TCACCACAGA TGTCATTACT GGCAGATATA ACAAAGGAAC CGCAACAGTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGGATTCC ATACAATTTT ATATCGGACA ACCGATGTGA ATTTAGAAGG TCAAATGCTT
 GATGGTTCTC GATACAGTGT GCCAGTAAAA TATTGGATGC CGTTATTAAG TCAAGGGGGC
 GTTGTCACAC AAATCGGGAT TCATGACTCC GACCATAAAT TGGATAAGTA TGGCGATAAA
 GAAGCCTTTA AAACCGATGC TGGTAGTAAT GGCTGTATCA ATACGCCAGG AACAGAAGTT
 TCAAAAATCT TTGATGTATC CTATGACGGA ATGCCGGTAA TTATTTATGG ACATATCTAT
 GATGATGCAC CAGGTGAATT TGATAAACCT GTAGATTACG GCGAAGAAGT ATAA

EF090-2 (SEQ ID NO:342)

MRNTRRQK SGKNNKKKVI ITS LVGLALV AGGSYVYFQS
 HFXPTTKVNG VSVGWLVNVA AEEKLAQVNQ TEEVVVQTGT KEEKIQLPKK YQLDQKFLKD
 HLHSSKVKLP LNEAFKKELE AKLATLSFPE GKPSKNASIR RGNCTFEIVP EEQGTVVDTQ
 RLNQIIADV EAGKGNQYN AKDFYKAPEI TKEDQTLKAT LTTLNNKLNK TITVDINGEK
 VAFDKTQIQN VLNDGTINK EKLTTWVTQL ETTYGSANQP VLFTDVHGTT RRFKNNGSYG
 WSIDGAKTQE LLVNALNSQE QTNAITAPLV GDTKENSIA NNYIEIDLKD QKMYCFIDGK
 KIVTTDVITG RYNKGTATVP GFHTILYRTT DVNLEGQMLD GSRYSPVKY WMPLLSQGGV
 VTQIGIHSD HKLDKYGDKE AFKTDAGSNG CINTPGTEVS KIFDVSYDGM PVIYGHYD
 DAPGEFDKPV DYGEV

EF090-3 (SEQ ID NO:343)

CAC AAAAGTAAAT GGAGTTTCTG TAGGCTGGTT AAATGTAAAT
 GCTGCAGAAG AAAAATTAGC GCAAGTTAAT CAAACCGAAG AAGTTGTGGT TCAAACGGGG
 ACAAAGAAG AAAAAATTCA ACTTCCTAAA AAATACCAAT TGGATCAAAA ATTTTAAAAA
 GACCATTTAC ACAGTAGCAA GGTGAAGCTA CCGTTAAACG AGGCATTCAA AAAAGAACTA
 GAAGCCAAAT TAGCAACTTT GAGTTTCCA GAGGGGAAAC CAAGCAAAAA TGCGAGTATC
 CGTCGAGGCA ATGGCACTTT TGAAATGTGT CCCGAAGAAC AAGGCACAGT AGTGACACA
 CAGCGCTTAA ACCAGCAGAT TATTGCGGAT GTTGAAGCGG GAAAAGGCAA CTATCAATAT
 AATGCCAAAG ATTTTATATA AGCCCTGAA ATTACAAAAG AGGATCAAAC GTTAAAGGCA
 ACATTGACAA CGTCAATAA CAAGTTAAAT AAAACAATTA CAGTTGATAT TAATGGTGAA
 AAAGTAGCCT TTGATAAAAC ACAAAATCAA AACGTGCTGA ATGATGATGG CACAATCAAC
 AAAGAAAAAC TAACTACTTG GGTGACACAA TTAGAAACAA CATATGGTTC TGCTAATCAA
 CCAGTTTAT TTACAGATGT TCACGGCAG ACACGTCGTT TAAAAACAA CGGAAGTTAT
 GGCTGGTCGA TTGATGGGGC CAAAACGCAA GAACTACTAG TAAACGCGCT GAATAGCCAA
 GAACAAACGA ATGCAATCAC TGCTCCGTTG GTTGGTGATA CCAAAGAAAA TAGTAAATT
 GCCAATAATT ACATTGAAAT TGATTTAAAA GATCAAAAAA TGTATTGTTT CATTGATGGC
 AAAAAATAG TCACCACAGA TGTCATTACT GGCAGATATA ACAAAGGAAC CGCAACAGTA
 CCAGGATTCC ATACAATTTT ATATCGGACA ACCGATGTGA ATTTAGAAGG TCAAATGCTT
 GATGGTTCTC GATACAGTGT GCCAGTAAAA TATTGGATGC CGTTATTAAG TCAAGGGGGC
 GTTGTCACAC AAATCGGGAT TCATGACTCC GACCATAAAT TGGATAAGTA TGGCGATAAA
 GAAGCCTTTA AAACCGATGC TGGTAGTAAT GGCTGTATCA ATACGCCAGG AACAGAAGTT
 TCAAAAATCT TTGATGTATC CTATGACGGA ATGCCGGTAA TTATTTATGG ACATATCTAT
 GATGATGCAC CAGGTGAATT TGATAAACCT GTAGATTACG GCGAAGAAGT AT

EF090-4 (SEQ ID NO:344)

TKVNG VSVGWLVNVA AEEKLAQVNQ TEEVVVQTGT KEEKIQLPKK YQLDQKFLKD
 HLHSSKVKLP LNEAFKKELE AKLATLSFPE GKPSKNASIR RGNCTFEIVP EEQGTVVDTQ
 RLNQIIADV EAGKGNQYN AKDFYKAPEI TKEDQTLKAT LTTLNNKLNK TITVDINGEK
 VAFDKTQIQN VLNDGTINK EKLTTWVTQL ETTYGSANQP VLFTDVHGTT RRFKNNGSYG
 WSIDGAKTQE LLVNALNSQE QTNAITAPLV GDTKENSIA NNYIEIDLKD QKMYCFIDGK
 KIVTTDVITG RYNKGTATVP GFHTILYRTT DVNLEGQMLD GSRYSPVKY WMPLLSQGGV
 VTQIGIHSD HKLDKYGDKE AFKTDAGSNG CINTPGTEVS KIFDVSYDGM PVIYGHYD

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

DAPGEFDKPV DYGEEV

EF091-1 (SEQ ID NO:345)

TAATTGGNGG AGATTTTAT GGCTAAAAA GGCGGATTTT TCTTAGNGC AGTAATTGGT
 GGAACAGCAG CAGCCGTTGC CGCATTATTA CTGACACAA AATCAGGTAA AGAATTACGT
 GATGATTTAT CAAATCAAAC AGATGATTTA AAAAACAAAG CGCAAGATTA CACAGATTAT
 GCTGTTCAAA AAGGAACAGA ATTAACAGAA ATCGCAAAAC AAAAAGCCGG CGTTTTATCA
 GATCAAGCCT CTGATTTGGC AGGTTCTGTC AAAGAAAAA CAAAAGATTC ATTGGATAAA
 GCACAAGGTG TTTCTGGCGA CATGCTTGAT AACTTTAAAA AACAAACAGG TGATTTATCT
 GATCAATTTA AAAAAGCAGC TGACGATGCT CAAGATCACG CAGAAGATTT AGGTGAAATT
 GCCGAAGATG CAGCAGAAGA TATCTATATT GACGTTAAAG ATTCTGCGGC AGCGGCCAAA
 GAAACTGTTT CTGCTGGTGT CGATGAAGCA ANAGAAACCA CCAAAGATGT TCCTGAAAAA
 GCTGCAGAAG CAAAAGAAGA TGTTAAAGAT GCAGCGAAAG ACGTAAAAA AGAATTTAAA
 GGGTAA

EF091-2 (SEQ ID NO:346)

MAKKG GFFLGAVIGG TAAVAALLL APKSGKELRD DLSNQTDDLK NKAQDYTDYA
 VQKGTELTEI AKQKAGVLSQ QASDLGSLV ETKDSDLKA QGVSGDMLDN FKKQTGDLSD
 QFKAADDAQ DHAEDLGEIA EDAAEDIYID VKDSAAAAKE TVSAGVDEAX ETTKDVPEKA
 AEAKEDVKDA AKDVKEFKG

EF091-3 (SEQ ID NO:347)

AT CAAATCAAAC AGATGATTTA AAAAACAAAG CGCAAGATTA CACAGATTAT
 GCTGTTCAAA AAGGAACAGA ATTAACAGAA ATCGCAAAAC AAAAAGCCGG CGTTTTATCA
 GATCAAGCCT CTGATTTGGC AGGTTCTGTC AAAGAAAAA CAAAAGATTC ATTGGATAAA
 GCACAAGGTG TTTCTGGCGA CATGCTTGAT AACTTTAAAA AACAAACAGG TGATTTATCT
 GATCAATTTA AAAAAGCAGC TGACGATGCT CAAGATCACG CAGAAGATTT AGGTGAAATT
 GCCGAAGATG CAGCAGAAGA TATCTATATT GACGTTAAAG ATTCTGCGGC AGCGGCCAAA
 GAAACTGTTT CTGCTGGTGT CGATGAAGCA ANAGAAACCA CCAAAGATGT TCCTGAAAAA
 GCTGCAGAAG CAAAAGAAGA TGTTAAAGAT GCAGCGAAAG ACGTAAAAA AGAATTTAAA
 GGGTAA

EF091-4 (SEQ ID NO:348)

SNQTDDLK NKAQDYTDYA
 VQKGTELTEI AKQKAGVLSQ QASDLGSLV ETKDSDLKA QGVSGDMLDN FKKQTGDLSD
 QFKAADDAQ DHAEDLGEIA EDAAEDIYID VKDSAAAAKE TVSAGVDEAX ETTKDVPEKA
 AEAKEDVKDA AKDVKEFKG

EF092-1 (SEQ ID NO:349)

TAAGGGGATG AAGAAAAAAT GGCAAAAAA ACAATTATGT TAGTTTGTTC CGCAGGAATG
 AGCAGCAGTT TATTAGTAAC AAAAATGCAA AAAGCAGCAG AAGATCGTGG CATGGAAGCA
 GACATCTTTG CAGTATCGGC TTCTGAAGCA GATACAACT TGGAAAAATA AGAGGTGAAT
 GTTTTACTTT TAGGTCCACA AGTTCGTTTC ATGAAAGGGC AATTTGAACA AAAATTACAA
 CAAAAGGGA TTCCTTTAGA TGTAATTAAC ATGGCAGATT ATGGCATGAT GAATGGCGAA
 AAAGTTTATG ATCAAGCAAT CTCATTAATG GGATAA

EF092-2 (SEQ ID NO:350)

MAKKT IMLVCSAGMS TSLLVTKMQK AAEDRGMEAD IFAVSASEAD TNLENKEVNV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LLLGPPQVRFM KGQFEQKLQP KGIPLDVINM ADYGMNNGEK VLDQAISLMG

EF092-3 (SEQ ID NO:351)

AG AAGATCGTGG CATGGAAGCA

GACATCTTTG CAGTATCGGC TTCTGAAGCA GATACAACT TGGAAAATAA AGAGGTGAAT
GTTTTACTTT TAGGTCCACA AGTTCGTTTC ATGAAAGGCG AATTGAACA AAAATTACAA
CCAAAAGGGA TTCCTTTAGA TGTAAATTAAC ATGGCAGATT ATGGCATGAT GAATGGCGAA
AAAGTTTATG ATCAAGCAAT CTCATTAAATG GGAT

EF092-4 (SEQ ID NO:352)

EDRGMEAD IFAVSASEAD TNLENKEVNV

LLLGPPQVRFM KGQFEQKLQP KGIPLDVINM ADYGMNNGEK VLDQAISLMG

EF093-1 (SEQ ID NO:353)

TAGTTTTTTT CCGATAAAGG GAGAATTTTA ATGAGGCAAA AATATTCAGG AAACTTATTG
TTCACGCGCA TGGCCATTGT TTATTTGATG AGTTTTCTCG CCTTCAGTT ACTAGAAGAA
CGTCAGTTAA CACAAAAATT TACGCAAGCT ACCCAGGAAT ACTATGCAGG GAAAAGTATC
TTTCATTTAT TTCTTGCAGA TGTTAAACAA AATAGACGAA AGTTAAAAAC AGAAGAAAGG
CTCGTATACG CGCAAGTGAC CCTCGATTAT ACATACAAAA ATGAACAATT AAGAATAACT
GTTTTATTAA ACAAATCTGG TCGAAAATAC CAATATCAAG AGAGAGTTTC TCATCAAAAA
AAAGCGGAAA CAATACTGGA ATAG

EF093-2 (SEQ ID NO:354)

M RQKYSNLLF TAMAIVYLMs FLALQLLEER QLTQKFTQAT QEYYAGKSIF

HLFLADVKQN RRKLKTEERL VYAQVTLDT YKNEQLRITV LLNKSGRKYQ YQERVSHQKK
AETILE

EF093-3 (SEQ ID NO:355)

CCTTCAGTT ACTAGAAGAA

CGTCAGTTAA CACAAAAATT TACGCAAGCT ACCCAGGAAT ACTATGCAGG GAAAAGTATC
TTTCATTTAT TTCTTGCAGA TGTTAAACAA AATAGACGAA AGTTAAAAAC AGAAGAAAGG
CTCGTATACG CGCAAGTGAC CCTCGATTAT ACATACAAAA ATGAACAATT AAGAATAACT
GTTTTATTAA ACAAATCTGG TCGAAAATAC CAATATCAAG AGAGAGTTTC TCATCAAAAA
AAAGCGGAAA CAATACTGG

EF093-4 (SEQ ID NO:356)

LQLLEER QLTQKFTQAT QEYYAGKSIF

HLFLADVKQN RRKLKTEERL VYAQVTLDT YKNEQLRITV LLNKSGRKYQ YQERVSHQKK
AETI

EF094-1 (SEQ ID NO:357)

TAAACATTTG AGACATTCAG AGGTGAATGT CTCTTTTTTA TTAATCAAAA ACGAAAGGGG
ATTAATTTATA TGAATAAAAC AACATTTAAA AATTGGTCTG TATTTGCGAC TTTGGCTCTA
TTAAGTCAAA CAATTGGCGG AACGATTGGT CCTACGATTG CTTTTGCCGA TGAAATTACT
CACCCCTCAAG AGGTAACAAT TCATTATGAC GTAAGTAAAC TGTATGAAGT TGACGGAAC
TTTAGCGATG GCAGCACGCT CTCAGAACGT ACTACGTCAT TATATGCAGA ATACAATGGT
GCAAAACAAA CAGTATTTTG TATTGAACCA GGTGTTAGTA TTCCAACAGA AGTGACGCAC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

```

GGTTATCAGA AAAACCCCTTT GCCATCAATG TCTGATAAAG CGAAACTAGT ATCGGTTCTT
TGGGAAAAGG CTGGAACAGA TATTGATACA AATATGGTTG CACAAAAGAT GATTTGGGAA
GAAGTGAACG GTTATAAACT CCATTCCATA AAAAGATTAG GTGGTGCTTC AGTTGATATA
AAATCTATTG AAGGAAAAAT TAATAAGGCA ATTGAGGAGT ATCAAAAAAA ACCAAGTTTT
CATAATACCA CTGTAAAAAC AATTTTAGGT CAATCGACAA CTTTAATAGA TAAAAATGAA
TTAAATTTAT CTGAGTTTGA TAAAGTCGTC CAAAATACGG CGAATATAGA TTACCGTGTA
ATTGGGAATC AATTAGTGCT TACTCCAAAC TCTAATTCCA AATCAGGAAC ATTAACATTG
AAAAAATCAG CTGGTACTGG AACTCCAGTC GCTTATAAAA AAGCAGGACT TCAAACGTG
ATGGCTGGTG CGCTTGATAA GCCCAATACC TACGCTATTA AAATTAATGT GGAAACTAAG
GTTCTTTTAA AGATCAAAAA AATCGATAAA GAATCAGGTG ATATTGTACC AGAAACGGTT
TTCCATTTAG ATTTTGGGAA AGCTTTACCT TCAAAAGATG TGACAACAGA TAAAGATGGG
ATTTCTATTT TGGATGGAAT TCCCCATGGT ACAAAGGTAA CTATTACTGA AAAATCGGTG
CCAGATCCTT ATATGATTGA TACCACACCC ATGGCTGCCA CCATTAAAGC GGGCGAGACC
ATTTCCATGA CTTCGAAAAA TATGCGACAA AAAGGTCAAA TTCTTTTAGA GAAGACTGGG
GTAGAAACAG GTACTGATCT TTGGAATGAC AATTATTCTC TAGCTGGAAG TACATTTGCC
ATTTCGTAAAG ACAGCCCAGC TGGTGAAATT GTCCAAGAAA TAACAACGGA TGAAAAAGGT
CGTGCGGAAA CACCAAAAGA GCTTGCTAAT GCTTTGGAAC TGGGAACCTA TTACGTGACA
GAAACTAAAT CTAGTAATGG TTTTCGTGAAT ACCTTCAAAC CAACAAAAGT CGAGTTAAAA
TATGCCAATC AAACCGTGGC TCTTGTTACC AGTAACGTAA AAGGGCAAAA CCAAGAAATT
ACTGGGGAAA CCACTTTGAC AAAAGAAGAC AAAGATACCG GTAATGAGAG TCAAGGGAAA
GCTGAGTTTA AAGGAGCTGA ATATACTCTC TTTACTGCAA AAGATGGTCA AGCTGTTAAA
TGGAGTGAAG CTTTTAAAAC AGAATTAGTG AAGGGAACGA AAGCTTCTGA TGAAACAGTG
ACTTTGGCTT TAGATGAAAA GAACCAAGTT GCCGTAAAC ACCTAGCAAT TAACGAGTAT
TTCTGGCAAG AAACCAAAGC ACCTGAAGGA TATACTTTGG ATGAAACGAA GTATCCTGTA
TCCATCAAAA AAGTTGATAA TAACGAAAAA AATGCCGTAA TFACTCGAGA TGTACGGCA
AAAGAACAAG TTATTCGCTT TGGCTTTGAT TTCTTTAAAT TTGCTGGATC GGCTGATGGC
ACTGCCGAAA CTGGATTTAA CGACTTATCT TTTAAAGTGT CGCCATTGGA AGGGACCAAN
GAAATCACAG GTGCTGAAGA TAAAGCGACC ACAGCTTGTA ACGAGCAATT AGGTTTGTAT
GGCTGAGGAT TTTTGAAGA TCTTCCTTAT GGGGATTATT TACTTGAAGA AATAGAGGCT
CCAGAAGGAT TTCAAAAAGAT TACACCACTA GAAATCCGTT CTACATTTAA GGAACAACAA
GACGACTATG CGAAGAGTGA GTATGTCTTT ACCATTACCG AAGAAGGACA AAAACAACCA
ATTAAGATGG TGACCGTTCC TTACGAGAAA CTAACATAA ACGAGTTTTT TGTAGTCTG
AACCGTTTGA TGCTTTATGA TTTGCCCCGAG AAAGAAGATA GTTTGACTTC TCTGCGACT
TGGAAGACG GAAATAAAAA ATTGAATACC CTTGATTTTA CCGAGCTAGT TGATAAATTG
AGATATAACT TGCATGAAAT CAAAGAAGAC TGGTATGTCG TAGCTCAAGC CATTGATGTG
GAAGCCACAA AAGCTGCCCA AGAAAAAGAC GAAAAAGCCA AACCGGTGGT GATTGCCGAA
ACAACCGCAA CGTTGGCGAA CAAAGAGAAA ACTGGAACCT GGAAAATTCT GCATAAATTA
ACCGCTGAAC AAGTTTTGGA TAAAAGCATC GTCTTGTTCA ATTATGTGTA TGAAAACAAG
GTAGCCTTTG AAGCAGGCAA TGAGCCAGTA GCGAAGGATG CTAGCTTGAA CAATCAAGCA
CAAACCGTCA ATTGTACGAT TGAACGCCAT GTTTCCATCC AAACAAAAGC CCACCTAGAA
GATGGTTTCG AAACTTTTAC TCATGGTGAC GTGATGGATA TGTITGATGA TGTGTCGGTT
ACCCATGATG TACTGGATGG CTCAAAAGAA GCTTTCGAAA CAATTCTGTA TGCTTTACTA
CCAGATGGTA CGAACAAAGA AATTTGGAAA TCTGGCAAAA TTGAGCATGA AGTGAATGAT
AAAGAATTTA CCAAAACCGT ACTTGCGGAA AAAGTAGATA CCGGAAAGTA TCCAGAAGGA
ACTAAGTTTA CTTTTACGGA AATCAATTAC GAAAAAGATG GAAACGTGAA TGAAAAACAC
AATGAAGATT TGAAAGAAAA ATCTCAAACC TTAACACCAA AAGAAGTGCC AACCATACCG
AGTACGCCAA AACCAACCGA AACACCAGCT GTTCCAAGTA ATTCTCAAGA ATCTAGTCCC
ACAGTGAAGA CATTCCTGCA AACTGGGGAG AAAAATTCCA ACGTTCTACT GTTAGTTGGC
TTTATCTTGA TTTTTTCGAC TGCTGGGTAT TATTTCTGGA ATCGCCGCAA TTAA

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EF094-2 (SEQ ID NO:358)

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MKKTTFFKN WSLFATLALL SQTIGGTIGP TIAFADEITH
PQEVTHYDV SKLYEVDGTF SDGSTLSERT TSLYAEYNGA KQTVFCIEPG VSIPTEVTHG

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

YQKNPLPSMS DKAKLVSVLW EKAGTDIDTN MVAQKMIWEE VNGYKLHSIK RLGGASVDIK
 SIEGKINKAI EEYQKKPSFH NTTVKTLGQ STTLIDKNEL NLSEFDKVVQ NTANIDYRVI
 GNQLVLTPNS NSKSGTLTLK KSAGTGTPVA YKKAGLQTVM AGALDKPNTY AIKINVETKG
 SLKIKKIDKE SGDIVPETVF HLDFGKALPS KDVTTDKDGI SILDGIPHGT KVTITEKSVP
 DPYMTDTPM AATIKAGETI SMTSKNMRQK GQILLEKTGV ETGTDLWNDN YSLAGNTFAI
 RKDSPAGEIV QEITTDEKGR AETPKELANA LELGTYVTE TKSSNGFVNT FKPTKVELKY
 ANQTVLVTS NVKGQNGEIT GETTLTKEDK DTGNESQGA EFKGAEYTLF TAKDGQAVKW
 SEAFKTELVK GTKASDETVT LALDEKNQVA VKHLAINEYF WQETKAPEGY TLDETKYPVS
 IKKVDNNEKN AVITRDVTAK EQVIRFGFDF FKFAGSADGT AETGFNDLSF KVSPLGTXE
 ITGAEDKATT ACNEQLGFDG YGKFENLPYG DYLLLEEIEAP EGFQKITPLE IRSTFKENKD
 DYAKSEYVFT ITEEGQKQPI KMTVPYEKL TNNEFSVSLN RLMLYDLPEK EDSLTSLATW
 KDGNNKLNLT DFTLVKDLR YNLHEIKEDW YVVAQAIDVE ATKAAQEKDE KAKPVVIAET
 TATLANKEKT GTWKILHKLK AEQVLDSIV LFNVYENKV AFEAGNEPVA KDASLNNQAQ
 TVNCTIERHV SIQTKAHLED GSQTFTHGDV MDMFDDSVT HDVLDGSKEA FETILYALLP
 DGTNKEIWKs GKIEHEVNDK EFTKTVLAEK VDTGKYPEGT KFTTFTEINYE KDGNVNGKHN
 EDLKEKSQTL TPKEVPTIPS TPKQPETPAV PSNSQESSPT VKTFPQTGEK NSNVLLLVGF
 ILIFSTAGYY FWNRRN

EF094-3 (SEQ ID NO:359)

CGA TGAAATTACT

CACCCTCAAG AGGTAACAAT TCATTATGAC GTAAGTAAAC TGTATGAAGT TGACCGAACT
 TTTAGCGATG GCAGCACGCT CTCAGAACGT ACTACGTCAT TATATGCAGA ATACAATGGT
 GCAAAACAAA CAGTATTTTG TATTGAACCA GGTGTTAGTA TTCCAACAGA AGTGACGCAC
 GGTATATCAGA AAAACCCTTT GCCATCAATG TCTGATAAAG CGAAACTAGT ATCGGTTCCTT
 TGGGAAAAGG CTGGAACAGA TATTGATACA AATATGCTTG CACAAAAGAT GATTTGGGAA
 GAAGTGAACG GTTATAAACT CCATTCCATA AAAAGATTAG GTGGTGCTTC AGTTGATATA
 AAATCTATTG AAGGAAAAAT TAATAAGGCA ATTGAGGAGT ATCAAAAAAA ACCAAGTTTT
 CATAATACCA CTGTAAAAAC AATTTTAGGT CAATCGACAA CTTTAAATAGA TAAAAATGAA
 TTAAATTTAT CTGAGTTTGA TAAAGTCGTC CAAAATACGG CGAATATAGA TTACCGTGTA
 ATTGGGAATC AATTAGTGCT TACTCCAAAC TCTAATTCCA AATCAGGAAC ATTAACATTG
 AAAAAATCAG CTGGTACTGG AACTCCAGTC GCTTATAAAA AAGCAGGACT TCAAACTGTG
 ATGGCTGGTG CGCTTGATAA GCCCAATACC TACGCTATTA AAATTAATGT GGAAACTAAG
 GGTTCCTTAA AGATCAAAAA AATCGATAAA GAATCAGGTG ATATTGTACC AGAAACGGTT
 TTCCATTTAG ATTTTGGGAA AGCTTTACCT TCAAAAGATG TGACAACAGA TAAAGATGGG
 ATTTCTATTT TGGATGGAAT TCCCCATGGT ACAAAGGTAA CTATTACTGA AAAATCGGTG
 CCAGATCCTT ATATGATTGA TACCACACCC ATGGCTGCCA CCATTAAAGC GGGCGAGACC
 ATTTCCATGA CTTCGAAAAA TATGCGACAA AAAGGTCAAA TTCTTTTAGA GAAGACTGGG
 GTAGAAACAG TACTGATCTT TTGGAATGAC AATTATTCTC TAGCTGAAA TACATTGGCC
 ATTCGTAAAG ACAGCCCAGC TGGTGAAATT GTCCAAGAAA TAACAACGGA TGA AAAAGGT
 CGTGCGGAAA CACCAAAAAGA GCTTGCTAAT GCTTTGGAAC TGGGAACCTA TTACGTGACA
 GAAACTAAAT CTAGTAATGG TTTCGTGAAT ACCTTCAAAC CAACAAAAGT CGAGTTAAAA
 TATGCCAATC AAACCGTGGC TCTTGTTACC AGTAACGTAA AAGGGCAAAA CCAAGAAATT
 ACTGGGAAA CCACTTTGAC AAAAGAAGAC AAAGATACCG GTAATGAGAG TCAAGGAAA
 GCTGAGTTTA AAGGAGCTGA ATATACTCTC TTTACTGCAA AAGATGGTCA AGCTGTAAAA
 TGGAGTGAAG CTTTAAAAAC AGAATTAGTG AAGGGAACGA AAGCTTCTGA TGAAACAG

EF094-4 (SEQ ID NO:360)

DEITH

PQEVTHYDV SKLYEVDGTF SDGSTLSERT TSLYAEYNGA KQTVFCIEPG VSIPTVTHG
 YQKNPLPSMS DKAKLVSVLW EKAGTDIDTN MVAQKMIWEE VNGYKLHSIK RLGGASVDIK
 SIEGKINKAI EEYQKKPSFH NTTVKTLGQ STTLIDKNEL NLSEFDKVVQ NTANIDYRVI
 GNQLVLTPNS NSKSGTLTLK KSAGTGTPVA YKKAGLQTVM AGALDKPNTY AIKINVETKG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

SLKIKKIDKE SGDIVPETVF HLDGFKALPS KDVTTDKDGI SILDGIPHGT KVTITEKSVP
 DPYIMIDTPM AATIKAGETI SMTSKNMRQK GQILLEKTGV ETGTDLWNDN YSLAGNTFAI
 RKDSPAGEIV QEITTDKGR AETPKELANA LELGTYVTE TKSSNGFVNT FKPTKVELKY
 ANQTVLVT NVKGQNEIT GETTLTKEDK DTGNESQKA EFKGAEYTLF TAKDGQAVKW
 SEAFKTELVK GTKASDET

EF095-1 (SEQ ID NO:361)

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 GAATTGATAG TAACGGGCAT CTGCCATATA TTAGTATTCC CCATACTAAT ACAGACAACCT
 GTTTTTGCAG AAACATTACC AAGTACAAAA CAAGTAAGAG AAGGAACCAA TCATTCAATTA
 ACAGCAGAAA AAGCCGAAAG TGAACAACCA CAGACAAAGG ATAACTACA TGATGAAGAA
 AACTGGCAT TGTCAAAAAG TGAGTTAATC GATAATGAGG CTAATGTTAC AAGTCAAACG
 ATTAGAGAAA GAATTGAGAC GCCTAACCTA ACTTATCGTT ATGGATTTAT TAATGAAGAG
 GGGCAGCCAG TAAACGCCAA TGAGATCCCT CTACAGTATC ATAGTTGGCA AGGCAATTCC
 CCAGATGGCA TAAATGTGTG GGAAGGTGAA AGTCAACCAG TGACAGCATC TACAGTGGCT
 AATTTAAAAG AAGTGGTAAT TCCAAGTGAG AAAGTAGCCG TCTATTCCGA CATGTCAACG
 GTGCTTGCAG CGAGTAATCA AACATTTTTT TTACCAAGAT ATTATACTTC TTTAAGCTTA
 TACAATAAGA AAGGGGAAAT TGATCCCAAT TATCCGCTGC CAACTATTTT CGACGCATCA
 GGAACCAAT ATCCAACAAC AATTTTCGCA TTTGAATTGG AAAAAATGTC TGCACAACAA
 TATAGTCAGA AAACAGGAGT AACGTTTAAAC ATTAGCGAGA GTCAAAAACCT AATCGTTTCCT
 TTGTACAACC AAGTGAAGGT TGATTTCATCG AATCAATCTG GGCTATTGAA TTACTTTAAA
 TTTTCAGGGC CGGTTTATTA TCATGTTACC AATCGCAAAG TGACAGAACA TTTTGTGGAT
 ACTCAAGGGA AACCAATCCC TCCACCACCG GGGTTTAGAC AAGGAAAGCA AACACTTATT
 GAGCGTGACC CTTACACCTT TAAACAGAAA GATCTTTTGC CAAGTAGCTA TGAAATTGAC
 TCAAAAACGT ATCAATTTCA AGGATGGTAT AAAGGGAAAA CGAAACCTGA AAATTTAGAA
 AAAAGCGTAA CGCCCAGTTA TGATATTACC TATGACGACA ATGATGATTT AACTGTTGTC
 TATAAGGAGA TACCTCAAAA AAATTATACA TTTGAGGATG TCAATGGTGT TGAAATTGCA
 CCACCATCTG ATTTTATTCA GGATCACCAC CAACCAATAA CTACGGATGG CTTTCGCTAT
 TTAGCTGGAA AAAAATGACC ACAACAATAC AGCGTTAACG GTAAAACTTA TTTATATCAA
 GGTGTGATC AAGATAAAAC NAAACAAGAG AGCTTAGAAA AAACGAAGCG ACCCATAAAC
 TCCCCTGTTT TTAATGAAAT GAACGCTATT ACAGCAGTGT ATAAGGAAAT AACTGCAAAA
 GCTGAAATGC AAATAGAAGG ACTAGTCAAA GTCATGCCAA GTGGTTATAT ACAAAATTGG
 CAGATTATGC TTACAAATGT GGGAGAAGTA CCGTTAAAAA AAATAAACTT AAAGCCAGCA
 AGTGGTTGGT CACCAGGTCT AGCTCGGCCA ATCCAAGTCA CGATTTCGTGT TGGATCTGAA
 CCAAACAAAA TTGTTTCCTAT TACTGATGAA AATTGGCGAG TTGGCATTAC TTTAAATACG
 GAAGTGCCCTA TTGGTCAGAC AGCAACTATT ATGATGACAA CAATTGCTAC AGGTGAACCA
 GATCAAGTGT TACAAGCGGC TGTGAAATG AATGGAAATT TTTCTGCTGT TCACGCAGCT
 GATACTGTCA GAATCCAACC TAAAAATCAA GAAATTGTGG CACCAGATGA GGAAGGTTTT
 ATCAGCACAC CAACTTTTGA TTTTGGCAAA GTCGCCATTT CTAGCAACAC GCAGCAACAT
 GGTTTAAAGC AGGCAGCAGA TTATTATGAA AATGGTCAGG AAAATCCATA TTTACGTTTG
 AAAAAATCAC AACCCAATTG GGCATAACT GCAGAACTAT CCCCCTTTGA AGGAAGAGTG
 GATCAACTAT CATCAATGAC AAAGTTATTG TTAGGAACAA CCAATGTTTC AGGTTTTATT
 CAGTACAATC AACCAACGGA AACTAAAGTT GCTCTTGGCA AAACAACCGC TATTCAATTA
 GTTGCCAACG GTGTAGCTAG CCATATTGTT GCCAATGGTC AGTTTGACGA AAGTGATGTT
 TATCAATTTG ATTTTCTTTT TGATCAAATC AAATTAGAAA TTCCAGCAA TCAAGGTAGA
 AAAGATCAAA CTTATCAAGC AATGGTGACT TGAATTTAG TGACAGGCC ATAA

EF095-2 (SEQ ID NO:362)

MKRKWKKE LIVTGICHIL VFPILIQTTV FAETLPSTKQ VREGTNHSLT
 AEKAESQPPQ TKDKLHDEET LALSKSELID NEANVTSQTI RERIETPNLT YRYGFINEEG
 QPVNANEILL QYHSWQGNP DGINWEGES QPVTASTVAN LKEVVIPSEK VAVYSDMSTV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LAASNQTFFL PRYYTSLSLY NKKGEIDPNY PLPTISDASG NQYPTTISQF ELEKMSAQOY
 SQKTGVTFNI SESQKLIVPL YNQVKVDSSN QSGLLNIFYKF SGPVYYHVTN RKVTEHFVDT
 QGKPIPPPPG FRQKQTLIE RDPYTFKQKD LLPSSYEIDS KTYQFQGWYK GKTKEPENLEK
 SVTPSYDITY DDNDLTLVVY KEIPQKNYTF EDVNGVEIAP PSDFIQDHQQ PITTDGFRLY
 AGKKLPQQYS VNGKTYLYQG WYQDKTKQES LEKTKRPINS PVFNEMNAIT AVYKEITAKA
 EMQIEGLVKV MPSGYIQIWQ IMLTNVGEVP LKKINLKPAS GWSPLARPI QVTIRVGSEP
 NKIVPITDEN WRVGITLNT EPIGQTATIM MTTIATGEPD QVLQAAVEMN GNFSAVHAAD
 TVRIQPKNQE IVAPDEEGFI STPTFDFGKV AISSNTQOHG LKQAADYYEN GQENPYLRLEK
 KSQPNWALTA ELSPFEGRVD QLSSMTKLLL GTTNVSGFIQ YNQPTETKVA LGKTTAIQLV
 ANGVASHIVA NGQFLESVDY QPDFSFDQIK LEIPANQGRK DQTYQAMVTW NLVTGP

EF095-3 (SEQ ID NO:363)

AAGTACAAAA CAAGTAAGAG AAGGAACCAA TCATTTCATTA
 ACAGCAGAAA AAGCCGAAAAG TGAACAACCA CAGACAAAGG ATAAACTACA TGATGAAGAA
 AACTGGCAT TGTCAAAAAG TGAGTTAATC GATAATGAGG CTAATGTTAC AAGTCAAACG
 ATTAGAGAAA GAATTGAGAC GCCTAACCTA ACTTATCGTT ATGGATTAT TAATGAAGAG
 GGGCAGCCAG TAAACGCCAA TGAGATCCTT CTACAGTATC ATAGTTGGCA AGGCAATTCC
 CCAGATGGCA TAAATGTGTG GGAAGGTGAA AGTCAACCAG TGACAGCATC TACAGTGGCT
 AATTPTAAAAG AAGTGGTAAT TCCAAGTGAG AAAGTAGCCG TCTATTCCGA CATGTCAACG
 GTGCTTGACG CGAGTAATCA AACATTTTTT TTACCAAGAT ATTATACTTC TTTAAGCTTA
 TACAATAAGA AAGGGGAAAT TGATCCCAAT TATCCGCTGC CAACTATTTT CGACGCATCA
 GGAAACCAAT ATCCAACAAC AATTTGCGAA TTTGAATTGG AAAAAATGTC TGCACAACAA
 TATAGTCAGA AACAGGAGT AACGTTTAAC ATTAGCGAGA GTCAAAAAC AATCGTTTCT
 TTGTACAACC AAGTGAAGGT TGATTCATCG AATCAATCTG GGCTATTGAA TTACTTTAAA
 TTTTCAGGGC CGGTTTATTA TCATGTTACC AATCGCAAAG TGACAGAACA TTTTGTGGAT
 ACTCAAGGGA AACCAATCCC TCCACCACCG GGGTTTAGAC AAGGAAAGCA AACACTTATT
 GAGCGTGACC CTTACACCTT TAAACAGAAA GATCTTTTGC CAAGTAGCTA TGAAATTGAC
 TCAAAAACGT ATCAATTTCA AGGATGGTAT AAAGGGAATA CGAAACCTGA AAATTTAGAA
 AAAAGCGTAA CGCCAGTTA TGATATTACC TATGACGACA ATGATGATTT AACTGTTGTC
 TATAAGGAGA TACCTCAAAA AAATTATACA TTTGAGGATG TCAATGGTGT TGAAATTGCA
 CCACCATCTG ATTTTATTCA GGATCACCAA CAACCAATAA CTACGGATGG CTTTCGCTAT
 TTAGCTGGAA AAAAAGTACC ACAACAATAC AGCGTTAAGC GTAAACTTAT TTTATATCAA
 GGTGGGTATC AAGATAAAAC NAAACAAGAG AGCTTAGAAA AAACGAAGCG ACCCATAAAC
 TCCCTGTTT TTAATGAAAT GAACGCTATT ACAGCAGTGT ATAAGGAAAT AACTGCAAAA
 GCTGAAATGC AAATAGAAGG ACTAGTCAAA GTCATGCCAA GTGGTTATAT ACAAATTTGG
 CAGATTATGC TTACAAATGT GGGAGAAGTA CCGTTAAAAA AAATAAACTT AAAGCCAGCA
 AGTGGTTGGT CACCAGGTCT AGCTCGGCCA ATCCAAGTCA CGATTTCGTG TGGATCTGAA
 CCAAAACAAA TTGTTCTTAT TACTGATGAA AATGGCGAG TTGGCATTAC TTTAAATACG
 GAAGTGCCTA TTGGTCAGAC AGCAACTATT ATGATGACAA CAATTGCTAC AGGTGAACCA
 GATCAAGTGT TACAAGCGGC GTTTGAAATG AATGGAAATT TTTCTGCTGT TCACGCAGCT
 GATACTGTCA GAATCCAACC TAAAAATCAA GAAATTTGTG CACCAGATGA GGAAGGTTTT
 ATCAGCACAC CAACTTTTGA TTTTGGCAAA GTCGCCATTT CTAGCAACAC GCAGCAACAT
 GGTTTAAAGC AGGCAGCAGA TTATTATGAA AATGGTCAGG AAAATCCATA TTTACGTTTG
 AAAAAATCAC AACCAATTG GGCATAACT GCAGAACTAT CCCCTTTTGA AGGAAGAGTG
 GATCAACTAT CATCAATGAC AAAGTTATTG TTAGGAACAA CCAATGTTTC AGGTTTATT
 CAGTACAATC AACCAACGGA AACTAAAGTT GCTCTTGGCA AAACAACCGC TATTCAATTA
 GTTGCCAACG GTGTAGCTAG CCATATTGTT GCCAATGGTC AGTTTGACGA AAGTGATGTT
 TATCAATTTG ATTTTCTTT TGATCAATC AAATTAGAAA TTCCAGCAAA TCAAGGTAGA
 AAAGATCAAA CTTATCAAGC AATGGTGACT TGAATTTAG TGACAGGCC A

EF095-4 (SEQ ID NO:364)

STKQ VREGTNHSLT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AEKAESEQPQ TKDKLHDEET LALSKSELID NEANVTSQTI RERIETPNLT YRYGFINEEG
 QPVNANEILL QYHSWQGNP DGINVWEGES QPVTASTVAN LKEVVIPSEK VAVYSDMSTV
 LAASNQTFFL PRYYSLSLY NKKGEIDPNY PLPTISDASG NQYPTTISQF ELEKMSAQQY
 SQKTGVTFNI SESQKLIVPL YNQVKVDSSN QSGLLNYFKF SGPVYHVTN RKVTEHFVDT
 QGKPIPPPPG FRQKQTLIE RDPYTFKQKD LLPSSYEIDS KTYQFQGWYK GKTKPENLEK
 SVTPSYDITY DDNDLTVVY KEIPQKNYTF EDVNGVEIAP PSDFIQDHQO PITTDGFRYL
 AGKKLPQQYS VNGKTYLYQG WYQDKTKQES LEKTKRPINS PVFNEMNAIT AVYKEITAKA
 EMQIEGLVKV MPSGVIQIWQ IMLTNVGEVP LKKINLKPAS GWSPLARPI QVTIRVGSEP
 NKIVPITDEN WRVGITLNT E VPIGQTATIM MTTIATGEPD QVLQAAVEMN GNFSAVHAAD
 TVRIQPKNQE IVAPDEEGFI STPTDFGKV AISSNTQOHG LKQAAADYYEN GQENPYLRLK
 KSQPNWALTA ELSPFEGRVD QLSSMTKLLL GTTNVSGFIQ YNQPTETKVA LGKTTAIQLV
 ANGVASHIVA NGQFDESVDY QDFDSFDQIK LEIPANQGRK DQTYQAMVTW NLVTGP

EF096-1 (SEQ ID NO:365)

TGAGGTGGCC AAGTTAAAAT GAAAAAATTA CAGTCACTTT TTATTGGAAT TATCGCTATT
 ATTGTCATCT TGTTTTTTGG CGTGCGCCAA TTGGAGAAAG CAAGTGGCAT GGCAGGAGCA
 GATACCTTGA CCATTTACAA TTGGGGGGAC TATATAGATC CGGCCTTGAT TAAGAAATTT
 GAAAAAGAAA CAGGCTATAA AGTCAATTAC GAAACCTTTG ATTCTAATGA AGCTATGTAT
 AAAAAAATTC AGCAAGGTGG CACAGCCTAT GATATTGCCA TTCCTTCTGA ATATATGATT
 CAAAAATGA TGAAGCGAA GATGCTTTTA CCACTTGATC ACAGCAAATT AAAAGGCTTA
 GAAAAATTG ATGCACGCTT TTTAGATCAA TCCTTTGATC CAAAAATAA GTTTTCCGTT
 CCGTACTTCT GGGGCACGTT GGGGATTATT TATAATGATA AATTTATTGA CGGCCGTCAG
 ATCCAACATT GGGATGATTT ATGGCGCCCG GAATTAAAAA ATAATGTCAT GCTGATTGAT
 GCGCTCGCG AAGTGTTAGG ATTATCTTTG AACAGTTTAG GCTATTCGTT AAACAGTAAA
 AACGACCAAC AATTACGTCA GGCTACCGAT AAGTTAAACC GATTAACGAA CAATGTCAAA
 GCAATTGTTG CCGATGAAAT CAAAATGTAC ATGGCTAATG AAGAAAGTGC AGTTGCTGTA
 ACTTTCTCTG GTGAAGCTGC TGAATGCTA GAAAACAATG AACATCTACA TTATGTGATT
 CCAGTGAAAG GCTCTAATCT CTGGTTTGAT AACATTGTGA TGCCTAAGAC AGCCAAAAAT
 AAAGAGGGTG CCTATGCATT TATGAACTTT ATGTTACGAC CAGAAAATGC GGCACAAAAT
 GCAGAATATA TTGGTTATTC CACACCAAAT AAAGAAGCTA AAAAATATT ACCAAAAGAA
 GTTGCCGAAG ATAAACAATT TTATCCAGAT GATGAACTA TCAAACATTT AGAAGTTTAC
 CAAGACTTAG GTCAAGAATA CTTAGGAATT TATAACGATC TGTCTTGGA GTTTAAGATG
 TATCGGAAAT AA

EF096-2 (SEQ ID NO:366)

MKKLQ SLFIGIIAI VILFFGVRQL EKASGMAGAD TLTIYNWGDY IDPALIKKFE
 KETGYKVNYE TFDSNEAMYT KIQQGGTAYD IAIPSEYMIQ KMMKAKMLLP LDHSLKLGLE
 NIDARFLDQS FDPKNKFSVP YFWGTLGIIY NDKFIDGRQI QHWDLLWRPE LKNNVMLIDG
 AREVLGLSLN SLGYSLSKN DQQLRQATDK LNRLTMNVKA IVADEIKMYM ANEESAVAVT
 FSGEAAEMLE NNEHLHYVIP SEGSLNLFWDN IVMPKTAKNK EGAYAFMFM LRPENAAQNA
 EYIGYSTPNK EAKKLLPKEV AEDKQFYPDD ETIKHLEVYQ DLGQEYLGIIY NDLFLEFKMY
 RK

EF096-3 (SEQ ID NO:367)

AAGTGGCAT GGCAGGAGCA
 GATACCTTGA CCATTTACAA TTGGGGGGAC TATATAGATC CGGCCTTGAT TAAGAAATTT
 GAAAAAGAAA CAGGCTATAA AGTCAATTAC GAAACCTTTG ATTCTAATGA AGCTATGTAT
 AAAAAAATTC AGCAAGGTGG CACAGCCTAT GATATTGCCA TTCCTTCTGA ATATATGATT
 CAAAAATGA TGAAGCGAA GATGCTTTTA CCACTTGATC ACAGCAAATT AAAAGGCTTA
 GAAAAATTG ATGCACGCTT TTTAGATCAA TCCTTTGATC CAAAAATAA GTTTTCCGTT
 CCGTACTTCT GGGGCACGTT GGGGATTATT TATAATGATA AATTTATTGA CGGCCGTCAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATCCAACATT GGGATGATTT ATGGCGCCCG GAATTAAAAA ATAATGTCAT GCTGATTGAT
 GGCCTCGCG AAGTGTTAGG ATTATCTTTG AACAGTTTAG GCTATTCGTT AAACAGTAAA
 AACGACCAAC AATTACGTCA GGCTACCGAT AAGTTAAACC GATTAACGAA CAATGTCAAA
 GCAATTGTTG CCGATGAAAT CAAAATGTAC ATGGCTAATG AAGAAAGTGC AGTTGCTGTA
 ACTTTCTCTG GTGAAGCTGC TGAAATGCTA GAAAACAATG AACATCTACA TTATGTGATT
 CCCAGTGAAG GCTCTAATCT CTGGTTTGAT AACATTGTGA TGCCTAAGAC AGCCAAAAAT
 AAAGAGGGTG CCTATGCATT TATGAACTTT ATGTTACGAC CAGAAAATGC GGCACAAAAT
 GCAGAATATA TTGGTTATTC CACACCAAAT AAAGAAGCTA AAAAATCTAT ACCAAAAGAA
 GTTGCCGAAG ATAAACAATT TTATCCAGAT GATGAACTA TCAAAACATT AGAAGTTTAC
 CAAGACTTAG GTCAAGAATA CTTAGGAATT TATAACGATC TGTTCCTGGA GTTTAAGATG
 TATCGGAAA

EF096-4 (SEQ ID NO:368)

SGMAGAD TLTIYNWGDY IDPALIKKFE
 KETGYKVNYE TFDSNEAMYT KIQQGGTAYD IAIPSEYMIQ KMMKAKMLLP LDHSLKLGLE
 NIDARFLDQS FDPKNKFSVP YFWGTLGIIY NDKFIDGRQI QHWDLLWRPE LKNNVMLIDG
 AREVLGLSLN SLGYSLNSKN DQQLRQATDK LNRLTNNVKA IVADEIKMYM ANEESAVAVT
 PSGEAAEMLE NNEHLHYVIP SEGSNLWFDN IVMPKTAKNK EGAYAFMFM LRPENAAQNA
 EYIGYSTPNK EAKKLLPKEV AEDKQFYPPD ETIKHLEVYQ DLGQEYLGIIY NDLFLEFKMY
 RK

EF097-1 (SEQ ID NO:369)

TAGAAGTATT CTAATTATCT ACATAGAGAG CGAGGGACAA GGAATATGAA GGAAAAAGAA
 ATGCATTGCG TCTTTTTTAA ACATAAGTTT GTGAAAGTAA CTCCCTATTT ACGTCGTTTT
 GGTCATCGTT TGAGTGGGAT GATTATGCCA AATTTGAGTA TTTTATTGTC GTGGAGCTTA
 TTGTCTTTGG TGGCTGGCTA TACGACTGGG AATCTACGGC TAGCTCTTTC TGAAGTCGAA
 ACGATAATGA TTCGAGTTGT TTTACCGATT CTAATTGGTT TTACAGCGCG AAAAATGTTC
 GAGGAACAAC GTGGCGGCGT TGTGCTGCT ATTGCGACAG TGGGCGTGAT TGTTCACACA
 GATGTTCCAC AGTTGTTTGG TGCTATGTTT ATTGGCCCTT TAGCAGGATA TACTTTCGCC
 AAAATTGAAC AAATTCTCTT ACCGAAAGTT AAAGAAGGCT ACGAGATGCT GACTAAAAAC
 TTTTATAGCAG GAATTGTGGG AGGACTGCTG TGCTGTTTTG GTATTCTGGT TGTAGCTCCG
 GCTGTTGAAA GCGCTAGTTT TTGGCTGTAT CAATTTCTTT CTGGTTAAT TGAAGCCAAT
 CTTTACCATT TGGTTCACGT TTTCTTAGAG CCTTAAAAG TGTATTTTTT TAATAATGCG
 ATTAACCATG GCTTATTAAC GCCTCTAGGT TTAGAAGGTG CTAGTCAAAC AGGTCAGTCC
 ATTTTATTTT TATTGGAAC AAACCTGGA CCAGGCGTGG GCGTTTTGGT TGCTTTTCTG
 CTGTTTGGGC CTGTAGGACA ACGAAAAACA GCAGGAGGTG CCACCATGAT TCAACTGATT
 GGGGGCATTG ATGAAATTTA TTTTCCGTTT GTTTTGATGG ACCCGCGCTT ATTTTATAGCA
 GTAATTGCTG GAGGAATGAG TGGTACGCTT GTTTTCAAA TATTTAATGT GGGTCTAAGT
 GCTCCAGCTT CGCCAGGTTT ATTGGTTGCG ATTTTAGCCA ATGCCCGAC TGATGCGAGG
 CTGGCGGTTT TTAGCGGAAT TTTTGTAGC TTTCTGTGCT CTTTGTCAAT AGCAAGCTTG
 TTATTAACAC GTCAACGAGG AATTGAACCA GTTTCAATGA TAAAGATGAA GGAGGAAGAC
 CAAGTGAAA CAGTCACACC TAACTATCAG CAAATTTTAT TTGTTTGTGA TGCAGGAATG
 GGCTCAAGTG CCATGGGGGC TAGTTTGCTA AGCCGACAAT TAAAAGCTGT GAACTTGGAG
 ATGCTGTGTA CTACACAGTC CGTTCATCAG ATGAAGTGGC AGCCTAAGAC ATTAGTGGTC
 ATTCAAGCAG AATTGAAACA GTTAGCACAA AAGTACGTCC CAGAAAAGGA TATGGTGAGT
 GTTCAAAATT TTTTAGAAAT TAAATCCTAT TACCCGCAAG TTTTAGCCAA ACTGACTGCT
 TCTTCTCAAG AGCAATCTTC ACTTGGTTCA GAGTCTACTG AAACGAACTC GACAAAACAA
 ATACAGAAGC TTGTTTTTTT ATATGCCGAG AATGTTGAG GATCGCAAAC AATGGGAATG
 GAATTATTGC GGCACCAAGC GGCGAAACAA GGAGTCGCGA TTGAAGTATC TAAAGAGCCA
 CTGGAACAG TCTTTTTTAC CAAGGAGACA ACCTACGTAG TGACTCGTGA ACTGGCGCAA
 GCCTATCATT TAGATCTAAC GCAACAAAAT TTATACGTAG TTACTAGTTT TTTGAATAAG
 AAAGAGTATC AAGAATGGCT GGAAGGAGGA GCTGATAGAT GTTTTTTAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF097-2 (SEQ ID NO:370)

MLTKNF LAGIVGGLLC CFGILVVAPA

VESASFWLYQ FSSWLEIANL LPLVHVFLFP LKVLFFNNAI NHGLLTPLGL EGASQTGQSI
 LFLLETNPGP GVGVLVAFLL FGPVGQRKTA GGATMIQLIG GIHEIYFPFV LMDPRLFLAV
 IAGGMSGTLV FQIFNVGLSA PASPGSLVAI LANAPTDARL AVFSGIFVSF LCSFAIASLL
 LKRQRGIEPV SMIKMKEEDQ VETVTPNYQQ ILFVCDAGMG SSAMGASLLS RQLKAVNLEM
 PVTYQSVHQM KWQPKTLVVI QAEKQLAQK YVPEKDMVSV QNFLEIKSY YPVLAKLTAS
 SQEQSSLGSE STETNSTKQI QKLVFLYAEN VRGSQTMGME LLRQQAQKQG VAIEVSKEPL
 ETVFFTKETT YVVTRELAQA YHLDLTQQNL YVVTSLNKK EYQEWLEGGA DRCF

EF097-3 (SEQ ID NO:371)

ACGAGG AATTGAACCA GTTTCATGA TAAAGATGAA GGAGGAAGAC

CAAGTGGAAG CAGTCACACC TAACTATCAG CAAATTTTAT TTGTTTGTGA TGCAGGAATG
 GGCTCAAGTG CCATGGGGGC TAGTTTGCTA AGCCGACAAT TAAAAGCTGT GAACTTGGAG
 ATGCCTGTGA CTTACCAGTC CGTTCATCAG ATGAAGTGGC AGCCTAAGAC ATTAGTGGTC
 ATTCAAGCAG AATTGAAACA GTTAGCACAA AAGTACGTCC CAGAAAAGGA TATGGTGAGT
 GTTCAAAATT TTTTAGAAAT TAAATCCTAT TACCCGCAAG TTTTAGCCAA ACTGACTGCT
 TCTTCTCAAG AGCAATCTTC ACTTGGTTCA GAGTCTACTG AAACGAACTC GACAAAACAA
 ATACAGAAGC TTGTTTTTTT ATATGCCGAG AATGTTTCGAG GATCGCAAAC AATGGGAATG
 GAATTATTGC GGCAACAAGC GGCGAAACAA GGAGTCGCGA TTGAAGTATC TAAAGAGCCA
 CTGGAACAG TCTTTTTTAC CAAGGAGACA ACCTACGTAG TGACTCGTGA ACTGGCGCAA
 GCCTATCATT TAGATCTAAC GCAACAAAAT TTATACGTAG TTACTAGTTT TTGAATAAG
 AAAGAGTATC AAGAATGGCT GGAAGGAGGA GCTGATAGAT GTTTTT

EF097-4 (SEQ ID NO:372)

RGIEPV SMIKMKEEDQ VETVTPNYQQ ILFVCDAGMG SSAMGASLLS RQLKAVNLEM

PVTYQSVHQM KWQPKTLVVI QAEKQLAQK YVPEKDMVSV QNFLEIKSY YPVLAKLTAS
 SQEQSSLGSE STETNSTKQI QKLVFLYAEN VRGSQTMGME LLRQQAQKQG VAIEVSKEPL
 ETVFFTKETT YVVTRELAQA YHLDLTQQNL YVVTSLNKK EYQEWLEGGA DRCF

EF098-1 (SEQ ID NO:373)

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 CTGTACCAA TGAGTGCATT AGCAGTCGAC GGTGGTGAAT ACCAAACAAA CGGAGCGATT
 CAATTTGCAC CAAATACGAA CCAACGAAT CCAGTTGATC CGACGAATCC AGACCCAGAT
 AAACCAATTA CACCAGTTGA TCCAAGTAT CCGACAGGGC CTAAGCCAGG GACAGCAGGT
 CCGTTATCCA TTGACTATGC ATCTAGCTTA TCTTTTGGGG AACAAACGAT TACCTCAAAA
 AATATGACCT ACTATGCAGA AACACAAAAA TACAAAGATA ACGCTGGTGC CGACCAAGAA
 GGCCCAAACT TTGTTCAAGT CTCAGATAAT CGTGGGACTG AGACAGGTTG GACGCTAAAA
 GTAAAACAAA ATGGTCAATT CAAAACGAA GCCAACCAAG AACTAACAGC GGCCAAAGTA
 ACTTTAAGCA ACGGACGCGT GGTTCAGCT TCACAATCTG CAAAGCCAAC GACAGCGCCA
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 GAAGGTGCGG GTACGTACTT AATGAGCTGG GGCATAGTG TAGATACCGC TAAAACAAGT
 ATTTCAATTAG AAGTACCTGG TTCAACCACA AAATATGCGA AAAAATACAC GACAACTTTT
 ACTTGGACTT TGACAGATAC ACCTGCTAAC ACAGGAACT AA

EF098-2 (SEQ ID NO:374)

MKKTVMTLT ATTTLGALAL VPMSALAVDG GEYQTNGAIQ FAPNTNPTNP VDPNTNPDPK
 PITVPDPTDP TGPKPGETAGP LSIDYASSLS FGEQTITSKN MTTAAETQKY KDNAGADQEG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

PNFVQVSDNR GTETGWTLKV KQNGQFKTEA NQELTAAKVT LSNGRVVSAS QSAKPTTAPA
 TIELNPTGAE SVVMAAGDKE GAGTYLMSWG DSVDTAKTSI SLEVPGSTTK YAKKYTTTTFT
 WTLTDTPANT GN

EF098-3 (SEQ ID NO:375)

AGTCGAC GGTGGTGAAT ACCAAACAAA CGGAGCGATT
 CAATTTGCAC CAAATACGAA CCCAACGAAT CCAGTTGATC CGACGAATCC AGACCCAGAT
 AAACCAATTA CACCAGTTGA TCCAACGTAT CCGACAGGGC CTAAGCCAGG GACAGCAGGT
 CCGTTATCCA TTGACTATGC ATCTAGCTTA TCTTTTGGGG AACAAACGAT TACCTCAAAA
 AATATGACCT ACTATGCAGA AACACAAAAA TACAAAGATA ACGCTGGTGC CGACCAAGAA
 GGCCCAAACT TTGTTCAAGT CTCAGATAAT CGTGGGACTG AGACAGGTTG GACGCTAAAA
 GTAAAAACAAA ATGGTCAATT CAAAACGTAA GCCAACCAAG AACTAACAGC GGCCAAAGTA
 ACTTTAAGCA ACGGACGCGT GGTTCAGCT TCACAATCTG CAAAGCCAAC GACAGCGCCA
 GCTACGATTG AATTAAACCC AACTGGGGCT GAATCAGTGG TCATGGCTGC TGGCGATAAA
 GAAGGTGCGG GTACGTACTT AATGAGCTGG GCGGATAGTG TAGATACCGC TAAAACAAGT
 ATTTCAATTAG AAGTACCTGG TTCAACCACA AAATATGCGA AAAAATACAC GACAACTTTT
 ACTTGGACTT TGACAGATAC ACCTGCTAAC ACAGGAAACT

EF098-4 (SEQ ID NO:376)

VDG GEYQTNGAIQ FAPNTNPTNP VDPTNPDPDK
 PITPVDPTDP TGPKPGTAGP LSI DYASSLS FGEQTITSKN MYYAETQKY KDNAGADQEG
 PNFVQVSDNR GTETGWTLKV KQNGQFKTEA NQELTAAKVT LSNGRVVSAS QSAKPTTAPA
 TIELNPTGAE SVVMAAGDKE GAGTYLMSWG DSVDTAKTSI SLEVPGSTTK YAKKYTTTTFT
 WTLTDTPANT GN

EF099-1 (SEQ ID NO:377)

TGATGTTGTA GAGGGCTGAT GAAATGTTTA TCAGTCTTCT TTTTATTGAA AGGAGAGATC
 ATGAAGAAAT TAGGCAAGGT TTTAATTGTT AGTGTGTTTA TTTTATTCTC TCCTTTTTTA
 TTATTTTTAG GTGTATTTTC TTCTAGTGAA AGCGGAGATT CTTCCTCAGT TCAGCCCGCT
 ACACCACAGG AAAAAGTAGC ATTAGAAGTT TCTAACTACG TGACGTCACA TGGCGGAACG
 TTGCAGTTTG CTTCGCTTG GATTGGCAAT ATGGAACATG AAAGTGGATT AAATCCTGCT
 AGAATTCAAA GTGATTTATC GTTTAATTCA GCGATAGCTT TTAATCCTTC GTTAGGCGGT
 TATGGAATTG GGTTAGGACA ATGGGATTCA GGACGAAGAG TTAATTTATT AAATTTTGCA
 AAAAGTCAAA AAAAGGAATG GAAATCAGTA GCTTTACAAA TGGATTTTGC GTGGAATAAG
 GATGGTTCTG ATAGTGACTT ACTTAAAGA ATGTCTAAAT CAAAAGATGT GAATACACTT
 GCGGTAGATA TTTTGAAGCT GTGGGAACGA GCTGGAACAA AAGATGATCC CGCAGAACAA
 GTAAAAAGAA AGGCTAGTGC TAATAATTGG TATAAACGAC TTTCTACAGG TTCCATGGGC
 GGAGGTTTCA CCAATGTTGG TGGAGGAAAA ATTGATGCCT TGGAAAAAGT GATGGGGCAA
 ACTATTAATG GTGGTCAATG TTATGGCTTA TCTGCTTTTT TTGTTGAAAA ACAAGGAGGT
 CTACAAATGA TGGGTACGGG GCATATGTTT GCGAGTGAAA TTGGTAATGA TTATCCTTGG
 AGTTCAATTG GTTGGACAGT CATAAAGAAT CCAAATTATT CAGATATTAA AGCAGGAGAT
 GTCATTAATT TTGGTCAAGG TGGTGTGGCT ACTAGTATTT ATGGGCATAC TGGTGTAGTG
 GCAAGTGTTG AAGGTAAAAA CAAGTTTACT ACTTATGAGC AAAACGCTGA ACAAGGTCAA
 ATTGTTGCTA AGTATTTTCG GACTTGGGGA TTAGATTTTC CACATGTGAC CAGCATAGTA
 AGGAAATAG

EF099-2 (SEQ ID NO:378)

MKCLS VFLLKGEIM KKLKVLIVS CFIFILPFL FLGVFSSSES GDSSQFQPAT
 PQEKVALEVS NYVTSHGGTL QFASAWIGNM EHESGLNPAR IQSDLFNSA IAFNPISLGGY
 GIGLQWDSG RRVNLLNFAK SQKKEWKSVA LQMDFAWNKD GSDSDLLKRM SKSKDVNTLA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

VDILKLWERA GTKDDPAEQV KRKASANNWY KRLSTGSMGG GSANVGGGKI DALEKVMGQT
 INGGQCYGLS AFFVEKQGG L QMMGTGHMFA SEIGNDYPWS SIGWTVIKNP NYSDIKAGDV
 INFGQGGVAT SIYGHTGVVA SVEGKNKFTT YEQNAEQGQI VAKYFRTWGL DFPHVTISIVR
 K

EF099-3 (SEQ ID NO:379)

TAGTGAA AGCGGAGATT CTTCCAGTT TCAGCCCGCT
 ACACCACAG AAAAAGTAGC ATTAGAAGTT TCTAAGTACG TGACGTCACA TGGCGGAACG
 TTGCAGTTTG CTTCCGCTTG GATTGGCAAT ATGGAACATG AAAGTGGATT AAATCCTGCT
 AGAATTCAAA GTGATTTATC GTTTAATTCA GCGATAGCTT TTAATCCTTC GTTAGGCGGT
 TATGGAATTG GGTAGGACA ATGGGATTCA GGACGAAGAG TTAATTTATT AAATTTTGCA
 AAAAGTCAA AAAAGGAATG GAAATCAGTA GCTTTACAAA TGGATTTTGC GTGGAATAAG
 GATGGTTCTG ATAGTGACTT ACTTAAAGA ATGTCTAAAT CAAAAGATGT GAATACACTT
 GCGGTAGATA TTTTGAAGCT GTGGGAACGA GCTGGAACAA AAGATGATCC CGCAGAACAA
 GTAAAAAGAA AGGCTAGTGC TAATAATTGG TATAAACGAC TTTCTACAGG TTCCATGGGC
 GGAGGTTTCA CCAATGTTGG TGGAGGAAAA ATTGATGCCT TGGAAAAAGT GATGGGGCAA
 ACTATTAATG GTGGTCAATG TTATGGCTTA TCTGCTTTTT TTGTTGAAAA ACAAGGAGGT
 CTACAAATGA TGGGTACGGG GCATATGTTT GCGAGTGAAA TTGTTAATGA TTATCCTTGG
 AGTTCAATTG GTTGACAGT CATAAGAAT CCAAATTATT CAGATATTAA AGCAGGAGAT
 GTCATTAATT TTGGTCAAGG TGGTGTGGCT ACTAGTATTT ATGGGCATAC TGGTGTAGTG
 GCAAGTGTG AAGGTAAAA CAAGTTTACT ACTTATGAGC AAAACGCTGA ACAAGGTCAA
 ATTGTTGCTA AGTATTTTCG GACTTGGGGA TTAGATTTTC CACATGTGAC CAGCATAGTA
 AGGAAAT

EF099-4 (SEQ ID NO:380)

SES GDSSQFPAT
 PQEKVALEVS NYVTSHGGTL QFASAWIGNM EHESGLNPAR IQSDLSFN SA IAFNPSLGGY
 GIGLGQWDSG RRVNLLNFAK SQKKEWKSV LQMDFAWNKD GSDSDLKRM SKSKDVNTLA
 VDILKLWERA GTKDDPAEQV KRKASANNWY KRLSTGSMGG GSANVGGGKI DALEKVMGQT
 INGGQCYGLS AFFVEKQGG L QMMGTGHMFA SEIGNDYPWS SIGWTVIKNP NYSDIKAGDV
 INFGQGGVAT SIYGHTGVVA SVEGKNKFTT YEQNAEQGQI VAKYFRTWGL DFPHVTISIVR
 K

EF100-1 (SEQ ID NO:381)

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 ACATTATTAG AAATGTTGAT TGTCTTATTG ATTATTTCCG TATTGATTTT ACTTTTTGTC
 CCTAACTTAG CGAAACATAA AGAAACAGTT GATAAAAAAG GCAATGAAGC AATCGTAAAA
 ATTGTAGAAT CACAAATCGA GCTCTACACA CTAGAAAAAA ATAAGACGCC TTCCTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGCAGTTAG ATAAATATAC AGCAGAAAAG
 CAATGA

EF100-2 (SEQ ID NO:382)

MKKKQKYAGF TLLEMLIVLL IISVLILLFV PNLAKHKETV DKKGNEAIVK
 IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLDKYTAEK Q

EF100-3 (SEQ ID NO:383)

TAA AGAAACAGTT GATAAAAAAG GCAATGAAGC AATCGTAAAA
 ATTGTAGAAT CACAAATCGA GCTCTACACA CTAGAAAAAA ATAAGACGCC TTCCTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGCAGTTAG ATAAATATAC AGCAGAAAAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAAT

EF100-4 (SEQ ID NO:384)

KETV DKKGNEAIVK

IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLDKYTAEK Q

EF100-1 (SEQ ID NO:385)

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 ACATTATTAG AAATGTTGAT TGTCTTATG ATTATTTCCG TATTGATTTT ACTTTTGTGTC
 CCTAATTAG CGAAACATAA AGAAACAGTT GATAAAAAAG GCAATGAAGC AATCGTAAAA
 ATTGTAGAAT CACAAATCGA GCTCTACACA CTAGAAAAAA ATAAGACGCC TTCCTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGCAGTTAG ATAAATATAC AGCAGAAAAAG
 CAATGA

EF100-2 (SEQ ID NO:386)

MKKKQKYAGF TLLEMLIVLL IISVLILLFV PNLAKHKETV DKKGNEAIVK

IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLDKYTAEK Q

EF100-3 (SEQ ID NO:387)

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ATTGTAGAAT CACAAATCGA GCTCTACACA CTAGAAAAAA ATAAGACGCC TTCCTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGCAGTTAG ATAAATATAC AGCAGAAAAAG
 CAAT

EF100-4 (SEQ ID NO:388)

KETV DKKGNEAIVK

IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLDKYTAEK Q

EF101-1 (SEQ ID NO:389)

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 GTAATTGCGG TTGGGGGCAT CGTAACGTG AATGCGTTAA ATAAAAATGC ACAACAAGTA
 GCTGTCAAGC AAGCGCCTAA AGATGACTGG GGAATTGACT ATTTTGACGT TCCCGACTTG
 CAACAAATTT ATATTAACGG TGTATCCAA CCGGAACAAA TGGAAGCCTT TCGCGTGAT
 CAAAAAATAA CAAAGGATCC AGAGATTAAG GTGAAAAACG GCGATGTCGT AGATGCAGGC
 ACAGAATTAT TTACTTATGA AGATGAGGCG GTCACAAAAG AAATTGAGGC ACAACAAAAT
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 GATAAATTTA ATAAACTAA AGAAGAAGAC CGCACGATGT CTGGTGATGA TTTAAATGAA
 CAATATCAAA CAGAAGTCGA TGCAGTAGAT GAAGAGATTA CCTTCACCAA TGAAACCTTA
 GCGGATTTAG GAGCGAAGCA ATATATTTCC ACAAAGGCTA ATTTCAAAG TCGTGATCA
 ATTCCAGAAG TAAAAGATGC CAATTCACCG ATTTTACGGT TAACTTCAGA AGATCTTTAT
 TTAGCTGGAA AAGTGAATGA AAAGGACTTG ACTAAAATTA GTGTTGGGCA AAAAGCTAAA
 CTAACITCTG TTTCCAACAA TGTGGTTGTG GATGGCTCAA TTTCTTACAT CGATGATAAT
 CCTCCTGAAG GCAACAGCGA TGCCGCGAGT GGCAATCCAG AGGGCGGCAC AACGATGTCT
 AGTTATAGCG TCAAAATGCG GTTGGCCAAT TTAGACAAAG TCAAAAATGG CTACCATATG
 CAAGCAACCA TTGATTTAGG CGATTTAGGG GCGATTGAGT TACCGAAAA AGCGATTCAA
 AAAGAGGGTG AACAGGCCA CGTTTTAGTG AATGATTTTG GAACCATCAT TCGTCGTGAT
 GTCCAAGTCG GGCAAGAAAA TGGCGACAAA ATGGCGATTG AATCTGGCTT AGAATCAGCC
 GACCGAGTGG TTATTTCTTC AAAAAACCA GTAAAAGTCG GTGATATTGT TGAATCAGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCAGCGATTG CTTCTGATGA ATCAGCAACC AACGAATCAA TGACAGATGC GTCGAAATAG

EF101-2 (SEQ ID NO:390)

MKKK TIIILGAVAV IAVGGIVTVN ALNKNAQQVA VKQAPKDDWG IDYFDVDPDQ
 QIYINGVIQP EQMEAFARDQ KITKDPEIKV KNGDVVDAGT ELFTYEDEAV TKEIEAQONS
 LAKLETKRAN IYNKWNRAID KFNKTKEEDR TMSGDDLNEQ YQTEVDAVDE EITFTNETLA
 DLGAKQYIST KANFKGRVSI PEVKDANSPI LRLTSEDLYL AGKVNEKDLT KISVGQKAKL
 TSVSNVVDV GSISYIDNPN PEGNSDAASG NPEGTTMSS YSVKIALANL DKVKNGYHMQ
 ATIDLGLDGA IELPKKAIQK EGEQAYVLVN DFGTIIRRDV QVGQENGDKM AIESGLESAD
 RVVISSKKPV KVGDIVESDA AIASDESATN ESMTDASK

EF101-3 (SEQ ID NO:391)

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 GCTGTCAAGC AAGCGCCTAA AGATGACTGG GGAATTGACT ATTTTGACGT TCCCGACTTG
 CAACAAATTT ATATTAACGG TGTCATCCAA CCGGAACAAA TGGAAGCCTT TCGCGGTGAT
 CAAAAAATAA CAAAGGATCC AGAGATTAAG GTGAAAAACG GCGATGTCGT AGATGCAGGC
 ACAGAAATAT TACTTTATGA AGATGAGGCG GTCACAAAAG AAATTGAGGC ACAACAAAAT
 AGCTTAGCCA AATTAGAAAC GAAGCGGGCG AATATCTATA ATAAGTGGAA TCGGGCCATT
 GATAAATTTA ATAAAACTAA AGAAGAAGAC CGCACGATGT CTGGTGATGA TTTAAATGAA
 CAATATCAAA CAGAAGTCGA TGCAGTAGAT GAAGAGATTA CCTTCACCAA TGAAACCTTA
 GCGGATTTAG GAGCGAAGCA ATATATTTCC ACAAAGGCTA ATTTCAAAGG TCGTGATCA
 ATTCCAGAAG TAAAAGATGC CAATTCACCG ATTTTACGGT TAACTTCAGA AGATCTTTAT
 TTAGCTGGAA AAGTGAATGA AAAGGACTTG ACTAAAATTA GTGTTGGGCA AAAAGCTAAA
 CTAACCTCTG TTCCAACAA TGTGGTTGTG GATGGCTCAA TTTCTTACAT CGATGATAAT
 CCTCCTGAAG GCAACAGCGA TGCCGCGAGT GGCAATCCAG AGGGCGGCAC AACGATGTCT
 AGTTATAGCG TCAAAATTGC GTTGGCCAAT TTAGACAAAG TCAAAAATGG CTACCATATG
 CAAGCAATCA TTGATTTAGG CGATTTAGGG GCGATTGAGT TACCGAAAAA AGCGATTCAA
 AAAGAGGGTG AACAGGCCTA CGTTTTAGTG AATGATTTTG GAACCATCAT TCGTCGTGAT
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 GACCGAGTGG TTATTTCTTC AAAAAACCA GTAAAGTCG GTGATATTGT TGAATCAGAT
 GCAGCGATTG CTTCTGATGA ATCAGCAACC AACGAATCAA TGACAGATGC GTCGAAAT

EF101-4 (SEQ ID NO:392)

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 QIYINGVIQP EQMEAFARDQ KITKDPEIKV KNGDVVDAGT ELFTYEDEAV TKEIEAQONS
 LAKLETKRAN IYNKWNRAID KFNKTKEEDR TMSGDDLNEQ YQTEVDAVDE EITFTNETLA
 DLGAKQYIST KANFKGRVSI PEVKDANSPI LRLTSEDLYL AGKVNEKDLT KISVGQKAKL
 TSVSNVVDV GSISYIDNPN PEGNSDAASG NPEGTTMSS YSVKIALANL DKVKNGYHMQ
 ATIDLGLDGA IELPKKAIQK EGEQAYVLVN DFGTIIRRDV QVGQENGDKM AIESGLESAD
 RVVISSKKPV KVGDIVESDA AIASDESATN ESMTDASK

EF102-1 (SEQ ID NO:393)

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 ATTAATTATA TGAAAAAAC AACATTTAAA AATGGTTCGT TATTTGCGAC TTTGGCTCTA
 TTAAGTCAAA CAATTGGCGG AACGATTGGT CCTACGATTG CTTTTGCCGA TGAAATTACT
 CACCCTCAAG AGGTAACAAT TCATTATGAC GTAAGTAAAC TGTATGAAGT TGACGGAAT
 TTTAGCGATG GCAGCAGCT CTCAGAACGT ACTACGTCAT TATATGCAGA ATACAATGGT
 GCAAAACAAA CAGTATTTTG TATTGAACCA GGTGTTAGTA TTCCAACAGA AGTGACGCAC
 GGTATCAGA AAAACCTTTT GCCATCAATG TCTGATAAAG CGAAACTAGT ATCGGTTCTT
 TGGGAAAAGG CTGGAACAGA TATTGATACA AATATGGTTG CACAAAAGAT GATTTGGGAA
 GAAGTGAACG GTTATAAACT CCATTCCATA AAAAGATTAG GTGGTGCTTC AGTTGATATA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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AAATCTATTG AAGGAAAAAT TAATAAGGCA ATTGAGGAGT ATCAAAAAAA ACCAAGTTTT
CATAATACCA CTGTAAAAAC AATTTTAGGT CAATCGACAA CTTTAATAGA TAAAAATGAA
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AAAAAATCAG CTGGTACTGG AACTCCAGTC GCTTATAAAA AAGCAGGACT TCAAACTGTG
ATGGCTGGTG CGCTTGATAA GCCCAATACC TACGCTATTA AAATTAATGT GGAAACTAAG
GGTTCTTTAA AGATCAAAAA AATCGATAAA GAATCAGGTG ATATTGTACC AGAAACGGTT
TTCCATTTAG ATTTTGGGAA AGCTTTACCT TCAAAAGATG TGACAACAGA TAAAGATGGG
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CCAGATCCTT ATATGATTGA TACCACACCC ATGGCTGCCA CCATTAAAGC GGGCGAGACC
ATTTCCATGA CTTGCAAAAA TATGCGACAA AAAGGTCAAA TTCTTTTAGA GAAGACTGGG
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CGTGCGGAAA CACCAAAAGA GCTTGCTAAT GCTTTGGAAC TGGGAACCTA TTACGTGACA
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TATGCCAATC AAACCGTGGC TCTTGTTACC AGTAACGTAA AAGGGCAAAA CCAAGAAATT
ACTGGGAAA CCACTTTGAC AAAAGAAGAC AAAGATACCG GTAATGAGAG TCAAGGAAA
GCTGAGTTTA AAGGAGCTGA ATATACTCTC TTTACTGCAA AAGATGGTCA AGCTGTTAAA
TGGAGTTAAG CTTTTAAAC AGAATTAGTG AAGGGAACGA AAGCTTCTGA TGAACAGTG
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TTCTGGCAAG AAACCAAAGC ACCTGAAGGA TATACTTTGG ATGAAACGAA GTATCCTGTA
TCCATCAAAA AAGTTGATAA TAACGAAAAA AATGCCGTAA TTACTCGAGA TGTTACGGCA
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GAAATCACAG GTGCTGAAGA TAAAGCGACC ACAGCTTGTA ACGAGCAATT AGGTTTTGAT
GGCTATGGTA AGTTTGAAAA TCTTCCTTAT GGGGATTATT TACTTGAAGA AATAGAGGCT
CCAGAAGGAT TTCAAAAGAT TACACCACTA GAAATCCGTT CTACATTTAA GGAAAACAAA
GACGACTATG CGAAGAGTGA GTATGTCTTT ACCATTACCG AAGAAGGACA AAAACAACCA
ATTAAGTATG TGACCTTCC TTACGAGAAA CTAACTAACA ACGAGTTTTT TGTAGTCTG
AACCGTTTGA TGCTTTATGA TTTGCCCGAG AAAGAAGATA GTTTGACTTC TCTTGCGACT
TGAAAGACG GAAATAAAAA ATTGAATACC CTTGATTTTA CCGAGCTAGT TGATAAATTG
AGATATAACT TGCATGAAAT CAAAGAAGAC TGGTATGTCG TAGCTCAAGC CATTGATGTG
GAAGCCACAA AAGCTGCCCA AGAAAAAGAC GAAAAAGCCA AACCGGTGGT GATTGCCGAA
ACAACCGCAA CGTTGGCGAA CAAAGAGAAA ACTGGAACCT GGAAAATTCT GCATAAATTA
ACCGCTGAAC AAGTTTGGGA TAAAAGCATC GTCTTGTTCA ATTATGTGTA TGAAAACAAG
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CAAACCGTCA ATTGTACGAT TGAACGCCAT GTTCCATCC AAACAAAAGC CCACCTAGAA
GATGGTTTCG AACTTTTAC TCATGGTGAC GTGATGGATA TGTTTGATGA TGTGTCGGTT
ACCATGATG TACTGGATGG CTCAAAAGAA GCTTTCGAAA CAATTCTGTA TGCTTTACTA
CCAGATGGTA CGAACAAAGA AATTGGGAAA TCTGGCAAAA TTGAGCATGA AGTGAATGAT
AAAGAATTTA CCAAAACCGT ACTTGCAGAA AAAGTAGATA CCGGAAAAGTA TCCAGAAGGA
ACTAAGTTTA CTTTACGGA AATCAATTAC GAAAAAGATG GAAACGTGAA TGGAAAACAC
AATGAAGATT TGAAAGAAAA ATCTCAAACC TTAACACCAA AAGAAGTGCC AACCATACCG
AGTACGCCAA AACACCGGA AACACCAGCT GTTCCAAGTA ATTCTCAAGA ATCTAGTCCC
ACAGTGAAGA CATTCGCGCA AACTGGGGAG AAAAATTCCA ACGTTCTACT GTTAGTTGGC
TTTATCTTGA TTTTTCGAC TGCTGGGTAT TATTTCTGGA ATCGCCGCAA TTAA

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EF102-2 (SEQ ID NO:394)

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MKKTTFKN WSLFATLALL SQTIGGTIGP TIAFADEITH
PQEVTHYDV SKLYEVDGTF SDGSTLSERT TSLYAEYNGA KQTVFCIEPG VSIPTEVTHG
YQKNPLPSMS DKAKLVSVLW EKAGTDIDTN MVAQKMIWEE VNGYKLHSIK RLGGASVDIK
SIEGKINKAI EEYQKKPSFH NTTVKILGQ STTLIDKNEL NLSEFDKVVQ NTANIDYRVI
GNQLVLTPTS NSKSGTLTLK KSAGTGTPVA YKKAGLQTM AGALDKPNTY AIKINVETKG

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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SLKIKKIDKE SGDIVPETVF HLDGKALPS KDVTDDKDI SILDGIPHGT KVTITEKSVP
DPYIMIDTPM AATIKAGETI SMTSKNMRQK GQILLEKTGV ETGTDLWNDN YSLAGNTFAI
RKDSPAGEIV QEITTTDEKGR AETPKELANA LELGTYVTE TKSSNGFVNT FKPTKVELKY
ANQTVALVTS NVKGQNEIT GETTLTKEDK DTGNESQGA EFKGAEYTLF TAKDGQAVKW
SEAFKTELVK GTKASDETVT LALDEKNQVA VKHLAINEYF WQETKAPEGY TLDETKYPVS
IKKVDNNEKN AVITRDVTAK EQVIRFGFDF FKFAGSADGT AETGFNDLSF KVSPLGTXE
ITGAEDKATT ACNEQLGFDG YGKFENLPYG DYLLLEEIEAP EGFQKITPLE IRSTFKENKD
DYAKSEYVFT ITEEGQKQPI KMTVPYEKL TNNEFSVSLN RLMLYDLPEK EDSLTSLATW
KDGNNKLNLT DFTELVDKLR YNLHEIKEDW YVVAQAIDVE ATKAAQEKDE KAKPVVIAET
TATLANKEKT GTWKILHKLT AEQVLDKSIV LFNYYENKV AFEAGNEPVA KDASLNNQAO
TVNCTIERHV SIQTKAHLED GSQTFTHGDV MDMFDDVSVT HDVLDGSKEA FETILYALLP
DGTNKEIWKS GKIEHEVNDK EFTKTVLAEK VDTGKYPEGT KFTTFEINYE KDGNNVNGKHN
EDLKEKSQTL TPKEVPTIPS TPKQPETPAV PSNSQESSPT VKTFPQTGEK NSNVLLLVGF
ILIFSTAGYY FWNRRN

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EF102-3 (SEQ ID NO:395)

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TTCTGGCAAG AAACCAAGC ACCTGAAGGA TATACTTTGG ATGAAACGAA GTATCCTGTA
TCCATCAAAA AAGTTGATAA TAACGAAAAA AATGCCGTAA TTA CTGAGA TGTTACGGCA
AAAGAACAAG TTATTCGCTT TGGCTTTGAT TTCTTTAAAT TTGCTGGATC GGCTGATGGC
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GACGACTATG CGAAGAGTGA GTATGTCTTT ACCATTACCG AAGAAGGACA AAAACAACCA
ATTAAGATGG TGACCGTTCC TTACGAGAAA CTAATAACA ACGAGTTTTT TGTTAGTCTG
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TGGAAGAGACG GAAATAAAA ATTGAATACC CTTGATTTTA CCGAGCTAGT TGATAAATTG
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EF102-4 (SEQ ID NO:396)

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ITGAEDKATT ACNEQLGFDG YGKFENLPYG DYLLLEEIEAP EGFQKITPLE IRSTFKENKD
DYAKSEYVFT ITEEGQKQPI KMTVPYEKL TNNEFSVSLN RLMLYDLPEK EDSLTSLATW
KDGNNKLNLT DFTELVDKLR YNLHEIKEDW YVVAQAIDVE ATKAAQEKDE KAKPVVIAET
TATLANKEKT GTWKILHKLT AEQVLDKSIV LFNYYENKV AFEAGNEPVA KDASLNNQAO
TVNCTIERHV SIQTKAHLED GSQTFTHGDV MDMFDDVSVT HDVLDGSKEA FETILYALLP
DGTNKEIWKS GKIEHEVNDK EFTKTVLAEK VDTGKYPEGT KFTTFEINYE KDGNNVNGKHN

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EDLKEKSQTL TPKEVPTIPS TPKQPETPAV PSNSQESSPT VK

EF103-1 (SEQ ID NO:397)

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 ATTACTTTAG TAACATTAAG TACGTTACTT ATAGCAGGTT ATGCAAGTCC AGCATTTGCA
 GATCATGCAG CCAATCCAAA TAGTGCTACA GCAAATTTAG GCAAACATCA AAACAATGGC
 CAAACAAGAG GCGACAAGGC GACTAAGATT TTATCTGGCA CGGACTGGCA AGGAACCCGT
 GTTTATGATG CTGCTGGTAA TGATTTAACG GCAGAAAATG CTAATTTTAT TGGTTTAGCA
 AAATATGATG GTGAAACCGG TTTTACGAG TTTTTCGACA AAAATACTGG GGAAACCCGT
 GGTGACGAAG GAACATTTTT TGTGACAGGT GATGGCACA AACGAATTTT AATTTCGCGG
 ACACAAAATT ATCAAGCCGT AGTGGATTTA ACCGAAGTGA GTAAAGACNA ATTTACTTAC
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 TATCATGGGA AAAAATTAGC TTTTACAAAT GGACGTGAAG CATTAAACCA TCAAACTGGC
 AAAATTGTGA CAAATAAATC AGGGGATAAA ATTTTAGGAA CAACCTTGTG GAATGGCACA
 AAAGTCGTAG ATAAAAACGG TAATGATGTG ACAGCGGCCA ATCAAAATTT CATTAGTTTA
 GCGAAATTTG ATCCAAACAC AAGTAAATAT GAATTTTTC AATTACAAAC AGGTGAAACC
 CGCGGCGACT TTGGGTACTT CCAAGTGGTG GACAATAACA AGATTCCGGC CCATGTATCT
 ATTGGTACGA ATCGTTACGG CGCGGCGCTA GAATTAACGG AACTAAACAA TGATCGATTT
 ACGTATACTC GAATGGGTAA AGATAATGCT GGTAAATGATA TTCAAGTGTT CGTGGAACAT
 GAACCTTACC AAGGCACATA TCATCCAGCC TTTACTTTCT AA

EF103-2 (SEQ ID NO:398)

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 DEGTFFVTGD GTRKILISRT QNYQAVVDLT EVSKDXFTYK RLKDKLGNL VEVYVEHIPY
 HGKKLAFTNG REALTNQTKG IVTNKSGDKI LGTTLWNGTK VVDKNGNDVT AANQNFISLA
 KFDPNSTSKYE FFLNLQGETR PDFGYFQVVD NTKIRAHVSI GTNRYGAAL LTELNNDRFT
 YTRMGKDNAG NDIQVFVEHE PYQGTYPAP TF

EF103-3 (SEQ ID NO:399)

TCATGCAG CCAATCCAAA TAGTGCTACA GCAAATTTAG GCAAACATCA AAACAATGGC
 CAAACAAGAG GCGACAAGGC GACTAAGATT TTATCTGGCA CGGACTGGCA AGGAACCCGT
 GTTTATGATG CTGCTGGTAA TGATTTAACG GCAGAAAATG CTAATTTTAT TGGTTTAGCA
 AAATATGATG GTGAAACCGG TTTTACGAG TTTTTCGACA AAAATACTGG GGAAACCCGT
 GGTGACGAAG GAACATTTTT TGTGACAGGT GATGGCACA AACGAATTTT AATTTCGCGG
 ACACAAAATT ATCAAGCCGT AGTGGATTTA ACCGAAGTGA GTAAAGACNA ATTTACTTAC
 AAGCGTTTAG GGAAAGATAA ACTGGGGAAT GATGTTGAAG TTTACGTGGA ACACATCCCT
 TATCATGGGA AAAAATTAGC TTTTACAAAT GGACGTGAAG CATTAAACCA TCAAACTGGC
 AAAATTGTGA CAAATAAATC AGGGGATAAA ATTTTAGGAA CAACCTTGTG GAATGGCACA
 AAAGTCGTAG ATAAAAACGG TAATGATGTG ACAGCGGCCA ATCAAAATTT CATTAGTTTA
 GCGAAATTTG ATCCAAACAC AAGTAAATAT GAATTTTTC AATTACAAAC AGGTGAAACC
 CGCGGCGACT TTGGGTACTT CCAAGTGGTG GACAATAACA AGATTCCGGC CCATGTATCT
 ATTGGTACGA ATCGTTACGG CGCGGCGCTA GAATTAACGG AACTAAACAA TGATCGATTT
 ACGTATACTC GAATGGGTAA AGATAATGCT GGTAAATGATA TTCAAGTGTT CGTGGAACAT
 GAACCTTACC AAGGCACATA TCATCCAGCC T

EF103-4 (SEQ ID NO:400)

HAANPNSATA NLGKHQNNQ
 TRGDKATKIL SGTDWQGRV YDAAGNDLTA ENANFIGLAK YDGETGFYEF FDKNTGETRG
 DEGTFFVTGD GTRKILISRT QNYQAVVDLT EVSKDXFTYK RLKDKLGNL VEVYVEHIPY

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

HGKKLAFTNG REALTNQTKG IVTNKSGDKI LGTTLWNGTK VVDKNGNDVT AANQNFISLA
 KFDPNSTSKYE FFLNLQTGETR GDFGYFQVVD NNKIRAHVSI GTNRYGAAL ETELNNDRFT
 YTRMGKDNAG NDIQVFVEHE PYQGTYYHPA

EF104-1 (SEQ ID NO:401)

TGAAAGGGGA TTAGTATGAA GAAAAAACT TTTTCTTTTG TGATGTTGAG TATACTTCTC
 GCACAAAATT TCGGGTTTGC CGTAAATGCC TATGCTGTAA CAACGACAGA AGCACAACAA
 GAGACCACTG ATACAGCAAA AAAAGAGGCA GAGTTATCGA ACTCAACACC ATCTTTACCT
 TTAGCAACAA CGACTACTTC AGAAATGAAT CAACCAACTG CAACAACTGA ATCGCAAAACC
 ACAGAGGCGA GCACAACAGC TTCCAGTGAT GCTGCTACAC CATCTGAACA ACAAACAACG
 GAGGACAAGG ACACCTCACT TAATGAAAAA GCCCTGCCAG ATGTTCAAGC GCCAATTACA
 GATGAACTAC TTGACAGTAT GAGTCTTGCG CCGATTGGTG GAACAGAATA CAGCCAAACA
 GAGGTTCCACC GCGAATTAAA TACAACACCG GTAACCGCTA CGTTCCAATT TGCTGTTGGA
 AACACAGGTT ATGCACCTGG ATCAGTTTAT ACAGTTC AAT TACCAGAACA TTTAGGTTAT
 TCAACTGTCA GCGGAGAAAT GACAGGCATT GCGCGAACTT GGGCAGTCGA TGCGGCGACC
 AAAACATTAA GTATTACGTT TAATCAACGA GTTTTCAGATA CTTCCTTTAA AGTAGAACTA
 AAAAGTTATC TAACAACAGA GCGGGAACCA TTAATCAAAA TTGAAACTCC AGGAAAAAAT
 AAAAAACCTC ACTCGTTTGA TTTATATGAA CAAGTGAAC CAATTCAATA TAACGAACGA
 ACCAGAACGA CCGGGTTAGA TGGCGAAATT TTTTATAATT TAGACCGGAC GTTAACTGGC
 AATCAAAACAT TAGAATTATT AACACAGAG ACGCCAGGCG CTGTCTTTGG AAAACAAGAT
 AACTTGGAAC CTCAAGTTTT CAGTTACGAT GTCGACATTA ATGGTCAAAT TTTACCAGAA
 ACGCAAACCT TGTTAACACC TGGCAAAGAT TATACATTAA GCGATAATTC ACTCGGGCGG
 ATTGCTGTAA CTGTTCCAAA CATGAATCAA CAAAAAGCCT ATTCCTTATC GATTAATCGG
 ACAATTTATT TAGAGAGTGC TTCGGACTAT AACTACTTAT ATTCGCAGCA GTATCCAACA
 ACAAAAATTG GGTCAATTTT TTTGAAAAGT ACGACAGGAA CTAAACAAAC AACCAGTTTT
 ACTGCTAAGA CGAGTCAAAAC AAGTAAAGTA ATTGCTGATC GTGAAATGCG TAGTATGTCC
 TATATCAGTT TTCAAAGCAA AGGGAAATAT TATGTAACAA TTTATGGCAC GTTAACAGAA
 ACAAAGTGG GTCAACAAAT CGTATTAGAG AGTACAAACG GTCAAGAAAT TAAGAATCCT
 AAATTTACGG CGTATGGTCC TTTATATGAA AATGTAAAT TGGGAAGACTA TTTTGATATT
 AAAACTGAAG GTGGCAAGCT CACTTTAACG GCCACAAAAG ATAGCTATTT AAGAATAAAT
 ATTTCTGATT TAACAATGGA TTTTGACAAG AAGGACATTA ATCTATCATT AAGTACACCT
 GTAATTGGTC CTAATAAAGC CATTCAATTA GTATCCGATC AATATATTGA ACCAATTAGT
 GTTGTTAATC CTTTGAATGC TGAACTGCT TGGGGTAATT ATGATCAAAA TGGTGCCTAT
 TCATCAAGAA CAACTGTCTC AGTTATGGGA AGCAAAGAGA AACCAGATTCA AAATTTAGAA
 ATTAAGTAA AGCATCCTAA TTATCTTTCA TTACGAGCTA CAAAAGAAAT TTATTTTAT
 TACAAGTTAG GAACGATTA TACAGTAACG CCAACGTCAG ATGGTTCAGT TATTAAGTTC
 ACTACGCCAA TAACCAACGA AATCCAAAT CCAATTGGTT TTAATTATGT GCCAGATAGT
 TTGCCAAAAG ATAAAAGTAT CCCAGTCGAT ACGATACCGA TAACAATGAG TGCTGAAGGT
 TTAAGTCCAG TTGATACGAC AGTAACTACT AATAGTAAGC GTGGTCTGA ACGAACACTT
 CAAAGTAGTA AAAATCAATT CCTTGTC AAT GCACGAAATG ATTCTTTTGA CTCCTAAGC
 GTCCGTACAA AAATTCAGC TGGCGCCGAT GTTCTTTTGG ACATTTATGA TGTTCACAAAC
 GATCAGGTAG ATTCAATTTA TCCACAATAC TGGGACCGCG GTCAATACTT TGATAAACCA
 ATGACGCCAA ACAGCCCTGG ATATCCAACG ATTACTTTTG ACGAAAATAC CAATAGTTAC
 ACGTTTGATT TTGGA AAAAC CAACAAACGT TACATTATTG AGTATAAAAA CGCCAATGGC
 TGGATCGACG TGCCAACTCT TTATATAACA GGGACAGCGA AAGAACCACA ATCGAATAAT
 AATGAAGGCT CTGCTTCGGT TTCTGTTCAA AATGAAGCGT TAGACATTTT GAGTGCAACA
 CAAGCGGCGA ATCCAACATT AAAAAATGTA ACAAACCGA CAGTAACAAC AAAAAATATT
 GATAATAAAA CACATCGTGT GAAAAATCCA ACGATTGAAT TAACACCAAA AGGCACAACC
 AATGCTCAAA TCGATTGAA TTCTATTACC GTGAAAGGCG TGCCAGAAGA TGCTTATTCA
 TTAGAGAAGA CTCACAAACG TCGGAAAGTC ATTTTAAAG ACTATACATT GACAGAAAAC
 ATTACGATTG AATACAATAC GGTCTCTGCA AACGCTGGCC AAATCTATAC AGAAACAACA
 ATCGACTCTG AAACATTGAA CCAGATGTCT GCTAGCAAGA AAAAAGTCAC CACTGCGCCA
 ATCACATTGA AATTCTCAGA AGGTGATGCG GAAGGTATTG TTTATTTAGC AACTGCCACA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTCTACACGC ATAACGTAGA GGATGAAAAC CAAGCAATTG CGAAGGTTTC TTTTGAAC TA
 ATTGATAATG TCACGCATAC AGCAACCGAA TTTACAACAG ATGAAAAAGG TCAATACTCC
 TTTGATGCCA TCATGACAGG TGATTATACT TTGCGAGTAA CGAATGTACC GCAGGAATAT
 TCCGTGGATG AAGAGTATTT GACAGGAAAA GCCATTAAGC TGGTCAAAGG AGACAACCAA
 CTAAAAATTC CATTAACGAA AACAATTGAT CACAGTCGTT TACAAGTCAA AGATTCAACG
 ATTTATGTCG GCGATTTCATG GAAACCAGAA GAGAACTTTG TTTCAAGCAAC AGATAAAACA
 GGTCAGACG TTTCCCTTCGA AAAAATCACT GTTTCAGGTC AAGTTGATAA CANCAAAGCA
 GGCGTTTATC CAATTATTTA CAGTGACGAA GGTAAAGAAG AAACAGCCTA TGTGACCGTC
 AAACCCGACC AATCTAAGTT AGAGGTCAAA GATACAACGA TTTATGTTGG TGATTCTGCG
 AAACCAGAAG ATAATTTTCGT TTCAGCGACA GACAAAACAG GTCAAGACGT NCCGTTTGAA
 AAAATTGATG TTCAGGGAAC AGTGAATGTT GATAAAATAG GCGATTATGA AATTGTCTAT
 AAAAATGGCA NAAAAGAAGC GAAAGCAATC GTTCATGTCC GTGATGACAG TCAGTTAGAG
 GTTAAAGATA CAACGATTTA TGTTGGTGAT TCGTGGAAAC CAGAAGATAA TTTCTGTTTCA
 GCAACAGACA AAACAGGCCA AGACGTTCCG TTTGAAAAAA TCACTGTTTC AGGTCAAGTT
 GATACTAGCA AAGCAGGCGT TTATCCAATC GTTTACAGTT ACGAAGGTAA AGAAGAAAACA
 GCTAATGTGA CTGTCAAACC CGACCAATCT AAGTTAGAGG TTAAAGATAC AACGATTTAT
 GTGGGCGATA AATGGGAACC AGAAGATAAT TTCGTTTCAG CAACAGACAA AACAGGTCAA
 GATGTCCCGT TTGAAAAAAT TGACGTTTCA GGAACAGTGA ATGTTGATAA AATAGGCGAT
 TATGAAATTG TCTATAAAAA TGGCACAAAA GAAGCGAAAG CAATCGTTCA TGTCCGTGAT
 GACAGTCAGT TAGAGGTCAA AGATACAACA ATTTATGTGG GTGATAAATG GGAAGCAGAA
 GATAACTTCG TTTCCGCGAC AGACAAAACA GGTCAAGACG TTCCGTTTGA AAAAATTGAT
 GTTCAGGGAA CAGTGAATGT TGATAAAATA GGCGATTATG AAATTGCTTA TAAAAATGGC
 ACAAAGAAG CGAAAGCAAT CGTTCATGTC CGTGATGATA GTCGTTTACA AGTCAAGGAT
 ACAACGATTT ATGTCGGCGA TTCNTGGANA CCAGAAGNGA ACTTTGTTTC AGCNACAGAT
 AAAACAGGTC AAGATGTCCC ATTCGAAAAA ATCACTGTT

EF104-2 (SEQ ID NO:402)

MKKKTFF SFVMLSILLA QNFGFAVNAY AVTTTEAQTE TTDATKEAE LSNSTPSLPL
 ATTTTSEMNO PTATTESQTT EASTTASSDA ATPSEQQTE DKDTSLNEKA LPDVQAPITD
 ELLDSMSLAP IGGTEYSQTE VHRELNTTPV TATFQFAVGN TGYAPGSVYT VQLPEHLGYS
 TVSGEVTGIG ATWAVIDAATK TLSITFNQRV SDTSFKVELK SYLTTEAEPL IKIETPGKNK
 KTYSFDLIEQ VEPIQYNERT RTTGLDGEIF YNLDRTLTGN QTLELLTTET PGAVFGKQDN
 LEPQVFSYDV DINGQILPET QTLTPGKDY TLDNSLGR IAVTVPMNQK KAYSLSINRT
 IYLESASDYN YLYSQYPTT KIGSISLKST TGTKQTTDFT AKTSQTSKVI ADREMRMSY
 ISFQSKGKYY VTIIYGLTET KVGQQIVLES TNGQEIKNPK FTAYGPLYEN VKLEDYFDIK
 TEGGKLTLTA TKDSYLRINI SLDLTMDFDKK DINLSLSTPV IGPKNKAIQLV SDQYIEPISV
 VNPLNAETAW GNYDQNGAYS SRTTVSVMGS KEKPIQNLEI KVKHPNYLSL RATKEIYFYY
 KLGTDYTVTP TSDGSVIKFT TPITNEIQIP IGFNYVPDSL PKDKSIPVDT IPITMSAEG
 TPVDITVTTN SKRGSERTLQ SSKNQFLVNA RNSFDSL SV RTKIPAGADV LFDIYDVSND
 QVDSIYPQYW DRGQYFDKPM TPNSPGYPTI TFDENTNSYT FDFGKTNKRY IIEYKNANGW
 IDVPTLYITG TAKEPQSNNN EGSASVSVQN EALDILSATQ AANPTLKNVT KTTVTTKNID
 NKTHRVKNPT IELTPKGTN AQIDLNSITV KGVPEDAYSL EKTNGAKVI FKDYTLTENI
 TIEYNTVSAN AGQIYTETTI DSETLNQMSA SKKKVTAPI TLKFSEGD AE GIVYLATATF
 YTHNVEDENQ AIAKVSFELI DNVTHTATEF TTDEKGQYSF DAIMTG DYTL RVTNVPQEYS
 VDEEYLTGKA IKLVKGDNL KIPLTKTIDH SRLQVKDSTI YVGDSWKPEE NFVSATDKTG
 QDVPFEKITV SGQVDNXXKAG VYPIIYSDEG KEETAYVTVK PDQSKLEVVD TTIYVGDSWK
 PEDNFVSATD KTGQDVPFEK IDVQGTNVND KIGDYEIVYK NGXKEAKAIV HVRDDSQLLEV
 KDTTIYVGDS WKPEDNFVSA TDKTGQDVFF EKITVSGQVD TSKAGVYPIV YSYEGKEETA
 NVTVKPDQSK LEVKDTTIYV GDKWEPEDNF VSATDKTGQD VPFEKIDVQG TVNVDKIGDY
 EIVYKNGTKE AKAIHVHVRD SQLVKDTTI YVGDKWEAED NFVSATDKTG QDVPFEKIDV
 QGTNVNDKIG DYEIVYKNGT KEAKAIVHVR DDSRLQVKDT TIYVGDSWXP EXNFVSATDK
 TGQDVPFEKI TV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF104-3 (SEQ ID NO:403)

TGTA CAACGACAGA AGCACAACA
 GAGACCACTG ATACAGCAAA AAAAGAGGCA GAGTTATCGA ACTCAACACC ATCTTTACCT
 TTAGCAACAA CGACTACTTC AGAAATGAAT CAACCAACTG CAACAACTGA ATCGCAAAACC
 ACAGAGGCGA GCACAACAGC TTCCAGTGAT GCTGTACAC CATCTGAACA ACAACAACG
 GAGGACAAGG ACACCTCACT TAATGAAAAA GCCCTGCCAG ATGTTCAAGC GCCAATTACA
 GATGAACATC TTGACAGTAT GAGTCTTGCG CCGATTGGTG GAACAGAATA CAGCCAAACA
 GAGGTTCCACC GCGAATTAAA TACAACACCG GTAACCGCTA CGTTCCAATT TGCTGTGGGA
 AACACAGGTT ATGCACCTGG ATCAGTTTAT ACAGTTCAAT TACCAGAACA TTTAGGTTAT
 TCAACTGTCA GCGGAGAAGT GACAGGCATT GCGCAACTT GGGCAGTCGA TGCGGCGACC
 AAAACATTAA GTATTACGTT TAATCAACGA GTTTCAGATA CTTCTTTAA AGTAGAATA
 AAAAGTTATC TAACAACAGA GCGGAACCA TTAATCAAAA TTGAAACTCC AGGAAAAAAT
 AAAAAACCT ACTCGTTTGA TTTATATGAA CAAGTGAAC CAATTCAATA TAACGAACGA
 ACCAGAACGA CGGGGTTAGA TGGCGAAATT TTTTATAATT TAGACCGGAC GTTAACGGC
 AATCAACAT TAGAATTATT AACAACAGAG ACGCCAGGCG CTGCTTTGG AAAACAAGAT
 AACTTGGAAC CTCAAGTTTT CAGTTACGAT GTCGACATTA ATGGTCAAAT TTTACCAGAA
 ACGCAAACCT TGTTAACACC TGGCAAAGAT TATACATTAA GCGATAATTC ACTCGGGCGG
 ATTGCTGTAA CTGTTCCAAA CATGAATCAA CAAAAAGCCT ATTCTTTATC GATTAAATCGG
 ACAATTTATT TAGAGAGTGC TTCGGACTAT AACTACTTAT ATTTCGAGCA GTATCCAACA
 AAAAAAATG GGTCAATTTT TTTGAAAAGT ACGACAGGAA CTAAACAAAC AACCAGTTTT
 ACTGCTAAGA CGAGTCAAAC AAGTAAAGTA ATTGCTGATC GTGAAATGCG TAGTATGTCC
 TATATCAGTT TTCAAAGCAA AGGGAAATAT TATGTAACAA TTTATGGCAC GTTAACAGAA
 ACAAAGTGG GTCAACAAAT CGTATTAGAG AGTACAAACG GTCAAGAAAT TAAGAAATCCT
 AAATTTACGG CGTATGTGCC TTTATATGAA AATGTAATAAT TGGAAGACTA TTTTGATATT
 AAAACTGAAG GTGGCAAGCT CACTTTAACG GCCACAAAAG ATAGCTATTT AAGAATAAAT
 ATTTCTGATT TAACAATGGA TTTTGACAAG AAGGACATTA ATCTATCATT AAGTACACCT
 GTAATTGGTC CTAATAAAGC CATTCAATTA GTATCCGATC AATATATTGA ACCAATTAGT
 GTTGTTAATC CTTTGAATGC TGAACCTGCT TGGGGTAATT ATGATCAAAA TGGTGCCTAT
 TCATCAAGAA CCAACTGTCT AGTTATGGGA AGCAAAGAGA AACCAGTTCA AAATTTAGAA
 ATTAAAGTAA AGCATCTTAA TTATCTTTCA TTACGAGCTA CAAAAGAAAT TTATTTTAT
 TACAAGTTAG GAACGGATTA TACAGTAACG CCAACGTCAG ATGGTTCAGT TATTAAGTTC
 ACTACGCCAA TAACCAACGA AATCCAAATT CCAATTGGTT TTAATTATGT GCCAGATAGT
 TTGCCAAAAG ATAAAAGTAT CCCAGTCGAT ACGATACCGA TAACAAAGAG TGCTGAAGGT
 TTAACCTCAG TTGATACGAC AGTAACACTT AATAGTAAGC GTGGTTCTGA ACGAACACTT
 CAAAGTAGTA AAAATCAATT CCTTGTCATG GCACGAAATG ATTCTTTTGA CTCCTAAGC
 GTCCGTACAA AAATTCACG TGGCGCCGAT GTTCTTTTGG ACATTTATGA TGTTTCAAAC
 GATCAGGTAG ATTCAATTTA TCCACAATAC TGGGACCGCG GTCAATACTT TGATAAACCA
 ATGACGCCAA ACAGCCCTGG ATATCCAACG ATTACTTTTG ACGAAAATAC CAATAGTTAC
 ACGTTTGATT TTGGAAAAAC CAACAAACGT TACATTATTG AGTATAAAAA CGCCAATGGC
 TGGATCGACG TGCCAACCTT TTATATAACA GGGACAGCGA AAGAACCACA ATCGAATAAT
 AATGAAGGCT CTGCTTCGGT TTCTGTTCAA AATGAAGCGT TAGACATTTT GAGTGCAACA
 CAAGCGGCGA ATCCAACATT AAAAAATGTA AAAAAACGA CAGTAACAAC AAAAAATATT
 GATAATAAAA CACATCGTGT GAAAAATCCA ACGATTGAAT TAACACCAA AGGCACAACC
 AATGCTCAAA TCGATTGAA TTCTATTACC GTGAAAGGCG TGCCAGAAGA TGCTTATTCA
 TTAGAGAAGA CTACAAACGG TGCGAAAGTC ATTTTAAAG ACTATACATT GACAGAAAAC
 ATTACGATTG AATACAATAC GGTCTCTGCA AACGCTGGCC AAATCTATAC AGAAACAACA
 ATCGACTCTG AAACATTGAA CCAGATGTCT GCTAGCAAGA AAAAGTACAC CACTGCGCCA
 ATCACATTGA AATTCTCAGA AGGTGATGCG GAAGGTATTG TTTATTTAGC AACTGCCACA
 TTCTACACGC ATAACGTAGA GGATGAAAAC CAAGCAATTG CGAAGGTTTC TTTTGAAC
 ATTGATAAAG TCACGATAC AGCAACCGAA TTTACAACAG ATGAAAAAGG TCAATACTCC
 TTTGATGCCA TCATGACAGG TGATTATACT TTGCGAGTAA CGAATGTACC GCAGGAATAT
 TCCGTGGATG AAGAGTATTT GACAGGAAAA GCCATTAGC TGGTCAAAGG AGACAACCAA
 CTAATAATTC CATTACGAA AACAATTGAT CACAGTCGTT TACAAGTCAA AGATTCAACG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATTTATGTCG GCGATTTCATG GAAACCAGAA GAGAACTTTG TTTCAGCAAC AGATAAAACA
 GGTCAAGACG TTCCCTTCGA AAAAATCACT GTTTCAGGTC AAGTTGATAA CANCAAAGCA
 GCGGTTTATC CAATTATTTA CAGTGACGAA GGTAAAGAAG AAACAGCCTA TGTGACCGTC
 AAACCCGACC AATCTAAGTT AGAGGTCAAA GATACAACGA TTTATGTTGG TGATTTCGTGG
 AAACCAGAAG ATAATTTTCGT TTCAGCGACA GACAAAACAG GTCAAGACGT NCCGTTTGAA
 AAAATTGATG TTCAGGGAAC AGTGAATGTT GATAAAATAG GCGATTATGA AATTGCTCTAT
 AAAAATGGCA NAAAAGAAGC GAAAGCAATC GTTCATGTCC GTGATGACAG TCAGTTAGAG
 GTTAAAGATA CAACGATTTA TGTGTTGAT TCGTGGAAC CAGAAGATAA TTTTCGTTTCA
 GCAACAGACA AAACAGGCCA AGACGTTCCG TTTGAAAAAA TCACTGTTTC AGGTCAAGTT
 GATACTAGCA AAGCAGGCGT TTATCCAATC GTTTACAGTT ACGAAGGTAA AGAAGAAACA
 GCTAATGTGA CTGTCAAACC CGACCAATCT AAGTTAGAGG TTAAAGATAC AACGATTTAT
 GTGGGCGATA AATGGGAACC AGAAGATAAT TTCGTTTCAG CAACAGACAA AACAGGTCAA
 GATGTCCCGT TTGAAAAAAT TGACGTTTCAG GGAACAGTGA ATGTTGATAA AATAGGCGAT
 TATGAAATTG TCTATAAAAA TGGCACAAAA GAAGCGAAAG CAATCGTTCA TGTCCGTGAT
 GACAGTCAGT TAGAGGTCAA AGATACAACA ATTTATGTGG GTGATAAATG GGAAGCAGAA
 GATAACTTCG TTTCCGCGAC AGACAAAACA GGTCAAGACG TTCCGTTTGA AAAAATTGAT
 GTTCAGGGAA CAGTGAATGT TGATAAAATA GGCGATTATG AAATTGTCTA TAAAAATGGC
 ACAAAGAAG CGAAAGCAAT CGTTCATGTC CGTGATGATA GTCGTTTACA AGTCAAGGAT
 ACAACGATTT ATGTCGGCGA TTCNTGGANA CCAGAAGNGA ACTTTGTTTC AGCNACAGAT
 AAAACAGGTC AAGATGTCCC ATTC

EF104-4 (SEQ ID NO:404)

VTTTEAQTE TTDATKEAE LSNSTPSLPL
 ATTTTSEMNO PTATTESQTT EASTTASSDA ATPSEQQTTE DKDTSLNEKA LPDVQAPITD
 ELLDSMSLAP IGGTEYSQTE VHRELNTTPV TATFQFAVGN TGYAPGSVYT VQLPEHLGYS
 TVSGEVTGIG ATWAVDAATK TLSITFNQRV SDTSFKVELK SYLTTEAEPL IKIETPGKNK
 KTYSFDLYEY VEPIQYNERT RTTGLDGEIF YNLDRTLGN QLELLTTET PGAVFGKQDN
 LEPQVFSYDV DINGQILPET QTLTTPGKDY TLDNSLGR IAVTPNMNQO KAYSL SINRT
 YLESASDYN YLYSQYPTT KIGSISLKST TGTQTTDFT AKTSQTSKVI ADREMRMSY
 ISFQSKGKYY VTIYGTLTET KVGQQIVLES TNGQEIKNPK FTAYGPLYEN VKLEDYFDIK
 TEGGKLTLTA TKDSYLRINI SDLTMDFDK DINLSLSTPV IGPNKAIQLV SDQYIEPISV
 VNPLNAETAW GNYDQNGAYS SRTTVSVMGS KEKPIQNLEI KVKHPNYLSL RATKEIYFYY
 KLGTDTYVTP TSDGSVIKFT TPITNEIQIP IGFNYVPDSL PKDKSIPVDT IPITMSAEG
 TPVDTTVTTN SKRGSERTLQ SSKNQFLVNA RNSFDSLSV RTKIPAGADV LFDIYDVSND
 QVDSIYPQYW DRGQYFDKPM TPNSPGYPTI TFDENTNSYT PFDGKTNKRY IIEYKNANGW
 IDVPTLYITG TAKEPQSNNN EGSASVSVQN EALDILSATQ AANPTLKNVT KTTVTTKNID
 NKTHRVKNPT IELTPKGTTN AQIDLNSITV KGVPELAYSL EKTNGAKVI PKDYTLTENI
 TIEYNTVSAN AGQIYTETTI DSETLNQMSA SKKKVTTAPI TLKFSEGD AE GIVYLATATF
 YTHNVEDENQ AIAKVSFELI DNVHTTATEF TTDEKGQYSF DAIMTGDYTL RVTNVPQEYS
 VDEEYLTGKA IKLVKGNQL KIPLTKTIDH SRLQVKDSTI YVGDSWKPEE NFVSATDKTG
 QDVPFEKITV SQQVDNXXKAG VYPIIYSDG KEETAYVTVK PDQSKLEVKD TTIYVGDSWK
 PEDNFVSATD KTGQDVPFEK IDVQGTVNVD KIGDYEIVYK NGXKEAKAIV HVRDDSQLEV
 KDTTIYVGDS WKPEDNFVSA TDKTGQDVPF EKITVSGQVD TSKAGVYPIV YSYEGKEETA
 NVTVPKPDQSK LEVKDTTIYV GDKWEPEDNF VSATDKTGQD VPFEKIDVQG TVNVDKIGDY
 EIVYKNGTKE AKAIVHVRDD SQLEVKDTTI YVGDKWEAED NFVSATDKTG QDVPFEKIDV
 QGTVNVDKIG DYEIVYKNGT KEAKAIVHVR DDSRLQVKDT TIYVGDSWXP EXNFVSATDK
 TGQDVPF

EF105-1 (SEQ ID NO:405)

TAAATGAAAA AAACAGTCGT CTAATCCTTG TTATTTCGAA CAATGTTGCT TGGCGCCACT
 GTTCCTGCTG AAGCGGCGAC GGTCGTTTTT GATAGCGAAC AGTCGATTGT TTTTACCCCA
 AGCACAGATG GGACGGATCC AGTAAATCCA GAAAATCCCG ATCCAGAAAA ACCAGTTTCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGTCGATC CAACGAATCC TGATGGACCT AATCCAGGTA CCCCTGGTCC ACTTTCCATC
 GATTATGCCT CAAGTTTGGA TTTTGGGAGT AATGAGATAT CGAATAAGGA TCAAACGTAT
 TTTGCCAGAG CGCAAACCTA TAGAAATCCA GATGGTTCAG CAAGTGAATT GGCAACTGCT
 AATTATGTAC AAGTAAGTGA TTTACGGGGA ACCAATGCTG GCTGGGTTTT AAAAGTGAAA
 CAAAATGGTC AATTTTCGTAA TGCAGAAACA TTACACAAAG AATTAACAGG CGCCACCGTC
 GCCTTTACTG AGCCCAAGTGT TCGCTCAAAT GCGACGGACG TATTGCCGCC AACTGCTACC
 GCAAACATTC AATTAGATGC TCGGGGCGCA GAAACTGTTG TCATGCAAGC CCCAGAAAAG
 ACCGGCGCCG GAACGTGGAT CACGCTGTGG GGGCAAGCAG AAAAAGTGAC CGAAAAAAT
 CAACAAGGAC AGCAAGTAA TGCCACAATC ACACGGGCAA TCTCACTAAC TGTTCCTGGG
 AAAACCCCTA AGGATGCAGT ACAATATAAA ACAACATTGA CTGCGCTACT TTCAGATGTA
 CCAGTAAATA ATGGAGGGAA ATAA

EF105-2 (SEQ ID NO:406)

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 VDPTNPDGPN PGTPGPLSID YASSLDGFSN EISNKDQTYF ARAQTYRNP GSASELATAN
 YVQVSDLRGT NAGWVLKVKQ NGQFRNAETL HKELTGATVA FTEPSVRSNA TDVLPPTATA
 NIQLDAAGAE TVVMQAPEKT GAGTWITLWG QAEKVTEKNQ QGQVQVNTIT RAISLTVPGK
 TPKDAVQYKT TLTWLLSDVP VNNGGK

EF105-3 (SEQ ID NO:407)

GGCGAC GGTCGTTTTT GATAGCGAAC AGTCGATTGT TTTTACCCCA
 AGCACAGATG GGACGGATCC AGTAAATCCA GAAAATCCCG ATCCAGAAAA ACCAGTTCGA
 CCAGTCGATC CAACGAATCC TGATGGACCT AATCCAGGTA CCCCTGGTCC ACTTTCCATC
 GATTATGCCT CAAGTTTGGA TTTTGGGAGT AATGAGATAT CGAATAAGGA TCAAACGTAT
 TTTGCCAGAG CGCAAACCTA TAGAAATCCA GATGGTTCAG CAAGTGAATT GGCAACTGCT
 AATTATGTAC AAGTAAGTGA TTTACGGGGA ACCAATGCTG GCTGGGTTTT AAAAGTGAAA
 CAAAATGGTC AATTTTCGTAA TGCAGAAACA TTACACAAAG AATTAACAGG CGCCACCGTC
 GCCTTTACTG AGCCCAAGTGT TCGCTCAAAT GCGACGGACG TATTGCCGCC AACTGCTACC
 GCAAACATTC AATTAGATGC TCGGGGCGCA GAAACTGTTG TCATGCAAGC CCCAGAAAAG
 ACCGGCGCCG GAACGTGGAT CACGCTGTGG GGGCAAGCAG AAAAAGTGAC CGAAAAAAT
 CAACAAGGAC AGCAAGTAA TGCCACAATC ACACGGGCAA TCTCACTAAC TGTTCCTGGG
 AAAACCCCTA AGGATGCAGT AC

EF105-4 (SEQ ID NO:408)

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 VDPTNPDGPN PGTPGPLSID YASSLDGFSN EISNKDQTYF ARAQTYRNP GSASELATAN
 YVQVSDLRGT NAGWVLKVKQ NGQFRNAETL HKELTGATVA FTEPSVRSNA TDVLPPTATA
 NIQLDAAGAE TVVMQAPEKT GAGTWITLWG QAEKVTEKNQ QGQVQVNTIT RAISLTVPGK
 TPKDAV

EF106-1 (SEQ ID NO:409)

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 AATCCCAATA ATTTAGGGGA TTTACCTGAG TATTTACGTT CAGTTGGTAT TAGACAAGAT
 GAAGGATTAT CAGAAAAAGA TTGGGCTGGA ACACGCGTTT ATGATCGAAA TGGGAATGAC
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 TATGAATTTT TTGATAAAGA GACTGGAGAA TCAACAGGAG ATGAAGGAAC CTTCCTTATG
 ACCGCTGGTA TTACAGATGT TTCCCGTCTT GTAATTATTT CTGAAACCAA AAATTATCAA
 GGTGTATACC CACTTAGAAC TTTATACCAA GATACTTTTA CGTATAGACA GATGGGGAAA
 GATAAAAACG GAAATGATAT TGAAGTTTTT GTAGAAAAA AAGCAACCTC AGGACCAGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TATGGTCGTC CGCAGCCATA CCCCAATAAT CGTCCCAGAA CACTAGAATT CACGAATGGA
 CGCCGTGCCA TGACAGAACA AACAGGCCAG ATTGATGTAA ATCGACAAGG GGATGAAATT
 ATTGGTAAAA CTCCTTTGA TGGGACACCG CAACTTCTTT GGAATGGCAC AAAAGTAGTG
 GATAAAGATG GCAATGACGT AACTTCGGCC AACCAAACT TTATCAGCTT AGCGAAATTT
 GACCAAGATA GCAGCAAATA TGAATTTTTT AATTACAAA CTGGTGAAAC TCGTGGCGAC
 TATGGCTACT TTAAAGTAGG AAATCAAAAT AAATTCCTG CCCATGTTTC CATTGGAACC
 AATCGCTATG GCGCTGTCTT AGAGTTAACA GAATGAATG ATAATCGTTT TACGTACACA
 CGAATGGGTA AAGATAACGA AGGAAACGAT ATCCAAGTCT ATGTGGAACA TGAACCATAC
 CAAGGAACCT TTAATCCTGA ATTTACCTTT TAA

EF106-2 (SEQ ID NO:410)

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 GLSEKDWAGT RYVDRNGNDL TDENQNLHA IKFDATTSFY EFFDKETGES TGDEGTFMT
 AGITDVSRLV IISSETKNYQG VYPLRTLYQD TFTYRQMGKD KNGNDIEVFV ENKATSGPVY
 GRPQYPNNR PRTLEFTNGR RAMTEQTGQI DVNRQGEII GKTSFDGTPQ LLWNGTKVVD
 KDNDVTSAN QNFISLAKFD QDSSKYEFFN LQTGETRGDY GYFKVGNQNK FRAHVSIGTN
 RYGAVALLETE LNDNRFTYTR MGKDNEGNDI QVYVEHEPYQ GTFNPEFTF

EF106-3 (SEQ ID NO:411)

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 TTAACAGATG AAAATCAAAA CCTATTACAT GCAATCAAAT TTGATGCAAC CACTAGTTTC
 TATGAATTTT TTGATAAAGA GACTGGAGAA TCAACAGGAG ATGAAGGAAC CTTCCTTTATG
 ACCGCTGGTA TTACAGATGT TTCCCGTCTT GTAATTATTT CTGAAACCAA AAATTATCAA
 GGTGTATACC CACTTAGAAC TTTATACCAA GATACTTTTA CGTATAGACA GATGGGGAAA
 GATAAAAACG GAAATGATAT TGAAGTTTTT GTAGAAAACA AAGCAACCTC AGGACCAGTT
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 TATGGCTACT TTAAAGTAGG AAATCAAAAT AAATTCCTG CCCATGTTTC CATTGGAACC
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EF106-4 (SEQ ID NO:412)

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 KDNDVTSAN QNFISLAKFD QDSSKYEFFN LQTGETRGDY GYFKVGNQNK FRAHVSIGTN
 RYGAVALLETE LNDNRFTYTR MGKDNEGNDI QVYVEHEPYQ GT

EF107-1 (SEQ ID NO:413)

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 CTTTATAGAG ACTATAGATT GAATTTTTAC ATAGAAAGAA GGAGCAAGAT GAAGCGAGTA
 AATTGGAAAA GATGGCTAGT TGTGGGTTA AGTTGTTCTT TGTTTATGGA TTCAGTGGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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CAGTCGAGTG ACGAAGCGAG CCAGACGACG CAAACAACCG AAGAGTCACA GGCAACGGTC
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GGTTATTCTT CTGTGGAAGG GCGCGAGATT CCCTTTTTCT TGTGGAGGA AGACGGGACG
TTGTTTGATC CCGACCGAAT TACGATGGCG GTCAATCTTT CCACGTTTTT GTTTTATGAA
GAGAAATTAC AACGAACCCC CCTTGAGCCC ACCACTGTGA ATGGCGGAAA GTTACTGTCT
ATTCCAACGT CACCAGCTTT TAAATATGAT ACAAATAACC AGAATCCAAG TAATATTTAT
GGCGTTTCTG AAGTGTCTGT TACTATTCCT AAGGAGTATC AAAGCCTGGA CATTTCGACCA
AGTACGTTTT ATACAGGAGA CACTACGCAA TATCCAGTGC CAACGGTTTT TCGCAACGTT
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GGGGATAAAA CCAAGTATCC AGTACCAAAT GAAGTGCGCC GTGGCATCGA AAACCCCGAC
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CAACAGTTCA CAGGCAGTGA CGTCTATCAG TTGGACTTCA CGTTTGCTAA CATCAAATA
GAAGTGCCAG CCAACCAAGG TATGGCTGGC CAACAATACC AAGCCGCCGT CACGTGGAAT
TTAGTGACTG GCCCTTAA

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EF107-2 (SEQ ID NO:414)

MKRVN

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SEAKTVPPQE TARIASRAIG YSSVEGREIP FFFVEEDGTL FDPDRITMAV NLSTFSFYEE

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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QDKKTIVTGE DFTFTQEGTL PERYTGS DGK TYLFGWYKG NAKPSTLETT KTPSYAVTYD
DNDDLHVVE EAVMKYTLTP AREALFGYVD EQGNLINPAK FKLSATMGES DGATGEMTTF
PTIDGIDMPA SQLKKLAIPQ KVTYTRPDDGT IVTYGPQEVs VEIPKYQTI SISPTTAYTG
DKTKYPVNE VRRGIENPDN IVSSLVGXXA YNLTKQSATR YTARRSYWXW GPTKTLYSMS
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GQNTKAFFVT KEQWTTGAGV SITLDQPLPA GGQLKMNLLG TAVTGNPGQV LTADVEVTGN
FGSLTAKDTV RIKDLQDEIT SPDGDGFIST PTFDFGKLAI SGSKQYGLK KAADYYGNGT
RNPYLRLNTS QANWSLTAQL SQPKSATDSL PTTTRLLLGTT AAAASF TDYN QPTETRTPLG
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VTGP

EF107-3 (SEQ ID NO:415)

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ACTAGTTTCG ACCAAAGACG AGGAACAGCG GGTCTCTGTG ATTATTATTT AACAAAGCGG
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GTCTACACTG TCGCAAAAGC TTTGCCGAAG ATCTACCAAG CTGGTGAAAA AACCTATATC
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ACGGGTCAAA ACACCAAAGC TTTTCTGTG ACCAAGAAGC AATGGACGAC CCGTGCAGGA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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GTGTCCATCA CGTTGGATCA GCCTTTACCA GCTGGCGGTC AATTAAAAAT GAACTTATTA
GGAACCGCCG TTACAGGAAA TCCTGGTCAA GTTTTAACCG CTGATGTTGA AGTAACGGGC
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ATTTCAGGAA GTAAGCAACA ATATGGTTTG AAGAAGGCCG CAGATTACTA CGGCAATGGC
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CTATCGCAAC CAAAATCAGC CACAGACAGC TTGCCAACAA CGACCCGCTT GTTGCTAGGA
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GGCAAGACCA GCACCGTGAC TTTAACC GCCAATACCG CAACAGCGGT GGTGCGAAAC
CAACAGTTCA CAGGCAGTGA CGTCTATCAG TTGGACTTCA CGTTTGCTAA CATCAAATA
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EF107-4 (SEQ ID NO:416)

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EF108-1 (SEQ ID NO:417)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACCGAGCCTT TGGCCACCAC TAAAACACCT AGCTATAAAG TCACGTATGA TGACAATGAT
 GATTTGACGG TGGTCTATGA GGAGTTTTC A GGTACGAGC TGCCTGCTTC GACCAATCAA
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 AGCTTAACAG CCAACAACAC AGCAACGAGT ATTATTGCCA ACAAGCAATT CACAGGTAGT
 AATGTTTATC AGTTGGACTT CACCTTCAAT AATGTCAAAC TTGAAGTGCC AGCCAATCAA
 GGTGTTAAAG GGCAACAATA CAAGGCCGCA GTTACATGGA ACCTAGTTAC AGGTCCTTAA

EF108-2 (SEQ ID NO:418)

MKQTKWQ RLATIGLCSS LVINAFSGVT AVAETVTIES SPTAESSAKE
 ETQASSVKEE TTKASTENSQ VTDTSQEEA TKEAEKEEPQ AEVEQAETPI IPKPKKINMK
 ATYSFSAETY QFGFVNESGQ LINPDIIPIT YSYAKGSWKT DGYNRKWTSM VQGSASTVGN
 LKNVIMPATS SVMPPGSPYE GTQEVYTNFS IRIKYYASA SLYNREGKID STYPLPAIAL
 AGTRPLSLTQ VSVISALALT SKGDNVYTPR ETFFGGDPAG VKFTNFLYRI NDFDVKGNNI
 GYKTVSSPIY YHLTNRRVTE NFVDTSGAKI TPPSNFTQ GK QTVINSDPYT FQSGFLPET

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

YKVGTKSYRF KGWYKGKTKT EPLATTKTPS YKVTYDDNDD LTVVYEEFSG YELPASTNQF
 GFVDEATNKL IAPDQVQMKY NLTLNENNK TVMSSNLTGT DTATLKNLSV PVNYFEQYRV
 NTFYGASDIT FTLPKRYKSI NITKSDGKTD PAFPLPKIYN IDQVEMSHMP VTTYNKLKQL
 SGQTFGFNAL ADQPEFYTKT LFGTESGIDD PVNYYTMSGP VYYYLENRKV TENFVDINGA
 KITPPTGFTQ GKKTIVITSDA YTFKQAGTLP DTYTTGGKTY KFKGWYKGKS ILNLTITTKA
 PSYQVITYDDN DDLNVVYEEE TVTTVYPSVD MNFVNEKGGG FTPALTFSGK YYAQSTSAYL
 RTDLYDVTSK NNGNGQYTVS INNGSMPLSQ ELLKKNNGQ PISATNRLQF NVDKLAIQQ
 LKYVDSIQLD TAQSSNLKSY RYVYTNNSSL VFDPNVAPAE VDLSSSESLN LNFDSDGTYF
 SNANNRLFYT HLGYSGTGPGV NYLLVMFLFN AKPADKSKLV YKVRKQVTE NFVDVNGAKI
 TAPTGTFTQGN QVPMNSNTFK YTAALKALPAT YTTGGKVYTF QGWYKGKTKP STLNKTITPT
 FNATFDGND MTAMYKEEIP TASVTLTRPK EVIDTNTNVI WTTTITNTSK APLQNLTLKK
 GPNWSAGLTI PTFMEVTPEG ETTKSIPVNS TLWTEGVPLP NAVPIGKKVS VAFTRATGK
 PNTVLKAEVV VFGGIKIDSTV DNFVRIRPND QEVVPTTEG FISVPTDFG QVGAGTKQQ
 HSLKQAADYY GNGTRNPYLR IKKTQPNWSL TAQLSQPKSA TDSLPTATRL LLGAAPVSSF
 TNYNQPTLTK NTVGTTSAIS LTANNTATSI IANKQFTGSN VYQLDFTFNN VKLEVPANQG
 VKGQQYKAAV TWNLVTGP

EF108-3 (SEQ ID NO:419)

CGT GACGATTGAA AGTAGTCCGA CCGCCGAAAG TAGTGCCAAG
 GAAGAGACGC AAGCAAGTAG CGTGAAGGAA GAAACAACGA AAGCCAGTAC GGAAAAAGT
 CAAGTAACAA CTGACACGAG TCAGGAAGAA GCAACGAAAG AAGCGGAGAA AGAAGAACCG
 CAAGCAGAAG TGGAACAAGC AGAAACACCA ATCATTCCTA AACCAAAAAA AATCAATATG
 AAGGCAACTT ATTCATTTTC TGCAGAACT TATCAGTTTG GATTTGTGAA TGAATCAGGT
 CAATTAATAA ATCCAGATAT TATACCAATT ACGTATAGCT ATGCCAAAGG ATCATGGAAG
 ACAGATGGTT ATAATCGAAA GTGGACTAGT ATGGTTCAAG GGAGTCTTC AACCGTAGGA
 AACTTAAAGA ATGTAATAAT GCCAGCACT TCTGTAGTTA TGCCACCAGG ACCGTCATAT
 GAAGGAATC AAGAGGTGTA CACAACTTT TCAATTCGCA TACCAAAATA TTATGCATCA
 GCGAGTCTCT ACAATAGAGA AGGTAAATTT GATTCTACTT ATCCGTTACC TGCTATTGCA
 CTAGCAGGTA CTAGACCGCT ATCTTTGACT CAAAGTAGTG TAATTAGTGC ATTGGCGCTG
 ACCAGTAAAG GAGACCAATGT TTATACACCA CGGGAAACAT TTTTGTGAGG AGATCCTGCA
 GGTGTAAAGT TTACTAATTT TTTGTATCGT ATAAATGACT TTGATGTGAA AGGTAATAAC
 ATAGGTTATA AGACTGTGAG TAGCCCAATC TATTACCATC TGACCAACCG CCGTGTCAAC
 GAAACTTCG TAGATACAAG TGGCGCCAAA ATCAGGCCAC CAAGTAATTT CACCAAGGG
 AAACAAACGG TCATTAACAG TGATCCTTAC ACGTTCCAAC AAAGTGGTTT TTTACCGGAG
 ACCTACAAAG TTGGCAGCAA ATCTTACCGA TTCAAAGGCT GGTACAAAGG GAAAACCAAA
 ACCGAGCCTT TGGCCACCAC TAAACACCT AGCTATAAAG TCACGTATGA TGACAAATGAT
 GATTGTACCG TGGTCTATGA GGAGTTTCA GGGTACGAGC TGCCTGCTTC GACCAATCAA
 TTTGGCTTTG TGGATGAAGC GACGAACAAA TTAATTGCCC CCGACCAAGT GCAGATGAAG
 TATAATCTTA CTTTAAATGA AAATAATAAA AAAACAGTAA TGAGCAGTAA CTTAACGGGG
 ACAGATACAG CGACACTGAA AAACITGTCC GTGCCTGTCA ACTATTTTGA ACAATATCGC
 GTCAATACGT TTTATGGCGC GAGTGACATT ACGTTTACAT TGCCCAACAG GTACAAATCA
 ATCAATATTA CCAATCAGA TGGCAAAACC GACCCAGCTT TTCCTCTTCC TAAATCTAT
 AATATAGATC AAGTAGAAAT GTCACACATG CCTGTGACCA CTTATAACAA GTTGAAACAG
 CTGTGGGGCC AAACGTTTGG CTTTAATGCT TTAGCCGATC AACCTGAATT TTATACGAAA
 ACGTTATTG GGACAGAGTC TGGCATCGAT GACCCAGTCA ATTATTATAC AATGAGTGGC
 CCTGTTTACT ATTATTTAGA AAACCGCAAA GTCACCGAGA ACTTCGTAGA CACCAACGGC
 GCTAAATCA CACCGCCAAC AGGTTTCACC CAAGGTAAAA AAACGGTGAT TACAAGCGAC
 GCCTACACTT TCAAACAAGC AGGCACCTTA CCAGACACTT ACACAACAGG CGGTAAGACC
 TACAAGTTA AAGGTTGGTA CAAAGGCAAG TCCATACTCA ACACATTGAC AACTACCAAA
 GCGCCAAGTT ATCAAGTGAC CTACGATGAC AATGATGATT TGAATGTGGT GTATGAAGAA
 GAAACAGTTA CGACAGTGTA TCCATCAGTC GATATGAACT TTGTGAATGA AAAAGGCGGG
 GCTTTCACAC CGGCGTTAAC TTTTAGTGGT AAGTACTATG CGCAAAGTAC GAGTGCCTAC
 TTAAGAACCG ATTTATATGA CGTGACCTCA AAAAATAATG GTAATGGGCA ATATACGGTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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AGTATTAATA ATGGTAGTAT GCCATTGTCC CAAGAATTAT TGAAAAAATA TAATAATGGA
CAACCAATCA GTGCTACCAA CAGATTACAG TTTAATGTTG ATAAATTAGC CATCGACCAA
CAACTAAAAT ATGTTGACAG CATTCAATTA GACACAGCTC AAAGTAGCAA TCTGAAATCC
TATAGATATG TGTACACGAA CAATAGCTCA CTGGTTTTTCG ACCCAAATGT AGCACCAGCA
GAGGTTGACC TTAGTTTACA ATCTCTTAAC TTGCTTAATT TTGATTCAGA TGGCACCTAT
TTTTCTAATG CAAATAATAG ACTTTTTTAC ACGCATTTAG GATATAGTGG CACACCAGGA
GTTAACATATC TTCTCGTAAT GTTTC'TTTT AAGCCCAAAC CTGCGGATAA GTCAAAACTT
GTCTACAAAG TCAC'TCGCAA ACAAGTCACC GAAAAC'TTCG TGGATGTCAA CCGTGCCAAA
ATCACTGCAC CAACAGGCTT CACCCAAGGT AACCAAGTAC CAATGAACAG TAACACCTTC
AAGTACACAG CGGCAAAAGC TTTACCAGCG ACGTATACTA CAGGTGGCAA AGTCTATACG
TTCCAAGGGT GGTATAAAGG GAAAACCAAG CCAAGTACGT TGAACAAAAC AACAACTCCA
ACGTTTCAATG CGACCTTTGA TGGCAATGAC GATATGACCG CCATGTATAA GGAAGAAAATA
CCAACAGCTA GTGTCACATT AACTCGACCA AAAGAAGTGA TTGATACGAA TACCAATGTA
ATCTGGACAA CAACGATCAC GAATACTAGC AAAGCACCCCT TACAAAATCT CACCTTGAAA
AAAGGGCCCA ATTGGTCAGC TGGTCTGACG ATCCCGACCT TTATGGAAGT GACACCAGAA
GGAGAAACGA CAAAATCAAT CCCAGTAAAT AGTACACTTT GGACAGAGGG GGTTCCTTTA
CCAAATGCGG TTCCTATCGG CAAAAAAGTT TCAGTTGCTT TCACAAC'TCG CGCAACAGGG
AAACCAAACA CTGTTTTGAA AGCAGAAGTT GTAGTATTTG GTGGTATTAA AGATAGTACA
GTGGATAACT TCGTGAGAAT TCGTCCAAAT GATCAAGAAG TAGTCACACC AACGACCGAA
GGCTTCATCA GTGTGCCAAC CTTCGACTTC GGCCAAGTGG GCGTTGCAGG AACTAAGCAA
CAACACAGCT TGAACAAGC CGCGGATTAC TACGGTAACG GCACACGGAA TCCGTATCTG
CGGATTAAAG AAACGCAACC CAATTGGAGC TTAACAGCGC AACTGTCAAC ACCAAAATCA
GCGACAGACA GCTTGCCCTAC AGCGACCCGC TTATTATTAG GGGCGGCGCC TGTCTCTAGC
TTTACCAATT ACAATCAACC AACCAGATTG AAAAATACGG TCGGTACCAC GAGTGCCATT
AGCTTAACAG CCAACAACAC AGCAACGAGT ATTATTGCCA ACAAGCAATT CACAGGTAGT
AATGTTTTATC AGTTGGACTT CACCTTCAAT AATGTCAAAC TTGAAGTGCC AGCCAATCAA
GGTGTTAAAG GGCAACAATA CAAGGCCGCA GTTACATGGA ACCTAGTTAC AG

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EF108-4 (SEQ ID NO:420)

VTIES SPTAESSAKE

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ETQASSVKEE TTKASTENSQ VTTDTSQEEA TKEAEKEEPQ AEVEQAETPI IPKPKKINMK
ATYSFSAETY QFGFVNESGQ LINPDIIPIT YSYAKGSWKT DGYNRKWTSM VQGSASTVGN
LKNVIMPATS VMPPPGPGSYE GTQEVYTNFS IRIPKYAYASA SLYNREGKID STYPLPAIAL
AGTRPLSLTQ SSVISALALT SKGDNVYTPR ETFFGGDPAG VKFTNPLYRI NDFDVKGNNI
GYKTVSSPIY YHLTNRRVTE NFVDTSGAKI TPPSNFTQ GK QTVINSDPYT FQSGFLPET
YKVGTKSYRF KGWYKGKTKT EPLATTKTPS YKVTYDDNDD LTVVYEEFSG YELPASTNQF
GFVDEATNKL IAPDQVQMKY NLTLNENNKK TVMSSNLTGT DTATLKNLSV PVNYFEQYRV
NTFYGASDIT FTLPKRYKSI NITKSDGKTD PAFPLPKIYN IDQVEMSHMP VTTYNKLKQL
SGQTFGFNAL ADQPEFYTKT LFGTESGIDD PVNYTMSGP VYYYLENRKV TENFVDNNGA
KITPPTGFTQ GKKTIVITSDA YTFKQAGTLP DTYTTGGKTY KFKGWYKGS ILNTLTTTKA
PSYQVYDDN DDLNVVYEEE TVTIVYPSVD MNFVNEKGA FTPALTFSGK YYAQSTSAYL
RTDLYDVTSK NNGNGQYTVS INNGSMPLSQ ELLKKYNNQ PISATNRLQF NVDKLAIQQ
LKYVDSIQLD TAQSSNLKSY RYVYTNNSSL VFDPNVAPAE VDLSSSESLNL LNFDSDGTYF
SNANNRLFYT HLGYSPTPGV NYLLVMFLFN AKPADKSKLV YKVTRKQVTE NFVDVNGAKI
TAPTGTQGN QVPMNSNTFK YTAALPAT YTTGGKVYTF QGWYKGKTKP STLNKTTTPT
FNATFDGND MTAMYKEEIP TASVTLTRPK EVIDTNTNVI WTTTITNTSK APLQNLTLKK
GPNWSAGLTI PTFMEVTPG ETTKSIPVNS TLWTEGVPLP NAVPIGKVS VAFTRATGK
PNTVLKAEVV VFGGIKSTV DNFVIRPNQ QEVVTPPTG FIVSPTFDG QVGVAGTKQQ
HSLKQAADYY GNGTRNPYLR IKKTQPNWSL TAQLSQPKSA TDSLPTATRL LLGAAPVSSF
TNYNQPTL NTVGTTSAIS LTANNTATS IANKQFTGSN VYQLDFTFNN VKLEVPANQ
VKGQQYKAAV TWNLV

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EF109-1 (SEQ ID NO:421)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AGGAGTAAAT TAATGAAAAA AAGTGTATA ACTAGTTCTA TGTTAGCGGT TTTGTTGTCG
 GGATTTCTCG TTACCCCTAT TTCTGCTTAC GCTTTGGAAC GCTCTAAGGG AACTACTGAA
 GAAACGGTGG CTTCAGAAAC ATCTCTAACG GAGCGACAAA TGAGTAGCGG TGTCACTGAA
 GAAATGAACC CAAGCATCAT AAATTCTCAA GAGGAAACAG AAACAACGTC CACTTCCTCA
 ACCTCCGATT CCACCACTGA AGTTTCTACA TCAGAAGTAA CAACTGTTAA TGATACAGAA
 NATAGTAGCG ACGTACTGAA ACTACTTTGG NAACATCACN AAGTAATGAG GACACACCTA
 TAG

EF109-2 (SEQ ID NO:422)

MKKSVI TSSMLAVLLS GFLVTPISAY ALERSKGTTE ETVASETSLT ERQMSSGVTE
 EMNPSIINSQ EETETTSTSS TSDSTTEVST SEVTTVNDTE XSSDVLKLLW XHHXVMRTHL

EF109-3 (SEQ ID NO:423)

GGAAC GCTCTAAGGG AACTACTGAA
 GAAACGGTGG CTTCAGAAAC ATCTCTAACG GAGCGACAAA TGAGTAGCGG TGTCACTGAA
 GAAATGAACC CAAGCATCAT AAATTCTCAA GAGGAAACAG AAACAACGTC CACTTCCTCA
 ACCTCCGATT CCACCACTGA AGTTTCTACA TCAG

EF109-4 (SEQ ID NO:424)

ERSKGTTE ETVASETSLT ERQMSSGVTE EMNPSIINSQ EETETTSTSS TSDSTTEVST S

EF110-1 (SEQ ID NO:425)

TAAATAAAAA TGGATAAGGA GTGGCATAAT CTTATGAAAA AGTTCTCCAT ACGAAAAATT
 AGTGCCTGGT TTTTCTTTCT GATTTTAGTA ACTTTGATCG CCGGTTTTAG CTTGTCTGCA
 AATGCAGAA AGTATATCGT TCCTGCCGAA AGTCATTAC GACAAAAAAG ATCGTTACTG
 GACCCCTGAG ACAGAAGACA AGAAGTGGCA GATACAACCG AAGCGCCTTT TCGCTCAATC
 GGAAGAATCA TTTCCCTG CAGTAAACCA GGCTATATTT CTTTAGGAAC AGGCTTTGTT
 GTTGAACCA ATACAATTGT CACCAATAAT CATGTGGCTG AAAGTTTTAA GAATGCCAAA
 GTATTAAATC CGAATGCCAA AGATGATGCT TGGTTTTATC CAGGTCGAGA TGGCAGTGCG
 ACACCATTTG GCAAATTCAG AGTGATTGAT GTAGCTTTTT CCCCGAATGC GGATATTGCG
 GTAGTGACTG TCGGCAACA AAACGATCGT CCAGATGGCC CAGAGTTGGG AGAAATTTTA
 ACGCCATTG TTTTGAAAAA GTTTGAATCT TCAGATACCC ATGTCACAAT ATCAGGCTAT
 CCAGGTGAGA AAAACACAC ACAATGGTCT CATGAAAAATG ATTTGTTTAC ATCTAACTTT
 ACAGACTTAG AAAATCCATT ACTATTTTAT GATATCGATA CAACCGGCGG TCAATCTGGT
 TCACCAATCT ATAATGATCA GGTGAAGTA GTTGGTGTTC ATTCCAATGG CGGCATTAAG
 CAAACAGGAA ATCATGGTCA AAGACTAAAT GAAGTGAATT ATAACTTTAT TGTTAATCGA
 GTGAATGAAG AAGAAAAATA ACGTTTATCC GCTGTGCCAG CAGCGTAA

EF110-2 (SEQ ID NO:426)

MKKFSIRKIS AGFLFLILVT LIAGFSLSAN AEEYIVPAES HSRQKRSLLD
 PEDRRQEVAD TTEAPFASIG RIISPASKPG YISLGTGFVV GTNTIVTNNH VAESFKNKV
 LNPNAKDDAW FYPGRDGSAT PFGKFKVIDV AFSPNADIAV VTVGKQND RP DGPELGEILT
 PFVLKKFESS DTHVTISGYP GEKNHTQWSH ENDLFTSNFT DLENPLLFYD IDTTGGQSGS
 PIYNDQVEVV GVHNSGGIKQ TGNHGQRLNE VNYNFIVNRV NEEENKRLSA VPAA

EF110-3 (SEQ ID NO:427)

AG AGTATATCGT TCCTGCCGAA AGTCATTAC GACAAAAAAG ATCGTTACTG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GACCCTGAGG ACAGAAGACA AGAAGTGGCA GATACAACCG AAGCGCCTTT TCGGTCAATC
 GGAAGAATCA TTTCCCTG CAGTAAACCA GGCTATATTT CTTTAGGAAC AGGCTTTGTT
 GTTGGAACCA ATACAATTGT CACCAATAAT CATGTGGCTG AAAGTTTAA GAATGCCAAA
 GTATTAAATC CGAATGCCAA AGATGATGCT TGGTTTATC CAGGTCGAGA TGGCAGTGCG
 ACACCATTTG GCAAAATCAA AGTGATGAT GTAGCTTTTT CCCCGAATGC GGATATGCG
 GTAGTGACTG TCGGCAAAACA AAACGATCGT CCAGATGGCC CAGAGTTGGG AGAAATTTTA
 ACGCCATTTG TTTTGAAAAA GTTTGAATCT TCAGATACCC ATGTCACAAT ATCAGGCTAT
 CCAGGTGAGA AAAACCAACAC ACAATGGTCT CATGAAAATG ATTTGTTTAC ATCTAACTTT
 ACAGACTTAG AAAATCCATT ACTATTTTAT GATATCGATA CAACCGCGG TCAATCTGGT
 TCACCAATCT ATAATGATCA GGTGGAAGTA GTTGGTGTTC ATTCCAATGG CGGCATTAAAG
 CAAACAGGAA ATCATGGTCA AAGACTAAAT GAAGTGAATT ATAACCTTTAT TGTTAATCGA
 GTGAATGAAG AAGAAAATAA ACGTTTATCC GCTGTGCCAG CAGCGT

EF110-4 (SEQ ID NO:428)

EYIVPAES HSRQKRSLLD

PEDRRQEVAD TTEAPFASIG RIISPASKPG YISLGTGFVV GTNTIVTNNH VAESFKNKV
 LNPNAKDDAW FYPGRDGSAT PFGKFKVIDV AFSPNADIAV VTVGKQND RP DGPELGEILT
 PFVLKKFESS DTHVTISGYP GEKNHTQWSH ENDLFTSNFT DLENPLLFYD IDTTGGQSGS
 PIYNDQVEVV GVHSGNGIKQ TGNHGQRLNE VNYNFIVNRV NEEENKRLSA VPAA

EF111-1 (SEQ ID NO:429)

TGATCAATAC ACTTCGATAC GGTGCTTTTT TTTCTAGAGA AAGTTGAATC TTTCAATAAT
 AAAAAGGGAT ACACCTCATT TGGCATAGTC CTTGCTGATA ATAAATCAGT GTATAAAGCG
 CTATCATTTT ATAGGAGGGG TTTTATGAAG GGTTTATCAA AAAAGAAACG GGTGCTACT
 TGGTTAGCGT TAGGAATCAC CGTAGTCAGC TGTTTTCGCT TAAGCAGGGA AGTGCAAGCA
 AGTGTGAAA GAACAAAAGT TGATGAATTT GCAAATGTTT TAGATGTGAG TGCATCACCA
 ACCGAACGGA CGAATGGCGT ATACGATACC AATTATTTTA ATAATTTTTT TGATTTAGGT
 GCATGGCATG GCTACTATTT ACCTGAAAAA AGCAATAAAG AGCTACTGGG TGGTTTTGCG
 GGGCCATTGA TTATTGCGGA AGAATATCCA GTAAACTTGG CGGCAAGTTT AAACAAATTA
 ACGGTCAAAA ATAAAAAAC GGGAGAAACC TATGATTTAA GCCAAAGCAA CCGCATGGAC
 CTGCTTTATT ATCTGGGCG CCTAGAGCAA ACCTATGAAT TAGACGATTT AACGATTCAT
 TTAGCTTTAA TTTTGTGAG CAATCGAAGC GCGCTTATCC AAACGACACT TGAAAACACT
 GGTGAAGAGC CTTGTGACT TGGAGCAAGC TGGACAGGTG CGGTCITTGA CAAAATTCOA
 GAGGGAACGG AAACCTTAGA TATTGGCACT CGTTTAACTG CTAAAGACAA TGACATTCAA
 GTGAATTTTG GTGAAGTCAG AGAAACGTGG AATTATTTTG CTACGAAAGA CACAAAATAT
 ACGATTCATC ATGCGGATAA AGTTTCAACA AAAATTGATA ATCGGAATTA TACAGCAACC
 GCTGAACCAA TTGAATTGAA GCCTAAACAA ACGTACAACA CCTATACGAC AGAAAGCTAT
 ACTTTTACAA AAGAAGAAGA GGCAAGGAA CAACAACAAG CACCCGAATA TACCAAAAAT
 GCGGCGCGCT ATTTCAAAGA GAACAAGCAA AGATGGCAAG GATATCTAGA TAAAACGTTT
 GATCAAAAGA AAACAGCAGA ATTTCTGAA TATCAAAATG CGCTAGTCAA ATCGATTGAA
 ACGATTAAATA CCAATTGGCG AAGTGGCGCA GGTGCCTTTA AGCATGACGG GATTGTTCCG
 TCCATGCTTT ATAAATGGTT TATTGGTATG TGGGCTTGGG ATTCGTGGAA AGCGGATGTA
 GCAACGCGTG ATTTTAAATCC TGAGTTAGCT AAAAATAATA TGCGGGCCTT GTTTGATTAT
 CAAAATTCAAA AAGATGATAC CGTACGTCCA CAAGATGCAG GAGCGATCAT TGATGCTGTC
 TTTTACAATC AAGACAGTGC GCGTGGTGGT GAAGGTGGCA ACTGGAATGA ACGAAATCT
 AAACCAACCAT TGGCTGCATG GGCAGTTTGG CATATTTATC AAGAAACCAA AGATAAGGAA
 TTTTAAAAAG AAATGTATCC CAACTTGTG GCTTATCATA ATTGGTGGTA TACCAACAGA
 GACCACAATA AAAATGGGAT AGCAGAATAT GGAAGCATGG TCAGTGATGC TCACTGGCAA
 AAAGAGGACA AGGATCAAAT CATTAAAGAT AAAAATGGCC ACCTAAAGTG GATGATGATG
 CTGTTATTTGA AGCAGCGCG TGGGAAAGTG GCATGGATAA CGCTACACGG TTTGACAAAG
 AAGGTGTGGG CAAAGGCGAC GTTGGAGTTA AAGTTTTTGA AAACAAAAAT AAAGGAAAAG
 TAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF111-2 (SEQ ID NO:430)

MKG LSKKKRVSTW

LALGITVWSC FALSREVQAS VERTKVDEFA NVLDVSASPT ERTNGVYDTN YFNNFSDLGA
 WHGYLPEKS NKELLGGFAG PLIIAEEYPV NLAASLNKLT VKNKKTGETY DLSQSNRMDL
 SYYPGRLEQT YELDDLTIHL ALIFVSNRTA LIQTTLENTG EEPLSLGASW TGAVFDKIQE
 GTETLDIGTR LTAKDNDIQV NFGEVRETWN YFATKDTKYT IHHADKVSTK IDNRNYTATA
 EPIELKPKQT YNTYTTESYT FTKEEEAKEQ QQAPEYTKNA ARYFKENKQR WQGYLDKTFD
 QKKTAEFPEY QNALVKSJET INTNWSAAG AFKHDGIVPS MSYKWFIMGW AWDSWKADVA
 TADFNPELAK NNMRALFDYQ IQKDDTVRPQ DAGAIIDAVF YNQDSARGGE GGNWNERNSK
 PPLAAWAVWH IYQETKDKEF LKEMYPKLVA YHNWWYTNRD HNKNGLIAEYG SMVSDAHWQK
 DDKDQIIKDK NGHLKWMMLL LLKQPRGKVA WITLHGLTKK VWAKATLELK FLKTKIKEK

EF111-3 (SEQ ID NO:431)

TGATGAATTT GCAAATGTTT TAGATGTGAG TGCATCACCA
 ACCGAACGGA CGAATGGCGT ATACGATACC AATTATTTTA ATAATTTTTC TGATTTAGGT
 GCATGGCATG GCTACTATTT ACCTGAAAAA AGCAATAAAG AGCTACTGGG TGGTTTTGCG
 GGGCCATGA TTATTGCGGA AGAATATCCA GTAAACTTGG CGGCAAGTTT AAACAAATTA
 ACGGTCAAAA ATAAAAAAC GGGAGAAACC TATGATTAA GCCAAAGCAA CCGCATGGAC
 CTGTCTTATT ATCTGGGCG CCTAGAGCAA ACCTATGAAT TAGACGATTT AACGATTCAT
 TTAGCTTTAA TTTTGTGTCAG CAATCGAAGC GCGCTTATCC AAACGACACT TGAAAACT
 GGTGAAGAGC CTTGTGCTACT TGGAGCAAGC TGGACAGGTG CCGTCTTTGA CAAAATTCAA
 GAGGGAACGG AAACCTTAGA TATTGGCACT CGTTTAACTG CTAAAGACAA TGACATTCAA
 GTGAATTTTG GTGAAGTCAG AGAAACGTGG AATTATTTTG CTACGAAAGA CACAAAATAT
 ACGATTTCATC ATGCGGATAA AGTTTCAACA AAAATTGATA ATCGGAATTA TACAGCAACC
 GCTGAACCAA TTGAATTGAA GCCTAAACAA ACGTACAACA CCTATACGAC AGAAAGCTAT
 ACTTTTACAA AAGAAGAAGA GGCAAGGAA CAACAACAAG CACCCGAATA TACCAAAAAT
 GCGGCGCGCT ATTTCAAAGA GAACAAGCAA AGATGGCAAG GATATCTAGA TAAAACGTTT
 GATCAAAAAGA AAACAGCAGA ATTTCTTGAA TATCAAAATG CGCTAGTCAA ATCGATTGAA
 ACGATTAAATA CCAATTGGCG AAGTGGCGCA GGTGCCTTTA AGCATGACGG GATTGTTCGG
 TCCATGTCTT ATAAATGGTT TATTGGTATG TGGGCTTGGG ATTCGTGGAA AGCGGATGTA
 GCAACGGCTG ATTTTAATCC TGAGTTAGCT AAAAATAATA TGCGGGCCTT GTTTGATTAT
 CAAATTCAAA AAGATGATAC CGTACGTCCA CAAGATGCAG GAGCGATCAT TGATGCTGTC
 TTTTACAATC AAGACAGTGC GCGTGGTGGT GAAGGTGGCA ACTGGAATGA ACGAAATTCT
 AAACCAACCAT TGGCTGCATG GGCAGTTTGG CATATTTATC AAGAAACCAA AGATAAGGAA
 TTTTAAAAAG AAATGTATCC CAAACTTGTG GCTTATCATA ATTGGTGGTA TACCAACAGA
 GACCACAATA AAAATGGGAT AGCAGAATAT GGAAGCATGG TCAGTGATGC TACTGGCAA
 AAAGACGACA AGGATCAAAT CATTAAAGAT AAAAATGGCC ACCTAAAGTG GATGATGATG
 CTGTTATTGA AGCAGCCGCG TGGGAAAGTG GCATGGATAA CGCTACACGG TTTGACAAAG
 AAGGTGTGGG CAAAGCGGAC GTTGGAGTTA AAGTT

EF111-4 (SEQ ID NO:432)

DEFA NVLDVSASPT ERTNGVYDTN YFNNFSDLGA

WHGYLPEKS NKELLGGFAG PLIIAEEYPV NLAASLNKLT VKNKKTGETY DLSQSNRMDL
 SYYPGRLEQT YELDDLTIHL ALIFVSNRTA LIQTTLENTG EEPLSLGASW TGAVFDKIQE
 GTETLDIGTR LTAKDNDIQV NFGEVRETWN YFATKDTKYT IHHADKVSTK IDNRNYTATA
 EPIELKPKQT YNTYTTESYT FTKEEEAKEQ QQAPEYTKNA ARYFKENKQR WQGYLDKTFD
 QKKTAEFPEY QNALVKSJET INTNWSAAG AFKHDGIVPS MSYKWFIMGW AWDSWKADVA
 TADFNPELAK NNMRALFDYQ IQKDDTVRPQ DAGAIIDAVF YNQDSARGGE GGNWNERNSK
 PPLAAWAVWH IYQETKDKEF LKEMYPKLVA YHNWWYTNRD HNKNGLIAEYG SMVSDAHWQK
 DDKDQIIKDK NGHLKWMMLL LLKQPRGKVA WITLHGLTKK VWAKATLELK

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF117-1 (SEQ ID NO:433)

TAATTCGATG GAGAAGGTGG TTTAGTGAAA AGATTTTCAT TTTTTTTACT AATTTTACTT
 GCTTTAACAG GTTGTAATC CGGTGAAAAA GAATTTGATG AAGAATCTCT TCAAAATCTA
 AAGGAAACGN CACAGTCTTA NTCAGAAACA GAATTACAAA ATGGTGACGT TCGTTTAAAT
 GAATATATTT CTTTGAAAGG GGAGATTGTT GAGAGTGACA GTCGTTCCAG TTTAATAAAA
 AAAGGTGATC GTTTTATTTT GAAAAGTGGT TCTAGTAAAT ATCAAGTTTN TAATGAGCAA
 AAGAAAAAAT TGAAGATTGG TGACGAAGTG ACAGTTTACG GAGAATATTA CGGCTTTTTG
 AAAGGGACAT TAATTGAAAG TGAGGAGAAT CATGATTCAG CCACGAATTA G

EF117-2 (SEQ ID NO:434)

VKR FSFFLLILLA LTGCKSGEKE FDEESLQNLK ETXQXSXSETE LQNGDVRLNE
 YISLKGEIVE SDSRSLIKK GDRFILKSGS SKYQVXNEQK KKLKIGDEVT VYGEYYGFLK
 GTLIESEENH DSATN

EF117-3 (SEQ ID NO:435)

TG AAGAATCTCT TCAAAATCTA
 AAGGAAACGN CACAGTCTTA NTCAGAAACA GAATTACAAA ATGGTGACGT TCGTTTAAAT
 GAATATATTT CTTTGAAAGG GGAGATTGTT GAGAGTGACA GTCGTTCCAG TTTAATAAAA
 AAAGGTGATC GTTTTATTTT GAAAAGTGGT TCTAGTAAAT ATCAAGTTTN TAATGAGCAA
 AAGAAAAAAT TGAAGATTGG TGACGAAGTG ACAGTTTACG GAGAATATTA CGGCTTTTTG
 AAAGGGACAT TAATTGAAAG TGAGGAGAAT CATGATTCAG CCACGAA

EF117-4 (SEQ ID NO:436)

EESLQNLK ETXQXSXSETE LQNGDVRLNE YISLKGEIVE SDSRSLIKK GDRFILKSGS
 SKYQVXNEQK KKLKIGDEVT VYGEYYGFLK GTLIESEENH DSATN

EF118-1 (SEQ ID NO:437)

TGAGGGGGAA AAAGTGTTT AAAAAGAAAA GTGGGGATTG TCGCAGGCGT TTTCTGTTCA
 GCTTTGTTAC TGACAGGTTG TGGCAAAAGT GCGAAAGATG AGTTCATTCA AGGAATCGGC
 AATCANAACG CACAAGAATC TGGGGTTTGN GATTTCTCTA TGTCATTAG TGACATGAAA
 TTTTCACAAG AAGATGGTGC ACAAACGAAT CCTATGATTG GGATGCTCAT CACGCAAATC
 AAAGACGCAT CGCTTCTGG GGAAGATTCA AGTAGATGCC AAAAAAGAAA AAGCATTCAA
 CTTAGAGATG AAATTAAAAG CGATGGGAAT GGATGTACCG ATTCATTGG TTGGATCGTT
 AGATAA

EF118-2 (SEQ ID NO:438)

VLKRKV GIVAGVFCSA LLLTGCGKSA KDEFIQIGN XNAQESGVXD FSMSISDMKF
 SQEDGAQTNP MIGMLITQIK DASLSGEDSS RCQKRKSIQL RDEIKSDGNG CTDFIGWIVR

EF118-3 (SEQ ID NO:439)

GAAAGATG AGTTCATTCA AGGAATCGGC
 AATCANAACG CACAAGAATC TGGGGTTTGN GATTTCTCTA TGTCATTAG TGACATGAAA
 TTTTCACAAG AAGATGGTGC ACAAACGAAT CCTATGATTG GGATGCTCAT CACGCAAATC
 AAAGACGCAT CGCTTCTGG GGAAGATTCA AGTAGATGCC AAAAAAGAAA AAGCATTCAA
 CTTAGAGATG AAATTAAAAG CGATGGGAAT GGATGTACCG ATTCATTGG TTGGATCGTT
 AGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF118-4 (SEQ ID NO:440)

KDEFIQGIGN XNAQESGVXD FSMSISDMKF SQEDGAQTNP MIGMLITQIK DASLSGEDSS
RCQKRKSIQL RDEIKSDGNG CTDFIGWIVR

EF119-1 (SEQ ID NO:441)

TAAAGAATAC CGAGTAAAT TTTCGGAAGG CTTTTTTTCA AAAATTGTAT ATGCAAAAGA
AGTGCAACGG AAAGGAGCTC GGAAATCGTG AATAAGCTAC CTTTACTTAT TTTATTGTTA
GGCGGAGTGT TGCTTGTTAG TGGCTGTCAA AGCCATAAGG AAGAAAACAA GTCTAGTAAA
GTATCGACAG AAGAAACGAC AGTGATTGAA ACAGTAGCAA GGAACAATC GAAGGAATCG
TTTACGAGTG AAGCAACTAA AAAACAGACA GAAACAACGA AATTAGAAGA ACCAGATCAT
GTAAACTTTC TAGAAGCTTA TGGAAATGCG TATGCGAACT TTACAAGTAT TAATGATCGC
AATGAAAAGC TAAAGCCCCT CATGACTGAA AAATGTATCA AAAAAAATGG AATTGATGTT
AAAAGTGGAG TAGCGTTAGT TTCCGTAGGA AAGGTTACAA CGATTTATAA AAATGATCAA
CATGAATATG CTTTACTTTT GGATTGTGAA CAAAATGGAA CGCAGACACG AGTGTTACTT
TTGGCTAAGG TGAAGAACAA TAAAATTTCT GAAATGACCT ATAATTCAGT TAAGCAAGAG
TATTAG

EF119-2 (SEQ ID NO:442)

VN KLPLLLILLG GVLLVSGCQS HKEENKSSKV STEETTVIET VAREQSKESF TSEATKKQTE
TTKLEEPDHV KLEAYGNAY ANFTSINDRN EKLKPLMTEK CIKKNIDVK TGVALVSVGK
VTTIYKNDQH EYALLLDCEQ NGTQTRVLLL AKVKNNKISE MTYNSVKQEY

EF119-3 (SEQ ID NO:443)

AGAAAACAA GTCTAGTAAA
GTATCGACAG AAGAAACGAC AGTGATTGAA ACAGTAGCAA GGAACAATC GAAGGAATCG
TTTACGAGTG AAGCAACTAA AAAACAGACA GAAACAACGA AATTAGAAGA ACCAGATCAT
GTAAACTTTC TAGAAGCTTA TGGAAATGCG TATGCGAACT TTACAAGTAT TAATGATCGC
AATGAAAAGC TAAAGCCCCT CATGACTGAA AAATGTATCA AAAAAAATGG AATTGATGTT
AAAAGTGGAG TAGCGTTAGT TTCCGTAGGA AAGGTTACAA CGATTTATAA AAATGATCAA
CATGAATATG CTTTACTTTT GGATTGTGAA CAAAATGGAA CGCAGACACG AGTGTTACTT
TTGGCTAAGG TGAAGAACAA TAAAATTTCT GAAATGACCT ATAATTCAGT TAAGCAAGAG
TAT

EF119-4 (SEQ ID NO:444)

ENKSSKV STEETTVIET VAREQSKESF TSEATKKQTE TTKLEEPDHV KLEAYGNAY
ANFTSINDRN
EKLKPLMTEK CIKKNIDVK TGVALVSVGK VTTIYKNDQH EYALLLDCEQ NGTQTRVLLL
AKVKNNKISE MTYNSVKQEY

EF120-1 (SEQ ID NO:445)

TGAATAGGCG TGAAAAGGG AATGTTAGCG TTTTTTGTCTG TGCTAGCGGT TTTATCATT
ACTGCTTGTC GGAACCAAAA AGNAAAGAAA GTAACCGCTT CAACGGAGGC ATCCTCTAAA
GTTGAAGAGA CGAATGAAAA AACGAGTGAA ACAATTGATA AGACAAACGA ACAAGCGAGC
AGCAGTGTCT AGTCTAACGA ATCAGTGAAA AATGAAGAGC CGACAGCTGA TGGAAACAAT
AGTCAGCTAA CTGTAGCTGA TTTAGATACT ACACGATTA ATGCTGGCGA TTTTACTACT
TTAGTTGGAA TATGGAAAAA TGGTAAAGGA GAGAGTTTGA TCATTCATCC TGATGGTAGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACAAATACCG GAGGAATGAT TACGAAGGAT TCACCTACTG ATGAGTCGCG ACCAATTACA
AGCTTAAGTA TTAGGTGGGG GCCTACTGGT GCTGCGCTAT TATTATATAA AATTGGTGTT

EF120-2 (SEQ ID NO:446)

VKKGMLAF FVVLAVLSLT ACREPKKKV TASTEASSKV EETNEKTSET IDKTNEQASS
SVESNESVKN EEPTADGNNS QLTVADLDTT AINAGDFTTL VGIWKNGKGE SLIIHPDGST
NTGGMITKDS PTDESRPITS LSIRWGPTGA ALLLYKIGV

EF120-3 (SEQ ID NO:447)

AAGAAA GTAACCGCTT CAACGGAGGC ATCCTCTAAA
GTTGAAGAGA CGAATGAAAA AACGAGTGAA ACAATTGATA AGACAAACGA ACAAGCGAGC
AGCAGTGTCC AGTCTAACGA ATCAGTGAAA AATGAAGAGC CGACAGCTGA TGGAAACAAT
AGTCAGCTAA CTGTAGCTGA TTTAGATACT ACAGCGATTA ATGCTGGCGA TTTTACTACT
TTAGTTGGAA TATGGAAAAA TGGTAAAGGA GAGAGTTTGA TCATTCATCC TGATGGTAGT
ACAAATACCG GAGGAATGAT TACGAAGGAT TCACCTACTG ATGAGTCGCG ACCAATTACA
AGCTTAAGTA TTAGGTGGGG GCCTACTGGT GCTGCGCTAT TATTATATAA AATTGGTGTT

EF120-4 (SEQ ID NO:448)

KKV TASTEASSKV EETNEKTSET IDKTNEQASS
SVESNESVKN EEPTADGNNS QLTVADLDTT AINAGDFTTL VGIWKNGKGE SLIIHPDGST
NTGGMITKDS PTDESRPITS LSIRWGPTGA ALLLYKIGV

EF121-1 (SEQ ID NO:449)

TGAAACACAA GGAGGAAATT TGTGAAAAAG TTGAGCTTTA AAAAAGTGAA GTGGGGCATG
CATTTTTTTAA TGGCTGTTGC GTTGATAGCG CCAAGTGTTA CTAGTACGGC ATATGCAGTA
GAAACAACGA GTCAACAAAG TTCAGAAGCA GTAACAAGTA CCACCGATT C AAGTAGAAAA
CAAGAACCAG TCATTACACA GGAAACAACA GACATCAAAC AAGAAGCACC AAATCAGGCT
ACGAGTGACA GTGTCAAGCA GTCACAAGAA ACCACAGCAC CAACAGAGAC GACGAATTTA
GAAACGTCAA TCGCTGAAAA AGAAGAAACG AGCACGCCGC AAAAATAAC AATTTTAGGT
ACGTCAGATG TTCATGGTCA ATTATGGAAT TGGTCTTATG AAGATGATAA AGAACTACCA
GTGGGTTTTGT CCCAAGTAAG TACAGTCGTT AACCAAGTCC GGGCACAAAA CCCAGCAGGC
ACCGTTTTTAA TTGATAATGG CGACAATATT CAAGGCAC TA TTTTAACAGA TGACTTGTAT
AATAAAGCGC CTTTAGTGAA TGAAAAGACC CATCCAATGA TCACCGCCAT GAATGTGATG
AAGTATGATG CAATGGTTTT GGGAAATCAT GAGTTTAATT TTGGTTTACC GTTAATCAAA
AAAATTCAAC AAGAAGCCAC TTTTCCAATC TTGTCTGCGA ATACCTACAA TAAGGAAGAT
GGTCTTCGTT TTGTTGAAGG GACTACCAG AAGGAACTTG ATTTTAATCA AGATGGGCAG
CCAGATTTAA AAGTTGGGAT TATCGGCTTA ACAATTCCGC ACATTCCTTT GTGGGATGGC
CCTCGTGTTA CTTGCGTTAA TTTTTTACCT TTGAAAGAAG AAGCAGAAAA AGCAGTTACT
GAGTTGAAAG CTAACGATCA GGCTGACATT ATTGTTGCCT CGATTTCATGC GGGACAACAA
AATAGTGATC CGGCTGCCAG TGCCGACCAA GTAATTGAAA ATGTCGCGGG GATTGATGCG
TATATTCTGG GTCATGACCA CCTTCTTTTT ACCAAGCAAG GAGCAGCGCC GAATGAAAAA
ACTGTACCGG TAGGGGGACC GAAAGATACG GGGACAGAAG TTGTCAAAAT TGATCTTTCA
GTTGCTAAAA ATGCCGATAA GTGGGAAGTG CAAGAAGGTA CAGCAACGAT TGTACCAACA
ACGAATGTTT CAGCAGATGA AGCAGTTAAG GCAGCGACAA AAGAATACCA TGAAAAAACG
CGAGCGTTTA TTCAGGAGGA GATCGGCACA GCAACAGCTG ATTTTTTACC AAAACAAGAA
ATTAAAGGAA TTCCCGAAGC ACAATTACAA CCAACAGCGA TGATTTCTTT AATTAATAAC
GTTCAAAAAG AAGTAACGGG CGCACAATTA AGTGCGGCAG CGCTGTTTAA ATACGACAGT
AAATTACCTG CGGGGAAGAT TTCTATGCC ACGATTTTTG ATATCTACAA ATACCCGAAT
ACCTTAGTGA GTGTTCCCAT TAACGGTGAA AACTTACTGA AGTATTTAGA AAAACAAGGG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCGTACTATA ACCAAACACA GCCAGATGAT TTGACCATTA GTTTTAATCC AAACATTTCGT
 GTATATAACT ATGACATGAT TTCTGGAGTG GACTACAAGA TTGACATTTT AAAACCAAGTG
 GGTGAACGAA TTGTAGATGC GAAAATTGAC GGCCAACCGC TGGATCCTGC CAAAGAATAT
 ACGATTGCTA TGAATAATTA TCGTTACGGC GGTTTAGCTA GCCAAGGGAT TCAAGTAGGG
 GAACCTATTA AAAATTCTGA TCCAGAAACC TTACGAGGAA TGATTGTTGA TTATATTAAG
 AAAAAAGGAA CTCTTGATCC AGAACAAGAA ATCGAACGAA ATTGGTCAAT TATTGGGACA
 AATTTTGATG AAAAATGGCG TGCCAAAGCA ATCGAATTAG TGAATGACGG CACTCTTCAA
 ATTCCGACTT CTCTTGATGG ACGTACACCA AACGCCGCCG CTATTACGAA ACAAGATGTC
 CGTAATGCGG GCTTTGATTT AGATAATGCA TATACCATTA TGCACACAAA TGACGTTTAT
 GGCCGACTAG AAGCAGGGAA AGGCGAATTA GGTATGGCGC GTCTAAAAAC CTTTAAAGAC
 CAAGAAAACC CAACCTTGAT GGTGGATGCA GGGGATGTTT TCCAAGGATT ACCAATCTCC
 AATTTCTCCA AAGGCGCGGA TATGGCCAAA GCAATGAATG AAGTTGGTTA TGATGCCATG
 GCGGTGGGAA ATCAGGAGTT TGATTTTGGT TTAGAGATTG CACTAGGTTA TAAAGACCAA
 CTGAATTTTC CGATTTTATC TAGTAATACG TATTACAAAG ATGGCAGTGG ACGGGTTTTT
 GATCCGTATA CAATCGTAGA AAAATCCGGG AAAAAGTTTG CCATTGTAGG TGTGACGACC
 CCAGAAACAG CAACGAAAAC ACACCCGAAA AACGTAGAGA AGGTGACATT TAAAGACCCG
 ATTCCAGAAG TAGAAGCAGT GATTAAGGAA ATTAAGAGA AGTACGCGGA TATNCAAGCT
 TTCGTGGTTA CTGGGCATTT AGGCGTAGAT GAAACGACGC CGCATATCTG GCGTGGTGAT
 ACGTAGCAG AAACCTTAG TCAAACATAT CCTGAGTTAG ATATCACTGT GATTGATGGA
 CATTCGCATA CAGCCGTCGA AAGTGGCAAA CGTTATGGCA AAGTGATCTA TGCTCAAACA
 GGTAATTATT TAAATAATGT TGGGATCGTC ACAGCACCAG AGAGTGAACC AACTAAGAAA
 ACAACAAAAT TGATTTACG AGCAGAGCTG CTAGAATTGC CAGAAAACCC GGCAGTTAAA
 GCCATCGTTG ATGAAGCAG TACGAATTTT AACGCTGAAA ATGAAAAAGT AATTGTCGAT
 TATATTCCAT TCACATTGGA TGGACAACGA GAAAATGTGC GCACACGAGA GACCAACTTA
 GGGAAATTTGA TTGGTGATGC GATTATGTCA TATGGCCAAG ACGCGTTTAG CCAACCTGCT
 GATTTTGCAG TAACTAATGG TGGCGGCATT CGCGCTGATA TTAAACAAGG GCCAATTAAA
 GTTGGGGATG TCATTGCTGT GTTACCTTTT GGCAATAGCA TTGCGCAAAAT TCAAGTAACC
 GCGCGCCAAG TTAAAGAAAT GTTTGAAATG TCTGTTCGTT CGATTCCACA AAAAGATGAG
 AATGGCACAA TTTTACTAGA TGATGCTGGC CAACCAAAAC TTGGCGCAAA TGGTGGTTTC
 CTACATGTTT CAAGCTCCAT TCGTATCCAC TATGATTCCA CAAAACCAGG TACTCGCTTG
 GCTAGTGACG AAGGCAATGA AACAGGACAA ACGATTGTCT GTAGTCGCGT ATTAGGAATA
 GAAATTAAAA ATCGGCAAAAC ACAAAGTTT GAACCATTTG ATGAGAAGAA ACAATACCGG
 ATGGCTACCA ATGATTTCTT AGCTGCTGGT GGTGATGGTT ACGATATGCT AGGTGGTGAA
 CGAGAAGAAG GGATTTCACT AGATTCTGTC TTAATTGAAT ACTTGAAAAG TGCAACCAGC
 TTGCGGTTGT ATCGTGCAGC AACGACGATT GATTTAGCAC AATATAAAGA ACCATTCCCA
 GGCGAACGAA TTGTTTCTAT TTCGGAAGAA GCTTACAAAG AGTTAATCGG TGGAGGAGAG
 ACGCCAAAAC CAGATCCAAA ACCAGACCCG AAACCAACAC CAGAAAACACC AGTAGCAACC
 AATAACAAA ACCAAGCGGG AGCAAGACAG AGCAATCCAT CCGTAACAGA GAAGAAAAAG
 TATGGCGGCT TTTTACCTAA AACGGGTACA GAAACAGAAA CGCTTGCAAT ATATGGTTTA
 CTGTTGCTTG GACTTCTTTC TTCTGGCTGG TATATTTATA AACGACGTAA CAAAGCTAGT
 TAG

EF121-2 (SEQ ID NO:450)

VKKL SFKKVKWGMH FLMAVALIAP SVTSTAYAVE TTSQSSSEAV TSTTDSSRKQ
 EPVITQETTD IKQEAPNQAT SDSVKQSQET TAPTETTNLE TSIAEKEETS TPQKITILGT
 SDVHQGLWNW SYEDDKELPV GLSQVSTVVN QVRAQNPAQT VLIDNGDNIQ GTILTDDLIN
 KAPLVNEKTH PMITAMNVMK YDAMVLGNHE FNFGLEPLIKK IQQEATFPIL SANTYNKEDG
 LRFVEGTTTK ELDFNQDGQP DLKVGIIGLT IPHIPLWDGP RVTSINFLPL KEEAEKAVTE
 LKANDQADII VASIHAGQON SDPAASADQV IENVAGIDAY ILGHDHLSFT KQGAAPNGKT
 VPVGGPKDTG TEVVKIDLSV AKNADKWEVQ EGTATIVPTT NVPADAEVKA ATKEYHEKTR
 AFIQEEIGTA TADFLPKQEI KGIPEAQLQP TAMISLINNV QKEVTGAQLS AAALFKYDSK
 LPAGKISYAT IFDIYKYPNT LVSVPINGEN LLKYLEKQGA YYNQTPQDDL TISFNPNIHV
 YNYDMISGVD YKIDISKPVG ERIVDAKIDG QPLDPAKEYT IAMNNYRYGG LASQGIQVGE

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

PIKNSDPETL RGMIVDYIKK KGTLDPEQEI ERNWSIIGTN FDEKWRAKAI ELVNDGTLQI
 PTSPDGRTPN AAAITKQDVR NAGFDLDNAY TIMHTNDVHG RLEAGKGELG MARLKTFFKDQ
 ENPTLMVDAG DVFQGLPISN FSKGADMAKA MNEVGYDAMA VGNHEFDGFL EIALGYKDQL
 NFPILSSNTY YKDGSGRVFD PYTIVEKSGK KFAIVGVVTP ETATKTHPKN VEKVTFKDPI
 PEVEAVIKEI KEKYADXQAF VVTGHLGVDE TTPHIWRGDT LAETLSQTYT ELDITVIDGH
 SHTAVESGKR YGKVIYAQTG NYLNNVGIVT APESEPTKKT TKLISAAELL ELPENPAVKA
 IVDEARTNFN AENEKVIVDY IPFTLDGQRE NVRTRETNLG NLIGDAIMSY GQDAFSQPAD
 FAVTNGGGIR ADIKQGPIKV GDVIAVLPFG NSIAQIQVTG AQVKEMFEMS VRSIPQKDN
 GTILLDDAGQ PKLGANGGFL HVSSSIRIHY DSTKPGTRLA SDEGNETGQT IVGSRVLGIE
 IKNRQTQKFE PLDEKKQYRM ATNDFLAAGG DGYDMLGGER EEGISLDSVL IEYLKSATSLS
 RLYRAATTID LAQYKEPFPF ERIVSISEEA YKELIGGET PKPDPKDPK PTPETPVATN
 KQNQAGARQS NPSVTEKKKY GGFLPKTGTE TETLALYGLL FVGLSSSGWY IYKRRNKAS

EF121-3 (SEQ ID NO:451)

ACAAAG TTCAGAAGCA GTAACAAGTA CCACCGATTC AAGTAGAAAA
 CAAGAACCAG TCATTACACA GGAAACAACA GACATCAAAC AAGAAGCACC AAATCAGGCT
 ACGAGTGACA GTGTCAAGCA GTCACAAGAA ACCACAGCAC CAACAGAGAC GACGAATTTA
 GAAACGTCAA TCGCTGAAAA AGAAGAAACG AGCACGCCGC AAAAAATAAC AATTTTAGGT
 ACGTCAGATG TTCATGGTCA ATTATGGAAT TGGTCTTATG AAGATGATAA AGAACTACCA
 GTTGGTTTGT CCCAAGTAAG TACAGTCGTT AACCAAGTCC GGGCACAAAA CCCAGCAGGC
 ACCGTTTTAA TTGATAATGG CGACAATATT CAAGGCACTA TTTTAACAGA TGACTTGTAT
 AATAAAGCGC CTTTAGTGAA TGAAAAGACC CATCCAATGA TCACCGCCAT GAATGTGATG
 AAGTATGATG CAATGGTTTT GGGAAATCAT GAGTTTAATT TTGTTTACC GTTAATCAAA
 AAAATTCAAC AAGAAGCCAC TTTTCCAATC TTGTCTGCGA ATACCTACAA TAAGGAAGAT
 GGTCCTCGTT TTGTTGAAGG GACTACCACG AAGGAACTTG ATTTTAATCA AGATGGGCAG
 CCAGATTTAA AAGTTGGGAT TATCGGCTTA ACAATTCGCG ACATTCCTTT GTGGGATGGC
 CCTCGTGTTA CTTTCGCTTAA TTTTTFACCT TTGAAAGAAG AAGCAGAAAA AGCAGTTACT
 GAGTTGAAAG CTAACGATCA GGCTGACATT ATTGTTGCCT CGATTCATGC GGGACAACAA
 AATAGTGATC CGGCTGCCAG TGCCGACCAA GTAATTGAAA ATGTCGCGGG GATTGATGCG
 TATATTCTGG GTCATGACCA CCTTTCCTTT ACCAAGCAAG GAGCAGCGCC GAATGGAAAA
 ACTGTACCGG TAGGGGGACC GAAAGATACG GGGACAGAAG TTGTCAAAAT TGATCTTTCA
 GTTGCTAAAA ATGCCGATAA GTGGGAAGTG CAAGAAGGTA CAGCAACGAT TGTACCAACA
 ACGAATGTTT CAGCAGATGA AGCAGTTAAG GCAGCGACAA AAGAATACCA TGAAAAACG
 CGAGCGTTTA TTCAGGAGGA GATCGGCACA GCAACAGCTG ATTTTTFACC AAAACAAGAA
 ATTAAAGGAA TTCCCGAAGC ACAATTACAA CCAACAGCGA TGATTTCTTT AATTAATAAC
 GTTCAAAAAG AAGTAACGGG CGCACAATTA AGTGCGGCAG CGCTGTTTAA ATACGACAGT
 AAATTACCTG CGGGGAAGAT TTCTATGCC ACATTTTGTG ATATCTACAA ATACCCGAAT
 ACCTTAGTGA GTGTTCCTAT TAACGGTGAA AACTTACTGA AGTATTTAGA AAAACAAGGG
 GCGTACTATA ACCAAACACA GCCAGATGAT TTGACCATTA GTTTTAATCC AAACATTCGT
 GTATATAACT ATGACATGAT TTCTGGAGTG GACTACAAGA TTGACATTTT AAAACCAAGT
 GGTGAACGAA TTGTAGATGC GAAAATTGAC GGCCAACCGC TGGATCCTGC CAAAGAATAT
 ACGATTGCTA TGAATAATTA TCGTTACGGC GGTTTAGCTA GCCAAGGGAT TCAAGTAGGG
 GAACCTATTA AAAATTCTGA TCCAGAAACC TTACGAGGAA TGATTGTTGA TTATATTAAG
 AAAAAGGAA CTCTTGATCC AGAACAAGAA ATCGAACGAA ATTGGTCAAT TATTGGGACA
 AATTTTGATG AAAAATGGCG TGCCAAAGCA ATCGAATTAG TGAATGACGG CACTCTTCAA
 ATTCCGACTT CTCTGATG ACGTACACCA AACGCCG

EF121-4 (SEQ ID NO:452)

QSSEAV TSTTDSRQK
 EPVITQETTD IKQEAPNQAT SDSVKQSQET TAPTETTLE TSIAEKEETS TPQKITILGT
 SDVHGQLWNW SYEDDKELPV GLSQVSTVVN QVRAQNPAQT VLIDNGDNIQ GTILTDDLIN

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

KAPLVNEKTH PMITAMNVMK YDAMVLGNHE FNFGLPLIKK IQQEATFPIL SANTYNKEDG
 LRFVEGTTTK ELDFNQDGQP DLKVGIIIGLT IPHIPLWDGP RVTSINFLPL KEEAEKAVTE
 LKANDQADII VASIHAGQQN SDPAASADQV IENVAGIDAY ILGHDHLSFT KQGAAPNGKT
 VPVGGPKDTG TEVVKIDLSV AKNADKWEVQ EGTATIVPTT NVPADAEVKA ATKEYHEKTR
 AFIQEEIGTA TADFLPKQEI KGIPEAQLQP TAMISLINNV QKEVTGAQLS AAALFKYDSK
 LPAGKISYAT IFDIYKYPNT LVSVPINGEN LLKYLEKQGA YYNQTPDDL TISFNPNIHV
 YNYDMISGVD YKIDISKVPV ERIVDAKIDG QPLDPAKEYT IAMNNYRYGG LASQGIQVGE
 PIKNSDPETL RGMIVDYIKK KGTLDPEQEI ERNWSIIGTN FDEKWRAKAI ELVNDGTLQI
 PTSPDGRTPN A

EF122-1 (SEQ ID NO:453)

TGAAACACAA GGAGGAAATT TGTGAAAAAG TTGAGCTTTA AAAAAGTGAA GTGGGGCATG
 CATTTTTTAA TGGCTGTTGC GTTGATAGCG CCAAGTGTTA CTAGTACGGC ATATGCAGTA
 GAAACAACGA GTCAACAAAG TTCAGAAGCA GTAACAAGTA CCACCGATT C AAGTAGAAAA
 CAAGAACCAG TCATTACACA GGAAACAACA GACATCAAAC AAGAAGCACC AAATCAGGCT
 ACGAGTGACA GTGTCAAGCA GTCACAAGAA ACCACAGCAC CAACAGAGAC GACGAATTTA
 GAAACGTCAA TTCGTGAAAA AGAAGAAACG AGCAGCGCCG AAAAAATAAC AATTTTAGGT
 ACGTCAGATG TTCATGGTCA ATTATGGAAT TGGTCTTATG AAGATGATAA AGAACTACCA
 GTTGGTTTGT CCCAAGTAAG TACAGTCGTT AACCAAGTCC GGGCACAAAA CCCAGCAGGC
 ACCGTTTTAA TTGATAATGG CGACAATATT CAAGGCACTA TTTTAACAGA TGACTTGTAT
 AATAAAGCGC CTTTAGTGAA TGAAAAGACC CATCCAATGA TCACCGCCAT GAATGTGATG
 AAGTATGATG CAATGTTTTT GGGAAATCAT GAGTTTAATT TTGTTTACC GTTAATCAAA
 AAAATTCAAC AAGAAGCCAC TTTTCCAATC TTGTCTGCGA ATACCTACAA TAAGGAAGAT
 GGTCCTCGTT TTGTTGAAGG GACTACCACG AAGGAACTTG ATTTTAATCA AGATGGGCAG
 CCAGATTTAA AAGTTGGGAT TATCGGCTTA ACAATTCGCG ACATTCCCTT GTGGGATGGC
 CCTCGTGTTA CTTGCTTAA TTTTTTACCT TTGAAAGAAG AAGCAGAAAA AGCAGTTACT
 GAGTTGAAAG CTAACGATCA GGCTGACATT ATTGTTGCCT CGATTTCATG GGGACAACAA
 AATAGTGATC CGGCTGCCAG GTAATTGAAA ATGTCGCGGG GATTGATGCG
 TATATTCTGG GTCATGACCA CCTTCTTTT ACCAAGCAAG GAGCAGCGCC GAATGAAAAA
 ACTGTACCGG TAGGGGGACC GAAAGATACG GGGACAGAAG TTGTCAAAAT TGATCTTTCA
 GTTGCTAAAA ATGCCGATAA GTGGGAAGTG CAAGAAGGTA CAGCAACGAT TGTACCAACA
 ACGAATGTTT CAGCAGATGA AGCAGTTAAG GCAGCGACAA AAGAATACCA TGAAAAACG
 CGAGCGTTTA TTCAGGAGGA GATCGGCACA GCAACAGCTG ATTTTTTACC AAAACAAGAA
 ATTAAGGAA TTCCCGAAGC ACAATTACAA CCAACAGCGA TGATTCTTTT AATTATAAAC
 GTTCAAAAAG AAGTAACGGG CGCACAAATTA AGTGCGGCAG CGCTGTTTAA ATACGACAGT
 AAATTACCTG CGGGGAAGAT TTCTATGCC ACGATTTTGT ATATCTACAA ATACCCGAAT
 ACCTTAGTGA GTGTTCCCAT TAACGGTGAA AACTTACTGA AGTATTTAGA AAAACAAGGG
 GCGTACTATA ACCAAACACA GCCAGATGAT TTGACCATTA GTTTTAATCC AAACATTCGT
 GTATATAACT ATGACATGAT TTCTGGAGTG GACTACAAGA TTGACATTTT AAAACCAGTG
 GGTGAACGAA TTGTAGATGC GAAAATTGAC GGCCAACCGC TGGATCCTGC CAAAGAATAT
 ACGATTGCTA TGAATAATTA TCGTTACGGC GGTTTAGCTA GCCAAGGGAT TCAAGTAGGG
 GAACCTATTA AAAATTCTGA TCCAGAAACC TTACGAGGAA TGATTGTTGA TTATATTAAG
 AAAAAAGGAA CTCTTGATCC AGAACAAGAA ATCGAACGAA ATTGGTCAAT TATTGGGACA
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 ATTCGACTT CTCTGATGG ACGTACACCA AACGCCGCCG CTATTACGAA ACAAGATGTC
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 GGCCGACTAG AAGCAGGGAA AGGCGAATTA GGTATGGCGC GTCTAAAAAC CTTTAAAGAC
 CAAGAAAACC CAACCTTGAT GGTGGATGCA GGGGATGTTT TCCAAGGATT ACCAATCTCC
 AATTCTTCCA AAGGCGCGGA TATGGCCAAA GCAATGAATG AAGTTGGTTA TGATGCCATG
 GCGGTGGGAA ATCAGAGTT TGATTGTGGT TTAGAGATTG CACTAGGTTA TAAAGACCAA
 CTGAATTTTC CGATTTTATC TAGTAATACG TATTACAAAG ATGGCAGTGG ACGGGTTTTT
 GATCCGTATA CAATCGTAGA AAAATCCGGG AAAAAGTTTG CCATTGTAGG TGTGACGACC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGAAACAG CAACGAAAAC ACACCCGAAA AACGTAGAGA AGGTGACATT TAAAGACCCG
 ATTCCAGAAG TAGAAGCAGT GATTAAGGAA ATTAAAGAGA AGTACGCGGA TATNCAAGCT
 TTCGTGGTTA CTGGGCATTT AGGCGTAGAT GAAACGACGC CGCATATCTG GCGTGGTGAT
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 CATTTCGCATA CAGCCGTCGA AAGTGGCAAA CGTTATGGCA AAGTGATCTA TGCTCAAACA
 GGTAATTATT TAAATAATGT TGGGATCGTC ACAGCACCAG AGAGTGAACC AACTAAGAAA
 ACAACAAAAA TGATTTTCAGC AGCAGAGCTG CTAGAATTGC CAGAAAACCC GGCAGTTAAA
 GCCATCGTTG ATGAAGCAGC TACGAATTTT AACGCTGAAA ATGAAAAAGT AATTGTCGAT
 TATATTCCAT TCACATTGGA TGGACAACGA GAAAATGTGC GCACACGAGA GACCAACTTA
 GGGAATTTGA TTGGTGATGC GATTATGTCA TATGGCCAAG ACGCGTTTAG CCAACCTGCT
 GATTTTGCAG TAACTAATGG TGGCGGCATT CGCGCTGATA TTAAACAAGG GCCAATTAAA
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 GCTAGTGACG AAGGCAATGA AACAGGACAA ACGATTGTCT GTAGTCGCGT ATTAGGAATA
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 AATAAACAAA ACCAAGCGGG AGCAAGACAG AGCAATCCAT CCGTAACAGA GAAGAAAAAG
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 TAG

EF122-2 (SEQ ID NO:454)

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 SDVHGQLWNW SYEDDKELPV GLSQVSTVNV QVRAQNPAGT VLIDNGDNIQ GTILTDDLIN
 KAPLVNEKTH PMITAMNVMK YDAMVLGNHE FNFGLPLIKK IQQEATFPIL SANTYNKEDG
 LRFVEGTTTK ELDFNQDQGP DLKVGIIIGLT IPHIPLWDGP RVTSNLNPLP KEEAEKAVTE
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 VPVGGPKDTG TEVVKIDLSV AKNADKWEVQ EGTATIVPTT NVPADAEVKA ATKEYHEKTR
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 PEVEAVIKEI KEKYADXQAF VVTGHLGVDE TTPHIWRGDT LAETLSQTYE ELDITVIDGH
 SHTAVESGKR YGKVIYAQTG NYLNNVGIVT APESEPTKKK TKLISAAELL ELPENPAVKA
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 RLYRAATTID LAQYKEPFPG ERIVSISEEA YKELIGGGET PKPDPKPKDPK PTPETPVATN
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EF122-3 (SEQ ID NO:455)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 CGTAATGCGG GCTTTGATTT AGATAATGCA TATACCATTA TGCACACAAA TGACGTTTCAT
 GGCCGACTAG AAGCAGGGAA AGGCGAATTA GGTATGGCGC GTCTAAAAAC CTTTAAAGAC
 CAAGAAAACC CAACCTTGAT GGTGGATGCA GGGGATGTTT TCCAAGGATT ACCAATCTCC
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 GCGGTGGGAA ATCAGCAGTT TGATTTTGGT TTAGAGATTG CACTAGGTTA TAAAGACCAA
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 GATCCGTATA CAATCGTAGA AAAATCCGGG AAAAAGTTTG CCATTGTAGG TGTGACGACC
 CCAGAAACAG CAACGAAAAC ACACCCGAAA AACGTAGAGA AGGTGACATT TAAAGACCCG
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 CATTCCGATA CAGCCGTCGA AAGTGGCAAA CGTTATGGCA AAGTGATCTA TGCTCAAACA
 GGTAATTTAT TAAATAATGT TGGGATCGTC ACAGCACCAG AGAGTGAACC AACTAAGAAA
 ACAACAAAAT TGATTTTCAGC AGCAGAGCTG CTAGAATTGC CAGAAAACCC GGCAGTTAAA
 GCCATCGTTG ATGAAGCAGC TACGAATTTT AACGCTGAAA ATGAAAAAGT AATTGTCGAT
 TATATTCCAT TCACATTGGA TGGACAACGA GAAAATGTGC GCACACGAGA GACCAACTTA
 GGGAAATTTGA TTGGTGATGC GATTATGTCA TATGGCCAAG ACGCGTTTAG CCAACCTGCT
 GATTTTGCAG TAACTAATGG TGGCGGCATT CGCGCTGATA TTAAACAAGG GCCAATTAAA
 GTTGGGGATG TCATTGCTGT GTTACCTTTT GGCAATAGCA TTGCGCAAAT TCAAGTAACC
 GGCGCCCAAG TTAAAGAAAT GTTTGAAATG TCTGTTCTGT CGATTCCACA AAAAGATGAG
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 GCTAGTGACG AAGGCAATGA AACAGGACAA ACGATTGTCT GTAGTCGCGT ATTAGGAATA
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 ATGGCTACCA AGATTTCCTT AGCTGCTGGT GGTGATGGTT ACGATATGCT AGGTGGTGAA
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 TTGCGGTTGT ATCGTGCAGC AACGACGATT GATTTAGCAG AATATAAAGA ACCATTCCCA
 GGCGAACGAA TTGTTTCTAT TTCGGAAGAA GCTTACAAAG AGTTAATCGG TGGAGGAGAG
 ACGCCAAAAC CAGATCCAAA ACCAGACCCG AAACCAACAC CAGAAACACC AGTAGCAACC
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EF122-4 (SEQ ID NO:456)

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 SHTAVESGKR YGKVIYAQTG NYLNNVGIVT APESEPTKKT TKLISAAELL ELPENPAVKA
 IVDEARTNFN AENEKVIVDY IPFTLDGQRE NVRTRETNLG NLIGDAIMSY GQDAFSQPAD
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 KQNQAGARQS NPSVTEKKKY GGF

EF123-1 (SEQ ID NO:457)

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 ATGAAAGAAA TGAGAAAGAA TGGTCCAATG GTAAACCGTT GGCTCTACGG GTTGATGTGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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ACGTTGAACC CTACAGCTAC AGAAGATGTG ACGTTTCTT ATGGACAACA GCAACGAGCG
TTGACGTTAA AGACTGGTAC TGATCCGACA GAATCAACGG CAATCACGAG TTCGCCAGCC
GCATCAGCGA ATGAAGGTTT AACAGAAGAA GCATCTACAA ACTCCTCTGT TCCTCGTTCG
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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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EF123-2 (SEQ ID NO:458)

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SANEGSTEEA STNSSVPRSS EETVASTTKA IESKTTESTT VKPRVAGPTD ISDYFTGDET

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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| PNKPGSGDLV | DAEGNVYGT | TISEDGTVRF | TFNERITSES | DIHGDFSLDT | HLNDS DGRGP |
| GDWVIDIPTQ | EDLPPVVIPI | VPDTEQQIDK | QGHFDRTPNP | SAITWTVDIN | QAMKDQTNPT |
| VTETWPTGNT | FKSVKVYELV | MNLDGTIKEY | GRELSPDEYT | VDKNGNVTIK | GD TNKAYRLE |
| YQTTIDEAVI | PDGGGDVFPK | NHATLTSDNN | PNGLD AEATV | TATYGKMLDK | RNIDYDEANQ |
| EFTWEINYN | GEQTIPKDQA | VITDTMGDNL | TFEPDSLHLY | SVTFDDKGNE | VVGAE LVEGK |
| DYKVVINGDG | SFAIDFLHDV | TGAVKIDYKT | KVDGIVEGDV | AVNNRVDVGT | GQHS EDDGTA |
| SQQNI IKNTG | AVDYQNSTIG | WTLAVNQNNY | LMENAVITDT | YEPVPG LTMV | PNSLVVKD TT |
| TGAQLTLGKD | FMVEITRNAD | GETGFKVSFI | GAYAKTSDAF | HITYTTFFDV | TELDANNPAL |
| DHYRNTAAID | WTDEAGNNHH | SEDSKPFKPL | PAPDLNAQKS | GVYNAVTK EI | TWTIAVNLSN |
| NRLVDAFLTD | PILTNTQTYLA | GSLKVYEGNT | KPDGSVEKVK | PTQPLTDITM | EEPSEKNQNT |
| WRVDFPNDSR | TYVIEFKTSV | DEKVIEGSAS | YDNTASYTNQ | GSSRDVTGKV | SIQHGGESVK |
| KGGEYHKDDP | DHVVWHVMIN | GAQSVLDDVV | ITDTPSPNQV | LDPESLVIYG | TNVTEDGTIT |
| PKSVILEEG | KDYTLEVTTD | NETGQQKIVV | KMAHIEAPYY | MEYRSLVTSS | AAGSTD TVSN |
| QV SITNGNSE | VVHGDDNGDV | VVDIDHSGGH | ATG TKGKIQL | KKTAMDETTI | LAGAHFQIWD |
| QAKTQVLREG | TVDATGVITF | GGLPQQQYIL | VETKAPEGYT | VSDELA GRV | ITIDEETS AE |
| GAQPTI IKND | VNKVFLEKMD | EKGKKLVNAR | FKLEHAVTTP | FTHWEEVPLA | PDR TNANGQL |
| EVD SLKPGLY | QFTEIEAPTC | YLLDTPKRF | IVTQNTSGQI | RDVHV KMLNY | QGS AE LIK KD |
| QAGNPLAGAE | FVSLD TTGQA | VREHLVSDAN | GKVTVTD LAP | GKYQFVETKA | PAGYLLNTEP |
| SAFTIAASDR | GKPATVIATA | NFVNYQGTAK | LIKKDVNGHL | LSGATFKVLD | AKGETIQTGL |
| TTNNQGEIVA | EHLAPGKYRF | VETKAPTGYL | LNTTPVPFEI | AEKNAGKPAV | VVASDNFVSY |
| KGAFQIVKTN | SADQPLAGAV | FELYDHNKQS | LGITATSGKD | GKIIFRDLAP | GTYYYKEIKA |
| PKLPDGADYI | IYPELVKVEI | RGDFKGDPEI | FQLGAFANFK | GRAVFKKIDA | NANPLPGTIF |
| KLYRIENGEK | IFEREVTA EK | DGSLAMEDLG | AGSYELDELD | ATDGYIVNKQ | PIYFVVKKNS |
| NDKQPLDELE | FVNYQAEVMG | RKVNEQQQTL | AGAVFAIYNA | DEQNQPQGS P | ITFLNRAGEK |
| VSEITTDK TG | EIYAKGLNEG | HYVLVETKAP | TGYLLD TTH | PFDTVTAQLGK | EQPIALGDLI |
| NYQGT AQLTK | ENETGEALAG | AVFKVIDETG | QTV DQG TNL M | SDKQGKVIAK | NLAPGTYRFV |
| ETQAPT SYLL | NETPSASFTI | AKDNQCKPAT | VVLKAPFINY | QGA AKLVKID | QQKNALAGAE |
| FKVDPELVGQ | TVARSLRSDN | QGLVQVNH LQ | PGKYTFVETK | APDGYQLSKQ | AVAF TIAATA |
| KDKPELVNAG | TFVNEKQPVS | KKTKPNQPTT | KQAARETGWL | GLPKTNTQVN | YFFVFI GLML |
| VGLASWLFYK | KSKK | | | | |

EF123-3 (SEQ ID NO:459)

GGAAGA GGTAAACAGC

| | | | | | |
|------------|------------|------------|-------------|------------|-------------|
| GATGGCCAGT | TAACGTTAGG | AGAAGTGAAG | CAAACCAGCC | AGCAAGAAAT | GACCTTAGCG |
| CTTCAAGGAA | AAGCACAACC | AGTAACACAA | GAGGTTGTAG | TGCATTATAG | TGCCAATGTG |
| TCAATCAAAG | CTGCACATTG | GGCAGCGCCC | AATAATACGC | GCAAGATTCA | AGTGGATGAC |
| CAGAAGAAAC | AGATTCAAAT | TGAATTGAAT | CAGCAAGCGT | TAGCAGATAC | GTTAGTCTTA |
| ACGTGAACCC | CTACAGCTAC | AGAAGATGTG | ACGTTTTCCT | ATGGACAACA | GCAACGAGCG |
| TTGACGTTAA | AGACTGGTAC | TGATCCGACA | GAATCAACGG | CAATCACGAG | TTCGCCAGCC |
| GCATCAGCGA | ATGAAGGTTT | AACAGAAGAA | GCATCTACAA | ACTCCTCTGT | TCCTCGTTCTG |
| TCCGAAGAAA | CTGTCGCCAG | CACGACAAAA | GCGATAGAAA | GTAAAACAAC | TGAATCGACG |
| ACTGTCAAAC | CGCGCGTAGC | AGGACCAACA | GATATCAGTG | ATTATTTTAC | AGGTGATGAA |
| ACAACGATTA | TCGATAATTT | TGAAGATCCG | ATTTATTTAA | ATCCTGATGG | AACACCAGCA |
| ACACCGCCGT | ATAAAGAAGA | TGTGACCATT | CATTGGA ACT | TTAACTGGTC | GATTCCAGAA |
| GATGTGCGAG | AACAAATGAA | AGCAGGCGAT | TACTTCGAGT | TTCAATTACC | TGGCAATTTG |
| AAACCTAATA | AACCAGGTTT | AGGTGATTTA | GTTGATGCAG | AAGGCAATGT | CTATGGAACC |
| TACACAATTA | GTGAAGATCG | TACGGTTCGT | TTTACCTTTA | ATGAGCGAAT | CACGTCTGAA |
| AGTGACATTG | ACGGGGACTT | TTCTTTAGAT | ACTCATTGTA | ATGATTGAGA | TGGGCGGGCC |
| CCAGGAGATT | GGGTGATTGA | TATTCTTACA | CAAGAAGATT | TGCCGCCTGT | AGTGATTCCA |
| ATTGTCCCAG | ATACCGAACA | ACAAATTGAT | AAACAAGGCC | ATTTTGATCG | AACGCCCAAT |
| CCTAGTGCGA | TTACTTGGAC | GGTAGATATC | AATCAAGCGA | TGAAAGATCA | AACAAATCCA |
| ACTGTGACGG | AAACATGGCC | AACAGGGAAT | ACCTTTAAGT | CCGTGAAAGT | CTATGAGTTA |

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTGATGAATC TTGATGGAAC AATTAAAGAA GTGGGTCGCG AACTTAGTCC AGATGAATAT
 ACCGTTGATA AAAATGGCAA TGTGACGATT AAAGGTGACA CCAACAAAGC GTATCGTCTT
 GAGTACCAAA CGACGATTGA CGAGGCGGTT ATTCCAGATG GCGGCGGCGA TGTGCCTTTT
 AAAAATCACG CGACGTTAAC AAGTGATAAT AATCCAAATG GGTTAGATGC TGAAGCAACT
 GTTACCGCCA CATATGGCAA AATGTTAGAC AAGCGCAATA TAGATTACGA CGAAGCCAAT
 CAAGAATTCA CTGGGGAAAT TAACTACAAC TATGGTGAAC AAACCATTCC AAAAGACCAA
 GCAGTCATTA CAGACACAAT GGGGGATAAT TTAACGTTTG AACCAGATTG TTTACATTTA
 TATTCAGTGA CATTTGATGA CAAAGGAAAT GAAAGTCGTTG GAGCAGAACT TGTGGAAGGA
 AAAGATTACA AAGTGGTAAT CAACGGAGAC GGTTCCTTTG CAATTGACTT TTTACATGAT
 GTGACTGGCG CAGTCAAGAT TGATTATAAA ACCAAAGTTG ATGGAATTGT CGAAGGCGAT
 GTTGCCGTGA ATAATCGTGT GGATGTTGGC ACTGGTCAGC ATTCAGAAGA TGATGGCACA
 GCCAGTCAAC AAAATATTAT TAAAAACACT GGTGCAGTTG ATTATCAAAA TTCAACGATT
 GGTGAGACGT TAGCTGTGAA TCAAAATAAT TATTTGATGG AAAATGCCGT GATTACGGAT
 ACGTACGAAC CAGTTCCTGG CTTAACTATG GTACCCAATT CGTTGGTTGT CAAAGATACA
 ACCACTGGTG CTCAGTTGAC GTTAGGCAAG GATTTTCATGG TAGAAATAAC TCGTAATGCA
 GATGGTGAAG CAGGCTTTAA GGTAAAGTTT ATAGGGGCGT ATGCCAAAAC AAGTGATGCC
 TTCCACATAA CTTATACTAC CTTTTTCGAT GTTACCGAGT TAGACGCTAA CAATCCTGCG
 TTGGACCATT ATCGAAATAC CGCTGCCATT GATTGG

EF123-4 (SEQ ID NO:460)

EEVNSD

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 KKQIQIELNQ QALADTLVLT LNPTATEDVT FSYGQQQRAL TLKTGTDPTT STAITSSPAA
 SANEGSTEEA STNSSVPRSS EETVASTTKA IESKTTESTT VKPRVAGPTD ISDYFTGDET
 TIIDNFEDPI YLNPDGTPAT PPYKEDVTIH WNFNWSIPED VREQMKAGDY FEFQLPGNLK
 PNKPGSGDLV DAEGNVYGTI TISEDGTVRF TFNERITSES DIHGDFSLDT HLNDSGDRGP
 GDWVIDIPTQ EDLPPVVIPI VPDTEQQIDK QGHFDRTPNP SAITWTVDIN QAMKDQTNPT
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 SQQNIKNTG AVDYQNSTIG WTLAVNQNNY LMENAVITDT YEPVPGLTMV PNSLVVKDIT
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 DHYRNTAAID W

EF124-1 (SEQ ID NO:461)

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 CAGAAGAAAC AGATTCAAAT TGAATTGAAT CAGCAAGCGT TAGCAGATAC GTTAGTCTTA
 ACGTTGAACC CTACAGCTAC AGAAGATGTG ACGTTTTCTT ATGGACAACA GCAACGAGCG
 TTGACGTTAA AGACTGGTAC TGATCCGACA GAATCAACGG CAATCACGAG TTCGCCAGCG
 GCATCAGCGA ATGAGGTTT CACAGAAGAA GCATCTACAA ACTCCTCTGT TCCTCGTTCC
 TCCGAAGAAA CTGTGCGCCAG CACGACAAAA GCGATAGAAA GTAAAACAAC TGAATCGACG
 ACTGTCAAAC CGCGCGTAGC AGGACCAACA GATATCAGTG ATTATTTTAC AGGTGATGAA
 ACAACGATTA TCGATAATTT TGAAGATCCG ATTTATTTAA ATCCTGATGG AACACCAGCA
 ACACCGCCGT ATAAAGAAGA TGTGACCATT CATTTGGAAT TTAACGGTTC GATTCCAGAA
 GATGTGCGAG AACAAATGAA AGCAGGCGAT TACTTCGAGT TTCAATTACC TGGCAATTTG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

| | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|
| AAACCTAATA | AACCAGGTTT | AGGTGATTTA | GTTGATGCAG | AAGGCAATGT | CTATGGAACC |
| TACACAATTA | GTGAAGATGG | TACGGTTCGT | TTTACCTTTA | ATGAGCGAAT | CACGTC TGAA |
| AGTGACATT | ACGGGGACTT | TTCTTTAGAT | ACTCATTGGA | ATGATTTCAGA | TGGGCGGGGC |
| CCAGGAGATT | GGGTGATTGA | TATTCCTACA | CAAGAAGATT | TGCCGCCTGT | AGTGATTCCA |
| ATTGTCCCAG | ATACCGAACA | ACAAATTGAT | AAACAAGGCC | ATTTTGATCG | AACGCCCAAT |
| CCTAGTGGCA | TTACTTGGAC | GGTAGATATC | AATCAAGCGA | TGAAAGATCA | AACAAATCCA |
| ACTGTGACGG | AAACATGGCC | AACAGGGAAT | ACCTTTAAGT | CCGTGAAAGT | CTATGAGTTA |
| GTGATGAATC | TTGATGGAAC | AATTAAAGAA | GTGGGTGCGG | AACTTAGTCC | AGATGAATAT |
| ACCGTTGATA | AAAATGGCAA | TGTGACGATT | AAAGGTGACA | CCAACAAAGC | GTATCGTCTT |
| GAGTACCAAA | CGACGATTGA | CGAGGCGGTT | ATTCCAGATG | GCGGCGGCGA | TGTGCCTTTT |
| AAAAATCAGC | CGACGTTAAC | AAGTGATAAT | AATCCAAATG | GGTTAGATGC | TGAAGCAACT |
| GTTACCGCCA | CATATGGCAA | AATGTTAGAC | AAGCGCAATA | TAGATTACGA | CGAAGCCAAT |
| CAAGAAATTC | CTTGGGAAAT | TAAC TACAAC | TATGGTGAAC | AAACCAITCC | AAAAGACCAA |
| GCAGTCATTA | CAGACACAAT | GGGGGATAAT | TTAACGTTTG | AACCAGATTTC | TTTACATTTA |
| TATTCACTGA | CATTTGATGA | CAAAGGAAAT | GAAGTCGTTG | GAGCAGAACT | TGTGGAAGGA |
| AAAGATTACA | AAGTGGTAAT | CAACGGAGAC | GGTTCCTTTG | CAATTGACTT | TTTACATGAT |
| GTGACTGGCG | CAGTCAAGAT | TGATTATAAA | ACCAAAGTTG | ATGGAATTGT | CGAAGGCGAT |
| GTTGCCGTGA | ATAATCGTGT | GGATGTTGGC | ACTGGTCAGC | ATTGAGAAGA | TGATGGCACA |
| GCCAGTCAAC | AAAATATTAT | TAAAAACACT | GGTGCAGTTG | ATTATCAAAA | TTCAACGATT |
| GGTTGGACGT | TAGCTGTGAA | TCAAATAAAT | TATTTGATGG | AAAATGCCGT | GATTACGGAT |
| ACGTACGAAC | CAGTTCCTGG | CTTAAC TATG | GTACCCAATT | CGTTGGTTGT | CAAAGATACA |
| ACCACTGGTG | CTCAGTTGAC | GTTAGGCAAG | GATTTTCATG | TAGAAATAAC | TCGTAATGCA |
| GATGGTGAAA | CAGGCTTTAA | GGTAAGTTTT | ATAGGGGCGT | ATGCCAAAAC | AAGTGATGCC |
| TTCCACATAA | CTTATACTAC | CTTTTTTCGAT | GTTACCGAGT | TAGACGCTAA | CAATCCTGCG |
| TTGGACCATT | ATCGAAATAC | CGCTGCCATT | GATTGGACCG | ATGAAGCAGG | AAACAATCAT |
| CATTGAGAAG | ATAGTAAACC | GTTTAAACCT | TTACCTGCTT | TTGATTTAAA | TGCGCAAAAA |
| AGCGGTGTTT | ACAATGCCGT | CACCAAAGAA | ATCACTTGGA | CGATTGCGGT | TAATTTAAGT |
| AATAATGAA | TAGTCGACGC | CTTTTTGACG | GATCCAATTT | TAACCAATCA | AACCTATTGT |
| GCTGGGAGCT | TGAAAGTCTA | TGAAGGCAAT | ACAAAGCCAG | ATGGTTCGGT | TGAAAAAGTG |
| AAACCAACGC | AACCGTTGAC | GGATATCACA | ATGGAAGAAC | CAAGCGAGAA | AAACCAAAAT |
| ACTTGGCGTG | TTGATTTTCC | TAATGATAGT | CGTACGTATG | TGATTGAATT | TAAGACGTCT |
| GTTGATGAAA | AAGTTATCGA | AGGTTCGGCT | AGTTATGACA | ATACCGCATC | TTATACAAAC |
| CAAGGTTCTT | CACGTGATGT | GACAGGAAAA | GTTTCTATTG | AACATGGTGG | CGAATCAGTG |
| AAAAAAGGTG | GCGAATACCA | CAAAGATGAT | CCAGATCATG | TGTACTGGCA | TGTAATGATC |
| AATGGCGCCC | AATCGGTTTT | AGACGATGTG | GTTATTACTG | ATACACCCTC | ACCAAACCAA |
| GTGCTAGATC | CCGAGTCATT | GGTGATTTAC | GGTACCAACG | TAACAGAAGA | CGGAAC TATT |
| ACGCCAGATA | AATCTGTTAT | TTTAGAAGAA | GGAAAAGATT | ACACACTGGA | AGTTACCACC |
| GATAATGAAA | CAGGACAACA | AAAAATTGTC | GTTAAAATGG | CCCATATTGA | AGCACCTTAT |
| TATATGGAAT | ATCGTAGTTT | AGTGACTTCT | TCAGCGGCGG | GGAGTACAGA | CACGGTATCC |
| AAACCAAGTGT | CAATTACTGG | AAATGGTTCA | GAAGTCGTTT | ATGGGGATGA | CAATGGCGAT |
| GTGGTCGTTG | ACATTGATCA | CAGTGGCGGG | CATGCCACAG | GGACTAAAGG | CAAAATTCAG |
| CTGAAGAAAA | CAGCCATGGA | TGAGACGACT | ATTTTAGCAG | GCGCCCATTT | CCAAATTTGG |
| GACCAAGCTA | AAACACAAGT | CCTACGTGAA | GGTACAGTAG | ATGCCACCGG | GGTTATCACA |
| TTTGGTGGGT | TGCCACAAGG | GCAATACATT | TTGGTGGAGA | CAAAAGCACC | AGAAGGCTAT |
| ACAGTTTCGG | ACGAATTAGC | TAAAGGCCGA | GTCATTACTA | TTGATGAAGA | AACTTCAGCC |
| GAAGGAGCAC | AACCAACCAT | TATTA AAAAC | GATGTCAATA | AAGTATTTT | AGAAAAAATG |
| GATGAGAAGG | GTAAAAAGTT | AGTCAATGCT | CGCTTTAAAT | TAGAGCATGC | CGTAACCACG |
| CCGTTTACTC | ATTGGGAAGA | AGTTCCCTTT | GCGCCGGATC | GAACCAACGC | GAATGGCCAG |
| TTAGAGGTGG | ATAGTTTAAA | ACCAGGGCTT | TATCAGTTCA | CAGAAATCGA | AGCACCGACA |
| GGCTATCTTT | TAGACACGAC | CCCCAAACGA | TTTCATCGTGA | CACAAAATAC | GAGCGGACAA |
| ATTCTGTGATG | TTTCATGTCAA | AATGCTTAAT | TACCAAGGTT | CTGCTGAAC | AATTA AAAAA |
| GACCAAGCAG | GCAATCCATT | AGCAGGTGCT | GAATTTTCAG | TCCTTGACAC | CACAGGACAA |
| GCAGTTCGAG | AACACTTAGT | TTCGGATGCA | AACGGAAAAG | TCACAGTGAC | GGATTTAGCC |
| CCAGGAAAAAT | ATCAATTTGT | GGAAACCAAA | GCGCCAGCAG | GGTACCTTTT | AAACACTGAA |

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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CCAAGTGCTT TCACGATTGC AGCAAGCGAT CGGGGCAAAC CAGCAACAGT TATAGCAACG
GCTAACTTTG TTAACATATCA AGGCACGGCT AAATTAATCA AAAAAGATGT GAATGGACAC
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TTTGTAGAAA CCAAAGCGCC AACAGGCTAT TTATTAAATA CCACGCCAGT CCCATTTGAA
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TACAAAGGGG CTTTCCAAAT CGTGAAAACG AATAGCGCAG ACCAACCATT AGCAGGTGCT
GTTTTTGAAT TATATGATCA CAATAAACAA TCATTAGGGA TTACAGCAAC GAGTGGCAAA
GATGGCAAAA TTATCTTTAG AGACTTGGCG CCAGGTACCT ATTATTACAA AGAAATCAAA
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TCAAATGATA AACAACCACT AGATGAGTTA GAGTTTGTA ATTATCAAGC AGAAGTAATG
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CTTGGTTTAC CGAAAACCAA CACACAAGTC AATTACTTCT TTGCTTTTAT CGGCCTCATG
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EF124-2 (SEQ ID NO:462)

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TIIDNFEDPI YLNPDGTPAT PPYKEDVTIH WNFNWSIPED VREQMKAGDY FEFQLPGNLK
PNKPGSGDLV DAEGNVYGTY TISEDGTVRF TFNERITSES DIHGDFSLDT HLNDSGRGP
GDWVIDIPTQ EDLPPVVIPI VPDTEQQIDK QGHFDRTPNP SAITWTV DIN QAMKDQTNPT
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SQQNIKNKG AVDYQNSTIG WTLAVNQNNY LMENAVITDT YEPVPLTMV PNSLVVKDTT
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DHYRNATAID WTDEAGNNHH SEDSKPFKPL PAFDLNAQKS GYNAVTK EI TWTI AVNLSN
NRLVDAFLTD PILTNQTYLA GSLKVYEGNT KPDGSVEKVK PTQPLTDITM EEPSEKNQNT
WRVDFPNDSR TYVIEFKTSV DEKVI EG SAS YDNTASYTNQ GSSRDVTGKV SIQHGGESVK
KGGEYHKDDP DHVYWHV MIN GAQSVLDDVV ITDTPSPNQV LDPESLVIYG TNVTEDGTIT

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 QAKTQVLREG TVDATGVITF GGLPQGQYIL VETKAPEGYT VSDELAKGRV ITIDEETSAE
 GAQPTIIKND VNKVFLEKMD EKGKKLVNAR FKLEHAVTTP FTHWEEVPLA PDRTNANGQL
 EVDSLKPGLY QFTEIEAPTG YLLDTPPKRF IVTQNTSGQI RDVHVKMLNY QGSaelIKKD
 QAGNPLAGAE FSVLDTTGQA VREHLVSDAN GKVTVTDLAP GKYQFVETKA PAGYLLNTEP
 SAFTIAASDR GKPATVIATA NFVNYQGTAK LIKKDVNGHL LSGATFKVLD AKGETIQTGL
 TTNNQGEIVA EHLAPGKYRF VETKAPTGYL LNTTPVPFEI AEKNAGKPAV VVASDNFVSY
 KGAFQIVKTN SADQPLAGAV FELYDHNKQS LGITATSGKD GKIIFRDLAP GTYYYKEIKA
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 KLYRIENGEK IFEREVTAEK DGSLAMEDLG AGSYELDELD ATDGYIVNKQ PIYFVVKNS
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 VSEITTDKTK EIIYAKLNEG HYVLVETKAP TGYLLDITLH PFDVTAQLGK EQPIALGDLI
 NYQGTAAQLTK ENETGEALAG AVFKVIDETG QTVDGQTNLM SDKQGKVIK NLAPGTYRFV
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 VGLASWLFYK KSKK

EF124-3 (SEQ ID NO:463)

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 GTTGATGAAA AAGTTATCGA AGGTTCGGCT AGTTATGACA ATACCGCATC TTATACAAAC
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 GCAGTTCGAG AACACTTAGT TTCGGATGCA AACGGAAAAG TCACAGTGAC GGATTTAGCC
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 TTATTAAGTG GTGCGACATT TAAAGTGCTT GATGCGAAGG GAGAAACGAT TCAACAGGC
 TTGACGACAA ATAATCAAGG G

EF124-4 (SEQ ID NO:464)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AF HITYTTFFDV TELDANNPAL

DHYRNTAAID WTDEAGNNHH SEDSKPFKPL PAFDLNAQKS GVYNAVTKEI TWTIAVNLSN
 NRLVDAFLTD PILTNQTYLA GSLKVYEGNT KPDGSVEKVK PTQPLTDITM EEPSEKNQNT
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 KGGEYHKDDP DHVYWHVMIN GAQSVLDDVV ITDTPSPNQV LDPESLVIYG TNVTEDGTIT
 PDKSVILEEG KDYTLEVITD NETGQQKIVV KMAHIEAPYY MEYRSLVTSS AAGSTDVTSN
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 QAKTQVLREG TVDATGVITF GGLPQGQYIL VETKAPEGYT VSEDELAGRV ITIDEETSAE
 GAQPTIIKND VNKVFLEKMD EKGKKLVNAR FKLEHAVTTP FTHWEEVPLA PDRTNANGQL
 EVDSLKPGLY QFTEIEAPTG YLLDTPPKRF IVTQNTSGQI RDVHVKMLNY QGSAELIKKD
 QAGNPLAGAE FSVLDTTGQA VREHLVSDAN GKVTVTDLAP GKYQFVETKA PAGYLLNTEP
 SAFTIAASDR GKPATVIATA NFVNYQGTAK LIKKDVNGHL LSGATFKVLD AKGETIQTGL
 TTNNQG

EF125-1 (SEQ ID NO:465)

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 GATGGCCAGT TAACGTTAGG AGAAGTGAAG CAAACCAGCC AGCAAGAAAT GACCTTAGCG
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 CAGAAGAAAC AGATTCAAAT TGAATTGAAT CAGCAAGCGT TAGCAGATAC GTTAGTCTTA
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 TTGACGTTAA AGACTGGTAC TGATCCGACA GAATCAACGG CAATCACGAG TTCGCCAGCC
 GCATCAGCGA ATGAAGGTTT AACAGAAGAA GCATCTACAA ACTCCTCTGT TCCTCGTTCCG
 TCCGAAGAAA CTGTGCGCCAG CACGACAAAA GCGATAGAAA GTAAACAAC TGAATCGACG
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 ATTGTCCCAG ATACCGAACA ACAAATTGAT AAACAAGGCC ATTTTGATCG AACGCCAAT
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 GTGATGAATC TTGATGGAAC AATTAAAGAA GTGGGTCGCG AACTTAGTCC AGATGAATAT
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 CAAGAATTCA CTTGGGAAAT TAACATAAC TATGGTGAAC AAACCATTC AAAAGACCAA
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 AAAGATTACA AAGTGTAAT CAACGGAGAC GGTTCCTTTG CAATTGACTT TTTACATGAT
 GTGACTGGCG CAGTCAAGAT TGATTATAAA ACCAAAGTTG ATGGAATTGT CGAAGGCGAT
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 GCCAGTCAAC AAAATATTAT TAAAAACACT GGTGCAGTTG ATTATCAAAA TTCAACGATT
 GGTGAGACGT TAGCTGTGAA TCAAAATAAT TATTTGATGG AAAATGCCGT GATTACGGAT
 ACGTACGAAC CAGTTCCTGG CTTAACTATG GTACCCAATT CGTTGGTTGT CAAAGATACA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

| | | | | | |
|-------------|-------------|-------------|------------|------------|-------------|
| ACCACTGGTG | CTCAGTTGAC | GTTAGGCAAG | GATTTCATGG | TAGAAATAAC | TCGTAATGCA |
| GATGGTGAAA | CAGGCTTTAA | GGTAAGTTTT | ATAGGGGCGT | ATGCCAAAAC | AAGTGATGCC |
| TTCCACATAA | CTTATACTAC | CTTTTTTCGAT | GTTACCGAGT | TAGACGCTAA | CAATCCTGCG |
| TTGGACCATT | ATCGAAATAC | CGCTGCCATT | GATTGGACGG | ATGAAGCAGG | AAACAATCAT |
| CATTCAGAAG | ATAGTAAACC | GTTTAAACCT | TTACCTGCTT | TTGATTTAAA | TGCGCAAAAA |
| AGCGGTGTTT | ACAATGCCGT | CACCAAAGAA | ATCACTTGGG | CGATTGCGGT | TAATTTAAGT |
| AATAATCGTT | TAGTCGACGC | CTTTTTTGACG | GATCCAATTT | TAACCAATCA | AACCTATTTG |
| GCTGGGAGCT | TGAAAAGTCTA | TGAAGGCAAT | ACAAAGCCAG | ATGGTTCGGT | TGAAAAAAGTG |
| AAACCAACGC | AACCGTTGAC | GGATATCACA | ATGGAAGAAC | CAAGCGAGAA | AAACCAAAAT |
| ACTTGGCGTG | TTGATTTTCC | TAATGATAGT | CGTACGTATG | TGATTGAATT | TAAGACGTCT |
| GTTGATGAAA | AAGTTATCGA | AGGTTCCGGCT | AGTTATGACA | ATACCGCATC | TTATACAAAC |
| CAAGGTTCTT | CACGTGATGT | GACAGGAAAA | GTTTCTATTG | AACATGGTGG | CGAATCAGTG |
| AAAAAAGGTG | GCGAATACCA | CAAAGATGAT | CCAGATCATG | TGTACTGGCA | TGTAATGATC |
| AATGGCGCCC | AATCGGTTTT | AGACGATGTG | GTTATTACTG | ATACACCCTC | ACCAAACCAA |
| GTGCTAGATC | CCGAGTCATT | GGTGATTTAC | GGTACCAACG | TAACAGAAGA | CGGAACTATT |
| ACGCCAGATA | AATCTGTTAT | TTTAGAAGAA | GGAAAAGATT | ACACACTGGA | AGTTACCACC |
| GATAATGAAA | CAGGACAACA | AAAAATTGTC | GTTAAAATGG | CCCATTATGA | AGCACCTTAT |
| TATATGGAAT | ATCGTAGTTT | AGTGACTTCT | TCAGCGGCGG | GGAGTACAGA | CACGGTATCC |
| AACCAAGTGT | CAATTACTGG | AAATGGTTCA | GAAGTCGTTT | ATGGGGATGA | CAATGGCGAT |
| GTGGTCGTTG | ACATTGATCA | CAGTGGCGGG | CATGCCACAG | GGACTAAAGG | CAAAATTCAG |
| CTGAAGAAAA | CAGCCATGGA | TGAGACGACT | ATTTTAGCAG | GCGCCCATTT | CCAAATTTGG |
| GACCAAGCTA | AAACACAAGT | CCTACGTGAA | GGTACAGTAG | ATGCCACCGG | GGTTATCACA |
| TTTGGTGGGT | TGCCACAAGG | GCAATACATT | TTGGTGGAGA | CAAAAGCACC | AGAAGGCTAT |
| ACAGTTTCGG | ACGAATTAGC | TAAAGGCCGA | GTCATTACTA | TTGATGAAGA | AACCTCAGCC |
| GAAGGAGCAC | AACCAACCAT | TATTA AAAAC | GATGTCAATA | AAGTATTTTT | AGAAAAAATG |
| GATGAGAAGG | GTAAAAAGTT | AGTCAATGCT | CGCTTTAAAT | TAGAGCATGC | CGTAACCACG |
| CCGTTTACTC | ATTGGGAAGA | AGTTCCTCTT | GCGCCGGATC | GAACCAACGC | GAATGGCCAG |
| TTAGAGGTGG | ATAAGTTTAA | ACCAGGGCTT | TATCAGTTCA | CAGAAATCGA | AGCACCGACA |
| GGCTATCTTT | TAGACACGAC | CCCCAAACGA | TTCATCGTGA | CACAAAATAC | GAGCGGACAA |
| ATTTCGTGATG | TTCATGTCAA | AATGCTTAAT | TACCAAGGTT | CTGCTGAACT | AATTAAAAAA |
| GACCAAGCAG | GCAATCCATT | AGCAGGTGCT | GAATTTTCAG | TCCTTGACAC | CACAGGACAA |
| GCAGTTCGAG | AACACTTAGT | TTCCGGATGCA | AACGGAAAAG | TCACAGTGAC | GGATTTAGCC |
| CCAGGAAAAT | ATCAATTTGT | GGAAACCAAA | GCGCCAGCAG | GGTACCTTTT | AAACACTGAA |
| CCAAGTGCTT | TCACGATTGC | AGCAAGCGAT | CGGGGCAAAC | CAGCAACAGT | TATAGCAACG |
| GCTAACTTTG | TTAACTATCA | AGGCACGGCT | AAATTAATCA | AAAAAGATGT | GAATGGACAC |
| TTATTAAGTG | GTGCGACATT | TAAAGTGCTT | GATGCGAAGG | GAGAAACGAT | TCAAACAGGC |
| TTGACGACAA | ATAATCAAGG | GGAAATTGTT | GCAGAGCACT | TAGCCCCAGG | AAAATATCGC |
| TTTGTAGAAA | CCAAAGCGCC | AACAGGCTAT | TTATTAATAA | CCACGCCAGT | CCCATTGTGA |
| ATTGCTGAGA | AAAATGCTGG | TAAACCGCG | GTCGTGGTTG | CTAGTGACAA | CTTTGTGAGT |
| TACAAAGGGG | CTTTCCAAAT | CGTGAAAACG | AATAGCGCAG | ACCAACCATT | AGCAGGTGCT |
| GTTTTTGAAT | TATATGATCA | CAATAAACAA | TCATTAGGGA | TTACAGCAAC | GAGTGGCAAA |
| GATGGCAAAA | TTATCTTTAG | AGACTTGCGG | CCAGGTACCT | ATTATTACAA | AGAAATCAAA |
| GCACCAAAAT | TACCAGATGG | CGCAGATTAT | ATTATTTATC | CTGAATTAGT | AAAAGTAGAA |
| ATTCGTGGTG | ATTTCAAAGG | TGATCCGGAG | ATTTTCCAAT | TAGGGGCCCT | CGCCAATTTT |
| AAAGGACCGG | CCGTCTTTAA | GAAAATTGAT | GCCAATGCGA | ACCCACTTCC | AGGAACGATT |
| TTTAAATTGT | ATCGAATCGA | AAACGGGGAA | AAAACTTTTG | AAAGAGAAGT | AAGTGTGAA |
| AAAGATGGTT | CATTGGCTAT | GGAGGATTTA | GGTGCTGGTA | GCTATGAATT | AGATGAAC TG |
| GATGCAACGG | ATGGCTATAT | CGTCAATAAA | CAACCCATTT | ATTTTGTAGT | GAAGAAGAAT |
| TCAAATGATA | AACAACCACT | AGATGAGTTA | GAGTTTGTA | ATTATCAAGC | AGAAGTAATG |
| GGACGTAAAG | TCAACGAGCA | AGGTCAAACC | TTAGCGGGTG | CAGTTTTTGC | AATTTACAAT |
| GCCGATGAGC | AGAATCAGCC | CCAAGGTTCA | CCGATAACAT | TCTTGAATCG | TGCAGGAGAA |
| AAAGTTTCTG | AAATAACAAC | GGATAAGACT | GGCGAAATTT | ACGCTAAAGG | GCTAAATGAA |
| GGGCATTACG | TTTTAGTGGA | AACGAAAGCA | CCAACAGGCT | ATCTGTTAGA | CACAACGCTA |
| CATCCATTTG | ATGTAACCGC | CCAATTAGGA | AAAGAGCAGC | CAATTGCTTT | AGGCGATCTT |

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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ATCAATTATC AAGGAACTGC TCAATTAACC AAAGAAAACG AAACAGGTGA AGCATTGGCA
GGTGCCTGT TTAAGGTCAT TGATGAAACA GGGCAAACCG TAGATGGACA AACCAATCTG
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TACCAAGGTG CTGCCAAGCT GGTGAAAAAT GATCAGCAAA AGAATGCCTT AGCAGGTGCT
GAATTTAAAG TGACAGATGC AGAGACAGGG CAAACTGTCG CTCGTTTATT ACGTTCTGAC
AACCAAGGTT TAGTTCAGT GAACCACTTA CAACCAGGAA AATATACCTT TGTGGAAACA
AAAGCACCGG ATGTTTACCA ACTGTCTAAG CAAGCTGTCG CATTCACTAT TCGGCAACA
GCGAAAGACA AACCTGAACT CGTGAATGCG GGCACGTTTG TTAACGAGAA ACAACCTGTA
TCCAAAAAAA CAAAACCAAA TCAGCCAACA ACGAAACAAG CAGCTAGAGA GACAGGTTGG
CTTGGTTTAC CGAAAACCAA CACACAAGTC AATTACTTCT TTGTCTTTAT CGGCCTCATG
TTGGTCGGTT TGGCAAGTTG GCTCTTCTAT AAAAAGAGCA AGAAATAA

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EF125-2 (SEQ ID NO:466)

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SANEGSTEEA STNSSVPRSS EETVASTTKA IESKTTTESTT VKPRVAGPTD ISDYFTGDET
TIIDNFEDPI YLNPDGTPAT PPYKEDVTIH WNFNWSIPED VREQMKAGDY FEFQLPGLNK
PNKPGSGDLV DAEGNVYGTI TISEDGTVRF TFNERITSES DIHGDFSLDT HLNDSGRGP
GDWVIDIPTQ EDLPPVVIPI VPDTEQQIDK QGHFDRTPNP SAITWTVGIN QAMKDQTNPT
VTETWPTGNT FKSVKVYELV MNLDGTIKEY GRELSPDEYT VDKNGNVTIK GDTNKAYRLE
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EFTWEINYNY GEQTIKPDQA VITDTMGDNL TFEPDSLHLY SVTFDDKGNE VVGAELEGGK
DYKVVINGDG SFAIDFLHDV TGAVKIDYKT KVDGIVEGDV AVNNRVDVGT GQHSDDGTA
SQQNIKNTG AVDYQNSTIG WTLAVNQNNY LMENAVITDT YEPVPGITMV PNSLVVKDIT
TGAQNTLGKD FMVEITRNAD GETGFKVSFI GAYAKTSDAF HITYTTFFDV TELDANNPAL
DHYRNTAAID WTDEAGNNHH SEDSKPFKPL PAFDLNAQKS GYVNAVTKEI TWTIAVNLN
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GAQPTIINKD VNKVFLEKMD EKGKLVNAR FKLEHAVTTP FTHWEEVPLA PDRTNANGQL
EVDLSKPGLY QFTEIEAPTG YLLDTPPKRF IVTQNTSGQI RDVHVKMLNY QGSAELIKKD
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SAFTIAASDR GKPATVIATA NFVNYQGTAK LIKKDVNGHL LSGATFKVLD AKGETIQTGL
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KLYRIENGK IFEREVTAEK DGSAMEDLG AGSYELDELD ATDGYIVNKQ PIYFVVKNS
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VSEITTDKTG EIYAKGLNEG HYVLVETKAP TGYLLDITLH PFDVTAQLGK EQPIALGLDI
NYQGTALTK ENETGEALAG AVFKVIDETG QTVGQTNLM SDKQGVIAK NLAPGTYRFV
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VGLASWLFYK KSKK

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EF125-3 (SEQ ID NO:467)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 TTGACGACAA ATAATCAAGG GGAAATTGTT GCAGAGCACT TAGCCCCAGG AAAATATCGC
 TTTGTAGAAA CCAAAGCGCC AACAGGCTAT TTATTAAATA CCACGCCAGT CCCATTGAA
 ATTGCTGAGA AAAATGCTGG TAAACCAGCG GTCGTGGTTG CTAGTGACAA CTTTGTGAGT
 TACAAAGGGG CTTTCCAAAT CGTGAAAACG AATAGCGCAG ACCAACCATT AGCAGGTGCT
 GTTTTTGAAT TATATGATCA CAATAAACAA TCATTAGGGA TTACAGCAAC GAGTGGCAAA
 GATGGCAAAA TTATCTTTAG AGACTTGGCG CCAGGTACCT ATTATTACAA AGAAATCAAA
 GCACCAAAAT TACCAGATGG CGCAGATTAT ATTATTTATC CTGAATTAGT AAAAGTAGAA
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 GGACGTAAAG TCAACGAGCA AGGTCAAACC TTAGCGGGTG CAGTTTTTGC AATTTACAAT
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 GCGAAAGACA AACCTGAAC TCGTAATGCG GGCACGTTTG TTAACGAGAA ACAACCTGTA
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EF125-4 (SEQ ID NO:468)

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 KGAFQIVKTN SADQPLAGAV FELYDHNKQS LGITATSGKD GKIIFRDLAP GTYYYKEIKA
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 FKVTDIETGQ TVARSLRSDN QGLVQVNLH PQKYTFVETK APDGYQLSKQ AVAFTIAATA
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EF126-1 (SEQ ID NO:469)

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 GAAGCGGTTA AAGCAGGAGA TACAGAAGGA ATGACCAATA CCGTGAAAGT GAAAGACGAC
 AGTCTGGCTG ATTGTAACCG GATATTGGAA GGACAAGCTA CTTTCCCAGT TCAAGCGGGT
 GAAACGGAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GTGGTAGTTT TTCAGATAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTTAGATGG TTACTTGCAT
AAGACCAATA CCAATGATTC AATCAATGAA TATCCAGATC CAAGACATCC TCTTCAAGTC
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GANGAAAATG GCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAAA TAACAAAGTA
ACTTTTACTA TGAACAAAAA AGATGACAGC TACTCTTACT TAGCTGGTCA TACATACACA
ATGACTATTA CCACTAAAAT TAAAACTGAC GCAACGGATG AAGAATTAGC GCCTTATATT
GAACAAGGCG GGATTCCCAA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTTG
CATTCCAACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCT
GAACCTAAAC AACCGCTAAA ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCACC
ACGAACCCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TTCATTTACC AATGACTAAT
ACAACAGTAA ATCCACTTTA CATGATCGCA GGTTTAATTG TCCTTATAGT GGCTATTAGC
TTTGGCATAA CAAAAAATAA AAAAAGAAAA AATTAG

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EF126-2 (SEQ ID NO:470)

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MF KKATKLLSTM VIVAGTVVGN FSPTLALAE AVKAGDTEGM TNTVKVKDDS
LADCKRILEG QATFPVQAGE TEPVDLVVVE DASGSFSDNF PHVRQAIDEV VQGLSDQDRV
MLASYRGGKQ FMFPDGKTKI NSADYDMNVR VNTQLTYDKS QFVSGFGDVR TYGGTPTAPG
LKLALDQYNG THGDLTNRKT YFLLVTDGVA NTRLDGYLHK TNTNDSINEY PDPRHPLOVS
VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPVFKQE
LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
NDVPVQINGQ TISATSTEGY VGNITIHVEV KENTAIDAAT LVSSGTMNQG TIAKEFPEAT

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

IPKNDNAHAC DVTPEPTIT KDIENTEHLDTNREDSFDW HVKTAFGNET STWTQASMVD
 DINKVLDIID VKVTDENGKD VTANGTVTQE NNKVTFEMNK QADSYDYLSG HTYTMITTTK
 IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHSNKPT VTPPPVDPNI AKDVEGQEHL
 DLTNRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDIT DVKVTDENGK DVTANGKVTQ
 ENNKVTFEMN XQADSYDYLS GHYTYMTITT KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHSNKPT TVTPPAPTPE DPTITKDIEG QEHLDTNDRD QEFKWNVKTA FGNETSTWTQ
 ASMVDINKV LDITDVKVXX ENKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLKPKKP LTPTNHQAPT NPVNFGRKAS KGIHLPMNT TVNPLYMIAG LIVLIVAISF
 GITKNKKRKN

EF126-3 (SEQ ID NO:471)

TGAA

GAAGCGGTTA AAGCAGGAGA TACAGAAGGA ATGACCAATA CGGTGAAAAGT GAAAGACGAC
 AGTCTGGCTG ATTGTAAACG GATATTGGAA GGACAAGCTA CTTTCCCAGT TCAAGCGGGT
 GAAACGGAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GTGGTAGTTT TTCAGATAAT
 TTTCCACATG TAAGACAAGC GATTGATGAA GTGGTTCAAG GCTTATCTGA TCAAGACCGC
 GTGATGCTGG CTTCATATCG CGGCGGAAAA CAATTTATGT TTCTGATGCG AAAGACAAAA
 ATTAATTCAG CTGATTATGA TATGAATGTG CGCGTCAATA CGCAATTGAC TTATGATAAA
 AGCCAATTTG TCTCTGGTTT TGGAGACGTT CGGACGTATG GTGGTACGCC AACC GCCCA
 GGATTGAAAC TCGCTTTAGA TACGTACAAT CAAACACACG GAGATTTAAC GAATCGAAAA
 ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTTAGATGG TTACTTGCAT
 AAGACCAATA CCAATGATTC AATCAATGAA TATCCAGATC CAAGACATCC TCTTCAAGTC
 TCAGTGAAT ATAGTAATGA CTACCAAGGT GCAGCAGCAG AAGTTTTCAG GTTAAACCAA
 GAAATTACTA ACCAAGGCTA TGAAATGATT AATGCGTATT GGGAAAGTGT TGAATCTTTA
 AGTTCAGTGA ATTCATACTT TGATAAATAT AAAACAGAAG TGGGTCCTTT TGTAACAA
 GAGTTGCAAC AAGGGTCTAG CACACCAGAA GATTTTATTA CAAGCCAATC TATTGATGAT
 TTTCAACCC AATTAACAA AATTGTCAAA GATCGTCTGG CGCAATCGAC ACCAGCAACA
 GCTTCATTAA CGATTGCCAA TCAATTGAT ATTCAATCTG CGACCGCTAC GGACGATGCT
 GGAAATGATG TGCCTGTTC AATTAAACGA CAAACCATTT CAGCAACTAG TACAGAAGGT
 TACGTAGGAA ACATCACGAT TCACTACGAA GTCAAAGAAA ATACAGCGAT TGAT

EF126-4 (SEQ ID NO:472)

EE AVKAGDTEGM TNTVKVKDDS

LADCKRILEG QATFPVQAGE TEPVDLVVVE DASGSFSDNF PHVRQAIDEV VQGLSDQDRV
 MLASYRGGKQ FMFPDGKTKI NSADYDMNVR VNTQLTYDKS QFVSGFGDVR TYGGTPTAPG
 LKLALDTYNQ THGDLTNRKT YFLLVTDGVA NTRLDGYLHK TNTNDSINEY PDPRHPLQVS
 VEYSNDYQGA AAEVLALNQE ITNQYEMIN AYWESVESLS SVNSYFDKYK TEVGPFVKQE
 LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
 NDVPVQINGQ TISATSTEGY VGNITIHIEV KENTAID

EF127-1 (SEQ ID NO:473)

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 ATGGTGATTG TCGCTGGAAC AGTTGTGGGA AATTTTCAGT CCACATTGGC TTTAGCTGAA
 GAAGCGGTTA AAGCAGGAGA TACAGAAGGA ATGACCAATA CGGTGAAAAGT GAAAGACGAC
 AGTCTGGCTG ATTGTAAACG GATATTGGAA GGACAAGCTA CTTTCCCAGT TCAAGCGGGT
 GAAACGGAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GTGGTAGTTT TTCAGATAAT
 TTTCCACATG TAAGACAAGC GATTGATGAA GTGGTTCAAG GCTTATCTGA TCAAGACCGC
 GTGATGCTGG CTTCATATCG CGGCGGAAAA CAATTTATGT TTCTGATGCG AAAGACAAAA
 ATTAATTCAG CTGATTATGA TATGAATGTG CGCGTCAATA CGCAATTGAC TTATGATAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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AGCCAATTG TCTCTGGTTT TGGAGACGTT CGGACGTATG GTGGTACGCC AACCGCCCCA
GGATTGAAAC TCGCTTTAGA TACGTACAAT CAAACACACG GAGATTTAAC GAATCGAAAA
ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTTAGATGG TTACTTGCAT
AAGACCAATA CCAATGATTC AATCAATGAA TATCCAGATC CAAGACATCC TCTTCAAGTC
TCAGTGGAAAT ATAGTAATGA CTACCAAGGT GCAGCAGCAG AAGTTTTAGC GTTAAACCAA
GAAATTACTA ACCAAGGCTA TGAAATGATT AATGCGTATT GGGAAAGTGT TGAATCTTTA
AGTTCAGTGA ATTCATACTT TGATAAATAT AAAACAGAAG TGGGTCCTTT TGTAACAA
GAGTTGCAAC AAGGGTCTAG CACACCAGAA GATTTTATTA CAAGCCAATC TATTGATGAT
TTTACAACCC AATTAAACA AATTGTCAAA GATCGTCTGG CGCAATCGAC ACCAGCAACA
GCTTCATTAA CGATTGCCAA TCAATTTGAT ATTCAATCTG CGACCGCTAC GGACGATGCT
GGAAATGATG TGCCTGTTCA AATTAACGGA CAAACCATTT CAGCAACTAG TACAGAAAGCT
TACGTAGGAA ACATCACGAT TCACTACGAA GTCAAAGAAA ATACAGCGAT TGATGCAGCA
ACCTTGTGTA GTAGTGGGAC AATGAATCAA GGAACAATTG CTAAGGAATT TCCAGAAGCG
ACGATTCCTA AAAATGACAA TGCGCATGCG TGTGACGTGA CGCCAGAAGA TCCAACGATT
ACAAAAGATA TCGAAAATCA AGAACACTTA GATTTAACCA ATCGTGAAGA TAGTTTCGAT
TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCCAGC CAGCATGGTG
GATGACATTA ATAAAGTGCT AGATATCATT GATGTGAAAG TCACCGACGA AAATGGTAAA
GATGTTACAG CTAACGGCAC AGTAACACAA GAAAATAACA AAGTAACTTT TGAAATGAAC
AAACAAGCAG ACAGCTATGA CTATTTAAGT GGTACATACG ATACAATGAC TATCACCCT
AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT
CCCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGACG TGTTACATTC CAACAAACCA
ACCGTAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAG ACAAGAACAT
TTAGATTTAA CCAACCGCGA TCAAGAATTT AAATGGAACG TCAAAACAGC TTTCGGTAAC
GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
ACTGATGTAA AAGTCACAGA TGAAAATGGT AAAGATGTTA CAGCTAACCG CAAAGTAACA
CAAGAAAATA ACAAAGTAAC TTTTGAAATG AACAANCAAG CNGACAGCTA TGACTATTTA
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AACGAAGGTG ACGTGTGCA TTCCAACAAA CCAACCGTAA CACCACCTGC ACCAACGCCA
GAAGATCCAA TGATTACAAA AGATATCGAA GGCCAAGAAC ATTTAGATTT AACCAACCGT
GACCAAGAAAT TTAATGGGAA CGTCAAAACA GCTTTTCGTA ACGAAACAAG CACATGGACC
CAAGCCAGCA TGGTGGATGA CATTAAATAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
GANGAAAATG GCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAAA TAACAAAGTA
ACTTTTACTA TGAACAAAAA AGATGACAGC TACTCTTACT TAGCTGGTCA TACATACACA
ATGACTATTA CCACTAAAAT TAAACTGAC GCAACGGATG AAGAATTAGC GCCTTATATT
GAACAAGGCG GGATTCCCAA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTTG
CATTCCAACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCTT
GAACCTAAAC AACCCTAAA ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCACC
ACGAACCCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TTCAATTTACC AATGACTAAT
ACAACAGTAA ATCCACTTTA CATGATCGCA GGTTTAATTG TCCTTATAGT GGCTATTAGC
TTTGGCATAA CAAAAATAA AAAAAGAAAA AATTAG

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EF127-2 (SEQ ID NO:474)

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MF KKATKLLSTM VIVAGTVVGN FSPTLALAE AVKAGDTEGM TNTVKVKDDS
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MLASYRGKQQ FMFPDGKTKI NSADYDMNVR VNTQLTYDKS QFVSGFGDVR TYGGTPPTAPG
LKLALDFTYNQ THGDLTNRKT YFLLVTDGVA NTRLDGYLHK TNTNDSINEY PDPRHPLQVS
VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPFFVKQE
LQQGSSSTPED FITSQSIDD FTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
LVNVPVINGQ TISASTEGY VGNITIHVEV KENTAIDAAT LVSSGTMTNQG TIAKEFPEAT
IPKNDNAHAC DVTPEPTIT KDIENQEHLD LTNREDSFDW HVKTAFGNET STWTQASMVD
DINKVLDIID VKVTDENGKD VTANGTVTQE NNKVTFEMNK QADSYDYLGS HTYTMITITK
IKTDATDEEL APYIEQGQIP NQADLNFNGE GDVLHSNKPT VTPPPVDPNI AKDVEGQEH

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

DLTNRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDIT DVKVTDENCK DVTANGKVTO
 ENNKVTFEMN XQADSYDYLS GHYTMITTT KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHSNKP TVTPPAPTPE DPTITKDIEG QEHLDTNRD QEFKWNVKA FGNETSTWTQ
 ASMVDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLKPKKP LPTPNHQAPT NPVNFKSAS KGIHLPMTNT TVNPLYMIAG LIVLIVAISF
 GITKNKKRKN

EF127-3 (SEQ ID NO:475)

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 ACGATTCTTA AAAATGACAA TCGCATGCG TGTGACGTGA CGCCAGAAGA TCCAACGATT
 ACAAAGATA TCGAAATCA AGAACAATTA GATTTAACCA ATCGTGAAGA TAGTTTCGAT
 TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCCAAGC CAGCATGGTG
 GATGACATTA ATAAAGTGCT AGATATCATT GATGTGAAAG TCACCGACGA AAATGGTAAA
 GATGTTACAG CTAACGGCAC AGTAACACAA GAAAATAACA AAGTAACCTT TGAAATGAAC
 AAACAAGCAG ACAGCTATGA CTATTTAAGT GGTTCATACG ATACAATGAC TATCACCCT
 AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT
 CCCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGACG TGTACATTTC CAACAAACCA
 ACCGTAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAGG ACAAGAACAT
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EF127-4 (SEQ ID NO:476)

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 DINKVLDIID VKVTDENGKD VTANGVTQE NNVKTFEMNK QADSYDYLSG HTYTMITTTK
 IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHSNKP VTPPPVDPNI AKDVEGQEH
 DLTNRDQEFK WNVKTAFGNE TSTWTQASMV DDIN

EF128-1 (SEQ ID NO:477)

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 GAAGCGGTTA AAGCAGGAGA TACAGAAGGA ATGACCAATA CGGTGAAAGT GAAAGACGAC
 AGTCGCGTG ATTGTAAACG GATATTGGAA GGACAAGCTA CTTTCCAGT TCAAGCGGGT
 GAAACGGAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GTGGTAGTTT TTCAGATAAT
 TTTCCACATG TAAGACAAGC GATTGATGAA GTGGTTCAAG GCTTATCTGA TCAAGACCGC
 GTGATGCTGG CTTTATATCG CGGCGGAAAA CAATTTATGT TTCTGATGG AAAGACAAAA
 ATTAATTCAG CTGATTATGA TATGAATGTG CGCGTCAATA CGCAATTGAC TTATGATAAA
 AGCCAAATTTG TCTCTGTTT TGGAGACGTT CGGACGTATG GTGGTACGCC AACCAGCCCCA
 GGATTGAAAC TCGCTTTAGA TACGTACAAT CAAACACACG GAGATTTAAC GAATCGAAAA
 ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTTAGATGG TTACTTGCAT
 AAGACCAATA CCAATGATTC AATCAATGAA TATCCAGATC CAAGACATCC TCTTCAAGTC
 TCAGTGGAAT ATAGTAATGA CTACCAAGGT GCAGCAGCAG AAGTTTATAG GTTAAACCAA
 GAAATTACTA ACCAAGGCTA TGAAATGATT AATGCGTATT GGGAAAGTGT TGAATCTTTA
 AGTTCAGTGA ATTCACTT TGATAAATAT AAAACAGAAG TGGGTCCTTT TGTAACAA
 GAGTTGCAAC AAGGGTCTAG CACACCAGAA GATTTTATTA CAAGCCAATC TATTGATGAT
 TTTACAACCC AATTAAACA AATTGTCAAA GATCGTCTGG CGCAATCGAC ACCAGCAACA
 GCTTCATTAA CGATTGCCAA TCAATTTGAT ATTCAATCTG CGACCGCTAC GGACGATGCT
 GGAAATGATG TGCCTGTTCA AATTAACGGA CAAACCATTT CAGCAACTAG TACAGAAGGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TACGTAGGAA ACATCAGGAT TCACTACGAA GTCAAAGAAA ATACAGCGAT TGATGCAGCA
 ACCCTTGTA GTAGTGGGAC AATGAATCAA GGAACAATTG CTAAGGAATT TCCAGAAGCG
 ACGATTCCCTA AAAATGACAA TGCGCATGCG TGTGACGTGA CGCCAGAAGA TCCAACGATT
 ACAAAGATA TCGAAAATCA AGAACACTTA GATTTAACCA ATCGTGAAGA TAGTTTCGAT
 TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCCAAGC CAGCATGGTG
 GATGACATTA ATAAAGTGCT AGATATCATT GATGTGAAAG TCACCGACGA AAATGGTAAA
 GATGTTACAG CTAACGGCAC AGTAACACAA GAAAATAACA AAGTAACTTT TGAAATGAAC
 AAACAAGCAG ACAGCTATGA CTATTTAAGT GGTTCATACGT ATACAATGAC TATCACCCT
 AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT
 CCCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGACG TGTTACATT CAAACAAACA
 ACCGTAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAGG ACAAGAACAT
 TTAGATTTAA CCAACCGCGA TCAAGAATTT AAATGGAACG TCAAAACAGC TTTTCGGTAA
 GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
 ACTGATGTAA AAGTCACAGA TGAAAATGGT AAAGATGTTA CAGCTAACGG CAAAGTAACA
 CAAGAAAATA ACAAAGTAAC TTTTGAAATG AACAANCAAG CNGACAGCTA TGACTATTTA
 AGTGGTCATA CGTACACAAT GACCATTACT ACTAAAATCA AAGCTAGCGC AACGGACGAA
 GAATTAGCAC CTTATATTGA ACAAGGTGGC ATTCCCAACC AAGCCGACTT GAACTTTGGC
 AACGAAGGTG ACGTGTGCA TTCCAACAAA CCAACCGTAA CACCACCTGC ACCAACGCCA
 GAAGATCCAA CGATTACAAA AGATATCGAA GGCCAAGAAC ATTTAGATTT AACCAACCGT
 GACCAAGAAT TTAAATGGAA CGTCAAAACA GCTTTTCGGT ACGAAACAAG CACATGGACC
 CAAGCCAGCA TGGTGGATGA CATTAAATAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
 GANGAAAATG CCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAAA TAACAAAGTA
 ACTTTTACTA TGAACAAAAA AGATGACAGC TACTCTTACT TAGCTGGTCA TACATACACA
 ATGACTATTA CCACTAAAAT TAAACTGAC GCAACGGATG AAGAATTAGC GCCTTATATT
 GAACAAGGCG GGATTCCCAA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTTG
 CATTCCAACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCT
 GAACCTAAAC AACCCTAAA ACCGAAAAA CCGTTGACGC CTACAAATCA TCAAGCACC
 ACGAACCCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TTCATTTACC AATGACTAAT
 ACAACAGTAA ATCCACTTTA CATGATCGCA GGTTTAATTG TCCTTATAGT GGCTATTAGC
 TTTGGCATAA CAAAAAATAA AAAAAGAAAA AATTAG

EF128-2 (SEQ ID NO:478)

MF KKATKLLSTM VIVAGTVVGN FSPTLALAE AVKAGDTEGM TNTVKVKDDSD
 LADCKRILEG QATFPVQAGE TEPVDLVVVE DASGSFSDNF PHVRQAIDEV VQGLSDQDRV
 MLASYRGKKQ FMFPDGKTKI NSADYDMNVR VNTQLTYDKS QFVSGFGDVR TYGGTPTAPG
 LKLALDTYNQ THGDLTNRKT YFLLVTDGVA NTRLDGYLHK TNTNDSINEY PDPRHPLQVS
 VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPFVKQE
 LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
 NDVPVQINGQ TISATSTEGY VGNITHIEV KENTAIDAAT LVSSGTMNQG TIAKEFPEAT
 IPKNDNAHAC DVTPEPTIT KDIENTEHLDT LNREDSFDW HVKTAFGNET STWTQASMVD
 DINKVLDIID VKVTDENGKD VTANGVTQ E NNKVTFEMNK QADSYDYLSE HTYTMITTTK
 IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHSNKPT VTPPPVDPNI AKDVEGQEHL
 DLTNRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDIT DVKVTDENGK DVTANGKVTQ
 ENNKVTFEMN XQADSYDYLSE HTYTMITTT KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHSNKP TVTPPAPTPE DPTITKDIEG QEHLDTNRD QEFKWNVKT FNETSTWTQ
 ASMVDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLPKKP LPTTNHQAPT NPVNFKKSAS KGIHLPMNT TVNPLYMIAG LIVLIVAISF
 GITKNKKRKN

EF128-3 (SEQ ID NO:479)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AGA TGAAAATGGT AAAGATGTTA CAGCTAACGG CAAAGTAACA
 CAAGAAAATA ACAAAGTAAC TTTTGAAATG AACAAANCAAG CNGACAGCTA TGA CTATTTTA
 AGTGGTCATA CGTACACAAT GACCATTACT ACTAAAATCA AAGCTAGCGC AACGGACGAA
 GAATTAGCAC CTTATATTGA ACAAGGTGGC ATTCCCAACC AAGCCGACTT GAACTTTGGC
 AACGAAGGTG ACGTGTGCA TTCCAACAAA CCAACCGTAA CACCACCTGC ACCAACGCCA
 GAAGATCCAA CGATTACAAA AGATATCGAA GGCCAAGAAC ATTTAGATTT AACCAACCGT
 GACCAAGAAT TTAAATGGAA CGTCAAAACA GCTTTCGGTA ACGAAACAAG CACATGGACC
 CAAGCCAGCA TGGTGGATGA CATTAAATAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
 GANGAAAATG GCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAAA TAACAAAGTA
 ACTTTTACTA CCACTAAAAAT TAAAACTGAC GCAACGGATG AAGAATTAGC GCCTTATATT
 ATGACTATTA CCACTAAAAAT TAAAACTGAC GCAACGGATG AAGAATTAGC GCCTTATATT
 GAACAAGGCG GGATTCCCAA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTTG
 CATTCCAACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCT
 GAACCTAAAC AACCGCTAAA ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCACCA
 ACGAACCCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TTCAT

EF128-4 (SEQ ID NO:480)

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 ENNKVTFEMN XQADSYDYL S GHTYTMITTT KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHSNKP TVTPPAPTPE DPTITKDIEG QEHLDLTNRD QEFKWNVKT FNETSTWTQ
 ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLKPKKP LTPTNHQAPT NPVNFGKSAS KGIH

EF129-1 (SEQ ID NO:481)

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 CAAGAAATTT CATCATTA AAAGCAAAACA GGGGATTTAG CTTCAACAAGT ATCTTCTTTA
 GAAGCAGAAG TATCTTCAGT ATTTGATGAA AGCATGGCTT TACGTGAACA AAAGCAAACA
 CTAAAAGCAA AATCAGAACA ATTACAACAA GAAATTACAA ACTTGAATCA ACGTATTGAA
 AAACGTAACG AAGCAATCAA AAATCAAGCA CGTGATGTTC AAGTTAATGG ACAAAGCACA
 ACAATGCTAG ATGCAGTTTT AGATGCGGAC TCAGTTGCAG ATGCAATCAG CCGTGTTCAA
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 GAAGCTGAAT TAGAAACAAA ACGTCAAGAT TTACTTTCTA AACAATCTGA ATTAAACGTA
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 AAACAAAAAG CAGCTGCTGA AGCAGAGCAA GCACGCTTAG CTGCTGAACA AAAAGCTGCA
 GCTGAAAAAG CCAACAAGC TGCTGCAAAA CCAGCTAAAG CTGAAGTGAA AGCAGAAGCA
 CCAGTTGCCCT CTTTCATCAAC AACAGAAGCA CAAGCACCAG CAAGCTCAAG CTCAGCAACT
 GAATCAAGCA CGCAACAAC AACTGAAACA ACTACACCAA GTACAGATAA TAGTGCAACA
 GAAAAACTG GCTCTTCTTC ATCAGAACAA CCAGTACAAC CTACAACACC AAGCGATAAT
 GGAAATAATG GTGGCCAAAC TGGTGGTGGA ACAGTTACAC CAACACCAGA ACCAACACCA
 GCGCCTTCTG CTGATCCAAC AATCAATGCA TTGAACGTTT TACGTCAATC ATTAGGTTTTA
 CGTCCAGTAG TATGGGATGC AGGTTTGGCA GCTTCTGCAA CTGCTCGTGC AGCACAAGTT
 GAAGCAGGTG GCATTCCAAA TGATCACTGG TCTCGTGGAG ATGAAGTTAT CGCAATTATG
 TGGGCGCCAG GTAACCTAGT AATCATGGCG TGGTACAATG AAACAAACAT GGTAACAGCT
 TCAGGAAGCG GTCACCGTGA TTGGGAAATT AACCCAGGTA TTACGCGTGT CGGTTTTGGT
 TACTCAGGTA GCACAATCGT AGGACACTCA GCCTAA

EF129-2 (SEQ ID NO:482)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

VKKRLFASV LLCSLTSAI ATPSIALADN VDKKIEKNQ EISSLKAKQG DLASQVSSLE
 AEVSSVFDES MALREQKQTL KAKSEQLQQE ITNLNQRIEK RNEAIKNQAR DVQVNGQSTT
 MLDAVLADDS VADAI SRVQA VSTIVSANND LMQQQKEDKQ AVVDKKAENE KVKQLEATE
 AELETKRQDL LSKQSELNVM KASLALEQSS AESSKAGLEK QKAAAEAEQA RLAAEQKAAA
 EKAKQAAAKP AKAEVKAEP VASSSTTEAQ APASSSSATE SSTQQTETT TPSTDNSATE
 NTGSSSSSEQP VQPTTPSDNG NNGGQTGGGT VTPTPPEPTPA PSADPTINAL NVLRQSLGLR
 PVVWDAGLAA SATARAAQVE AGGIPNDHWS RGDEVIAIMW APGNSVIMAW YNETNMVTAS
 GSGHRDWEIN PGITRVGFGY SGSTIVGHSA

EF129-3 (SEQ ID NO:483)

GGAC AATGTTGATA AAAAAATTGA AGAAAAAAT
 CAAGAAATTT CATCATTTAA AGCAAAACAA GGGGATTTAG CTTCACAAGT ATCTTCTTTA
 GAAGCAGAAG TATCTTCAGT ATTTGATGAA AGCATGGCTT TACGTGAACA AAAGCAAACA
 CTAAAGCAA AATCAGAACA ATTACAACA GAAATTACAA ACTTGAATCA ACGTATTGAA
 AAACGTAACG AAGCAATCAA AAATCAAGCA CGTGATGTTC AAGTTAATGG ACAAAGCACA
 ACAATGCTAG ATGCAGTTTT AGATGCGGAC TCAGTTGCAG ATGCAATCAG CCGTGTTCAC
 GCTGTTTCAA CAATCGTAAG TGCCAACAAC GACTTAATGC AACAAACAAA AGAAGACAAA
 CAAGCCGTTG TTGATAAAAA AGCTGAAAAC GAGAAAAAAG TGAAACAAC TGAAGCAACA
 GAAGCTGAAT TAGAAACAAA ACGTCAAGAT TTACTTTCTA AACAACTGA ATTAAACGTA
 ATGAAAGCTT CATTAGCATT AGAACAATCA TCAGCTGAAA GTTCTAAAGC TGGCTTAGAA
 AAACAAAAAG CAGCTGCTGA AGCAGAGCAA GCACGCTTAG CTGCTGAACA AAAAGCTGCA
 GCTGAAAAAG CCAAACAAGC TGCTGCAAAA CCAGCTAAAG CTGAAGTGAA AGCAGAAGCA
 CCAGTTGCCT CTTCATCAAC AACAGAAGCA CAAGCACCAG CAAGCTCAAG CTCAGCAACT
 GAATCAAGCA CGCAACAAAC AACTGAAACA ACTACACCAA GTACAGATAA TAGTGCAACA
 GAAAATACTG GCTCTTCTTC ATCAGAACAA CCAGTACAAC CTACAACACC AAGCGATAAT
 GGAAATAATG GTGGCCAAAC TGGTGGTGGA ACAGTTACAC CAACACCAGA ACCAACACCA
 GCGCCTTCTG CTGATCCAAC AATCAATGCA TTGAACGTTT TACGTCAATC ATTAGGTTTA
 CGTCCAGTAG TATGGGATGC AGGTTTGGCA GCTTCTGCAA CTGCTCGTGC AGCACAAGTT
 GAAGCAGGTG GCATTCCAAA TGATCACTGG TCTCGTGGAG ATGAAGTTAT CGCAATTATG
 TGGGCGCCAG GTAACTCAGT AATCATGGCG TGGTACAATG AAACAAACAT GGTAACAGCT
 TCAGGAAGCG GTCACCGTGA TTGGGAAATT AACCCAGGTA TTACGCGTGT CGGTTTGGT
 TACTCAGGTA GCACAATCGT AGGACACTCA GCC

EF129-4 (SEQ ID NO:484)

DN VDKKIEKNQ EISSLKAKQG DLASQVSSLE
 AEVSSVFDES MALREQKQTL KAKSEQLQQE ITNLNQRIEK RNEAIKNQAR DVQVNGQSTT
 MLDAVLADDS VADAI SRVQA VSTIVSANND LMQQQKEDKQ AVVDKKAENE KVKQLEATE
 AELETKRQDL LSKQSELNVM KASLALEQSS AESSKAGLEK QKAAAEAEQA RLAAEQKAAA
 EKAKQAAAKP AKAEVKAEP VASSSTTEAQ APASSSSATE SSTQQTETT TPSTDNSATE
 NTGSSSSSEQP VQPTTPSDNG NNGGQTGGGT VTPTPPEPTPA PSADPTINAL NVLRQSLGLR
 PVVWDAGLAA SATARAAQVE AGGIPNDHWS RGDEVIAIMW APGNSVIMAW YNETNMVTAS
 GSGHRDWEIN PGITRVGFGY SGSTIVGHSA

EF130-1 (SEQ ID NO:485)

TGATACATTA AAAGGAGGGA AAATATGCGC CAAAAGAGA AAAAAAGAGG AAAAAATTGG
 TTAATCAACA GTTTATTAGT TTTACTATTT ATCATTTGGCT TAGCCTTAAT TTTTAACAAT
 CAGATACGTA GTTGGGTGGT TCAACAAAAT AGCCGCTCGT ACGCCGTTAG CAAGTTGAAA
 CCAGCTGATG TGAAGAAAAA TATGGCTCGT GAAACAACGT TTGACTTTGA TTCAGTTGAG
 TCCTTGAGCA CAGAAGCGGT GATGAAAGCC CAATTGAAA ACAAACCTT ACCTGTGATT
 GGTGCCATTG CGATACCAAG TGTGGAATT AATTGCCCCA TTTTAAAGG ATTGTCCAAT
 GTCGCTTTAT TAACTGGTGC CGGGACCATG AAAGAAGATC AAGTCATGGG GAAAAACAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TATGCCTTGG CTAGTCATCG AACGGAAGAT GCGGTTTCCT TATTTTCACC TTTAGAAAGA
 ACCAAAAAAG ACGAACTCAT TTATATCACT GATTTATCTA CTGTTTATAC ATACAAAATA
 ACTTCTGTAG AAAAAATCGA ACCAACCCGT GTTGAGTTAA TTGATGACGT TCCTGGTCAA
 AATATGATTA CCTTAATTAC CTGTGGCGAT TTACAAGCAA CGACGCGAAT TGCTGTTCAA
 GGAACATTAG CAGCAACGAC GCCTATTAAA GACGCCAACG ACGATATGTT GAAGGCTTTC
 CAATTGGAGC AAAAAACTTT AGCCGATTGG GTGGCTTAA

EF130-2 (SEQ ID NO:486)

YIKRRENMRP KEKRGKKNWL INSLLVLLFI IGLALIFNNQ IRSWVVQQNS RSYAVSKLKP
 ADVKKNMARE TTFDFDSVES LSTEAVMKAQ FENKNLPVIG AIAIPSVEIN LPIFKGLSNV
 ALLTGAGTMK EDQVMGKNKY ALASHRTEDG VSLFSPLERT KKDELIYITD LSTVYTYKIT
 SVEKIEPTRV ELIDDPVGQN MITLITCGDL QATTTRIAVQG TLAATTPIKD ANDDMLKAFQ
 LEQKTLADWV A

EF130-3 (SEQ ID NO:487)

CGTTAG CAACTTGAAA
 CCAGCTGATG TGAAGAAAAA TATGGCTCGT GAAACAACGT TTGACTTTGA TTCAGTTGAG
 TCCTTGAGCA CAGAAGCGGT GATGAAAGCC CAATTTGAAA ACAAAAACCTT ACCTGTGATT
 GGTGCCATTG CGATACCAAG TGTCGAAATT AATTIGCCCA TTTTAAAGG ATTGTCCAAT
 GTCGCTTTAT TAACTGGTGC CGGGACCATG AAAGAAGATC AAGTCATGGG GAAAAACAAT
 TATGCCTTGG CTAGTCATCG AACGGAAGAT GCGGTTTCCT TATTTTCACC TTTAGAAAGA
 ACCAAAAAAG ACGAACTCAT TTATATCACT GATTTATCTA CTGTTTATAC ATACAAAATA
 ACTTCTGTAG AAAAAATCGA ACCAACCCGT GTTGAGTTAA TTGATGACGT TCCTGGTCAA
 AATATGATTA CCTTAATTAC CTGTGGCGAT TTACAAGCAA CGACGCGAAT TGCTGTTCAA
 GGAACATTAG CAGCAACGAC GCCTATTAAA GACGCCAACG ACGATATGTT GAAGGCTTTC
 CAATTGGAGC AAAAAACTTT AGCCGATTGG GTGGCT

EF130-4 (SEQ ID NO:488)

VSKLKP
 ADVKKNMARE TTFDFDSVES LSTEAVMKAQ FENKNLPVIG AIAIPSVEIN LPIFKGLSNV
 ALLTGAGTMK EDQVMGKNKY ALASHRTEDG VSLFSPLERT KKDELIYITD LSTVYTYKIT
 SVEKIEPTRV ELIDDPVGQN MITLITCGDL QATTTRIAVQG TLAATTPIKD ANDDMLKAFQ
 LEQKTLADWV A

EF131-1 (SEQ ID NO:489)

TAGGCGGAGG TAAGCGGTAT GCGTAAACGA CATGCAAAGA AAAGACATGG AGGAGTGAAT
 TGGCTTTTTA TAGTATGTTT GTTGGTGGTG ATTGGTGGTA GTGGTTATTT AATAAAAACG
 TTCTTTTTCA CTAGAGATTC ACAAGTTAGT CAAGAATCGA AAGTGGTCTT GGAAGAAGAT
 CGCCGAAGTG ATAATTATGC GAATTTAACG AAAGAAATAG TTGCACCAGA TAGTGGCGAA
 CTTGATCAAA AAATTCAAGA AACAAATTAT ATTGGTTCGG CTTTGATCAT TAAAGATGAT
 CAGGTTTTAG TAAATAAAGG ATATGGCTTT GCCAATTTTG AAAAGCAACA AGCCAACACG
 CCAAACACAA GGTTCAGAT TGGCTCAATT CAAAAATCTT TTACCACAAC CTTGATCTTA
 AAAGCAATTG AAGAAGGTAA ACTTACATTA GATACAAAAC TCGCTACGTT TTATCCGCAA
 ATTCAAGGTG CTGAGGATAT TACGATTAGC GATATGTTGA ATATGACAAG TGGTTTAAAG
 TTATCAGCAA TGCCTAATAA TATCGTTACC GATGAAGAAA TTATTCAATT TGTAAACAA
 AATACCATGT AAGTCAATAA AGGAAAATAC AATTATTCCC CAGTAAATTT TGTCCTTTTA
 GCAGGAATGT TAGAGAAAAT GTATCAACGT ACCTATCAAG AATTATTTAA TAATCTTTAT
 CACAAAACGG CTGGTTTTAA GAATTTTGGC TTCTATGAAA CCTTATTGGA ACAGCCCAAT
 AATTCAACAA GTTATAAATG GACAGAAGAT AATTCATATA ACCAAGTGCT CTCAATTCCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCAGCTAGTT TTGCCCATGA ATTTGGGACT GGTAATGTGG ATATGACGAC AGGTGATTTG
 TATTGGTACT TACATCAATT AACGAGTGGA CATTTAGTTT CCACCGCACT TTTGCAAAAA
 TTATGGACGT CTTCTCAGCA AAGCTCTTAT CATGGCGGCA TCTATGTTCA TGATAATTAT
 TTACGTTTAC ACGGCGTTGA AGCGGGTCAA CAAGCCCTGG TTTTATTTTC AAAAGATATG
 AAGACAGGGG TCATATTGCT AACTAACTGT GTGAATCCAG CGAAATACAA AGAATTAATT
 GGTTCTGTGT TCCATGATGT AACCAATTGA ACTGTTAAAT TTAA

EF131-2 (SEQ ID NO:490)

MRKRH AKKRHGGVNW LFIVCLLVVI GSGYLIKTF FFTRDSQVSQ ESKVVLEEDR
 RSDNYANLTK EIVAPDSGEL DQKIQETNYI GSALIIKDDQ VLVNKGYGFA NFEKQANTP
 NTRFQIGSIQ KSFTTTLILK AIEEGKLTLD TKLATFYPQI QGAEDITISD MLNMTSGLKL
 SAMPNNIVTD EEIIQFVKQN TIQVNKGKYN YSPVNFVLLA GMLEKMYQRT YQELFNLYH
 KTAGLKNFGF YETLLEQPNN STSYKWTEEN SYNQVLSIPA ASFAHEFGTG NVDMTTGDLY
 WYLHQLTSGH LVSTALLQKL WTSSQQSSYH GGIYVHDNYL RLHGVEAGQQ ALVLFKDKM
 TGVILLTNCV NPAKYKELIG SLFHDVTNLT VKF

EF131-3 (SEQ ID NO:491)

TTT AATAAAAAACG
 TTCTTTTCA CTAGAGATTC ACAAGTTAGT CAAGAATCGA AAGTGGTCTT GGAAGAAGAT
 CGCCGAAGTG ATAATTATGC GAATTTAACG AAAGAAATAG TTGCACCAGA TAGTGGCGAA
 CTTGATCAAA AAATTCAGA AACAAATTAT ATTGGTTCGG CTTTGATCAT TAAAGATGAT
 CAGGTTTGTAG TAAATAAAGG ATATGGCTTT GCCAATTTTG AAAAGCAACA AGCCAACACG
 CCAAACACAA GGTTCAGAT TGGCTCAATT CAAAATCTT TTACCACAAC CTTGATCTTA
 AAAGCAATTG AAGAAGGTAA ACTTACATTA GATACAAAAC TCGCTACGTT TTATCCGCAA
 ATTCAAGGTG CTGAGGATAT TACGATTAGC GATATGTTGA ATATGACAAG TGGTTTAAAG
 TTATCAGCAA TGCCTAATAA TATCGTTACC GATGAAGAAA TTATTCAATT TGTTAAACAA
 AATACCATTC AAGTCAATAA AGGAAAATAC AATTATTCCC CAGTAAATTT TGTCTTTTA
 GCAGGAATGT TAGAGAAAAT GTATCAACGT ACCTATCAAG AATTATTAA TAATCTTTAT
 CACAAAACGG CTGGTTTAAA GAATTTTGGC TTCTATGAAA CCTTATTGGA ACAGCCCAAT
 AATTCAACAA GTTATAAATG GACAGAAGAT AATTCATATA ACCAAGTGCT CTCAATTCCT
 GCAGCTAGTT TTGCCCATGA ATTTGGGACT GGTAATGTGG ATATGACGAC AGGTGATTTG
 TATTGGTACT TACATCAATT AACGAGTGGA CATTTAGTTT CCACCGCACT TTTGCAAAAA
 TTATGGACGT CTTCTCAGCA AAGCTCTTAT CATGGCGGCA TCTATGTTCA TGATAATTAT
 TTACGTTTAC ACGGCGTTGA AGCGGGTCAA CAAGCCCTGG TTTTATTTTC AAAAGATATG
 AAGACAGGGG TCATATTGCT AACTAACTGT GTGAATCCAG CGAAATACAA AGAATTAATT
 GGTTCTGTGT TCCATGATGT AACCAATTGA ACTGTTAAAT TT

EF131-4 (SEQ ID NO:492)

LIKTF FFTRDSQVSQ ESKVVLEEDR
 RSDNYANLTK EIVAPDSGEL DQKIQETNYI GSALIIKDDQ VLVNKGYGFA NFEKQANTP
 NTRFQIGSIQ KSFTTTLILK AIEEGKLTLD TKLATFYPQI QGAEDITISD MLNMTSGLKL
 SAMPNNIVTD EEIIQFVKQN TIQVNKGKYN YSPVNFVLLA GMLEKMYQRT YQELFNLYH
 KTAGLKNFGF YETLLEQPNN STSYKWTEEN SYNQVLSIPA ASFAHEFGTG NVDMTTGDLY
 WYLHQLTSGH LVSTALLQKL WTSSQQSSYH GGIYVHDNYL RLHGVEAGQQ ALVLFKDKM
 TGVILLTNCV NPAKYKELIG SLFHDVTNLT VKF

EF132-1 (SEQ ID NO:493)

TAGTTTTCTAATCTCACCAAAACAAAAATTTTAAAGAAAGAGAGATCGTTATGATGAGAAAATGGAAAGTAGTA
 GTGGGAAGTCTGGGAATGTTGATTGCTCTTTTATATTCCGGGCATGTTCAACAAATAGTAAAGACAAAGATACAGTG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCTTCGAACGAAAAATTAAAGGTAGTAGTTACTAATTCGATTTTAGCAGATATTACTGAAAAATATAGCAAAAGATAAA
 ATTGATTTACACAGTATCGTACCTATTGGGAAAGATCCCCACGAATATGAACCTTTGCCTGAAGATGTTCAAAAAACT
 TCAAAAGCAGATTTGATTTTTTATAACGGTGTTAACTTGGAmACTGGAGGAAATGCTTGGTTTACAAAATTAGTAAAA
 mATGCGAACAAAGAGGAAAAACAAAGACTATTTTGCAGCAAGTGATGGCATAGATGTTATTTACTTAGAGGGTCAGAGT
 GAGAAAGGGAAGGAAGATCCCCATGCTTGGTTAAATTTAGAAAACGGTATTATTTACGCTAAAAATATTGAAAAATGG
 TTACCGGAAAAAGATCCTGATAATAAAAAATTCATAAAAGAAAACTAGATAAGTATATTGAAAAGTTGGATTCTCTA
 GACAAAGAAGCTAAATCTAAATTTGCTTCAATTCCGAATGATAAAAAAATGATTGTTACAAGTGAAGGATGCTTTAAA
 TATTTCTCGAAAGCGTATAATGTGCCTTCTGCTTACATTTGGGAAATCAACACTGAAGAAGAAGGAACACCAGATCAA
 ATAAACACTTAGTTGAAAAATTACGCACAACAAAAGTTCCCTCCTTATTTCGTAGAAAGTAGTGTGGACGATAGACCG
 ATGAAAACAGTATCAAAAGATACCAATATTCCTATCTATTCAACGATTTTACTGATTCAATTGCAGAAAAAGGACAA
 GATGGTGATAGTTACTATGCGATGATGAAATGGAACCTGGATAAAAAATTGCTGAAGGCCTTTTCGAAATAA

EF132-2 (SEQ ID NO:494)

MMRKWKVVVGSGLMLIALFIFGACSTNSKDKDTVASNEKLKVVVTNSILADITENIAKDKIDLHSIVPIGKDPHEYEP
 LPEDVQKTSKADLIFYNGVNLXTGGNAWFTKLKXANKEENKDYFAASDGIDVIYLEGQSEKGDPHAWLNLENGII
 YAKNIEKWLAEKDPDNKKFYKENLDKYIEKLDSLDEAKSKFASIPNDKMKMIVTSEGCFKYFSKAYNVPSAYIWEINT
 EEEGTPDQIKHLVEKLRTTKVPSLFVSSVDDRPMKTVSKDTNIPYSTIFTDSIAEKGQDGSYYAMMKWNLDKIAE
 GLSK.

EF132-3 (SEQ ID NO:495)

ATGTTCAACAAATAGTAAAGACAAAGATACAGTGGCTTCGAACGAAAAATTAAAGGTAGTAGTTACTAATTCGATTTT
 AGCAGATATTACTGAAAAATATAGCAAAAGATAAAATTGATTTACACAGTATCGTACCTATTGGGAAAGATCCCCACGA
 ATATGAACCTTTGCCTGAAGATGTTCAAAAACTTCAAAAGCAGATTTGATTTTTTATAACGGTGTTAACTTGGAmAC
 TGGAGGAAATGCTTGGTTTACAAAATTAGTAAAAmATGCGAACAAAGAGGAAAAACAAAGACTATTTTGCAGCAAGTGA
 TGGCATAGATGTTATTTACTTAGAGGGTCAGAGTGAGAAAGGGAAGGAAGATCCCCATGCTTGGTTAAATTTAGAAAA
 CGGTATTATTTACGCTAAAAATATTGAAAAATGGTTAGCGGAAAAAGATCCTGATAATAAAAAATTCATAAAAGAAAA
 TCTAGATAAGTATATTGAAAAGTTGGATTCTCTAGACAAAGAAGCTAAATCTAAATTTGCTTCAATTCGAATGATAA
 AAAAAATGATTGTTACAAGTGAAGGATGCTTTAAATATTTCTCGAAAGCGTATAATGTGCCTTCTGCTTACATTTGGGA
 AATCAACACTGAAGAAGAAGGAACACCAGATCAAATAAAACACTTAGTTGAAAAATTACGCACAACAAAAGTTCCCTC
 CTTATTCGTAGAAAGTAGTGTGGACGATAGACCGATGAAAACAGTATCAAAAGATACCAATATTCCTATCTATTCAAC
 GATTTTTACTGATTCAATTGCAGAAAAAGGACAAGATGGTGATAGTTACTATGCGATGATGAAATGGAACCTGGATAA
 AATTGCTGAAGGCCTTTTCGAAA

EF132-4 (SEQ ID NO:496)

CSTNSKDKDTVASNEKLKVVVTNSILADITENIAKDKIDLHSIVPIGKDPHEYEP
 LPEDVQKTSKADLIFYNGVNLXTGGNAWFTKLKXANKEENKDYFAASDGIDVIYLEGQSEKGDPHAWLNLENGII
 YAKNIEKWLAEKDPDNKKFYKENLDKYIEKLDSLDEAKSKFASIPNDKMKMIVTSEGCFKYFSKAYNVPSAYIWEINT
 EEEGTPDQIKHLVEKLRTTKVPSLFVSSVDDRPMKTVSKDTNIPYSTIFTDSIAEKGQDGSYYAMMKWNLDKIAEGLSK

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| Query | GenBank Access. No. | GenBank Gene Description | BLAST Score | BLAST P-Value |
|---------|---------------------|---------------------------------------------------------------------|-------------|---------------|
| EF002-2 | gi 2338759 | (AF018073) periplasmic sorbitol-binding protein, SmoE [Rhodobacter | 113 | 3.60E-18 |
| EF003-2 | gi 1552773 | hypothetical [Escherichia coli] >gnl PID d1012634 hypothetical 29.4 | 278 | 1.20E-53 |
| EF003-2 | gi 2196996 | lipoprotein homolog [Treponema pallidum] >gi 2108234 29K protein | 309 | 3.30E-44 |
| EF003-2 | gi 146649 | lipoprotein-28 precursor [Escherichia coli] >gi 290510 | 263 | 9.20E-40 |
| EF003-2 | gi 148838 | 28 kDa membrane protein [Haemophilus influenzae] | 197 | 2.10E-39 |
| EF003-2 | gi 1573614 | 28 kDa membrane protein (hlpA) [Haemophilus influenzae] | 197 | 7.80E-39 |
| EF003-2 | gi 2314748 | (AE000654) outer membrane protein [Helicobacter pylori] | 263 | 4.60E-37 |
| EF003-2 | gi 349530 | lipoprotein [Pasteurella haemolytica] >gi 150508 lipoprotein | 189 | 4.10E-29 |
| EF003-2 | gnl PID e118435 | similar to hypothetical proteins [Bacillus subtilis] | 158 | 2.70E-26 |
| EF003-2 | gi 349532 | lipoprotein [Pasteurella haemolytica] >pir JN0753 JN0753 outer | 200 | 1.20E-25 |
| EF003-2 | gi 1336657 | lipoprotein [Bacillus subtilis] | 182 | 2.70E-25 |
| EF003-2 | gnl PID e233873 | hypothetical protein [Bacillus subtilis] >gnl PID e1182900 | 186 | 1.30E-23 |
| EF003-2 | gi 294071 | lipoprotein 3 [Pasteurella haemolytica] | 199 | 6.60E-23 |
| EF003-2 | gi 349531 | lipoprotein [Pasteurella haemolytica] >pir JN0752 JN0752 outer | 198 | 1.30E-20 |
| EF003-2 | gi 294070 | lipoprotein 2 [Pasteurella haemolytica] | 198 | 1.80E-20 |
| EF005-2 | gi 537235 | Kenn Rudd identifies as gpmB [Escherichia coli] >gi 1790856 | 127 | 6.20E-12 |
| EF006-2 | gi 1552773 | hypothetical [Escherichia coli] >gnl PID d1012634 hypothetical 29.4 | 255 | 1.40E-60 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|-----------------|------------------------------------------------------------------|------|-----------|
| EF006-2 | gi 349532 | lipoprotein [Pasteurella haemolytica] >pir JN0753 JN0753 outer | 221 | 6.40E-49 |
| EF006-2 | gi 2314748 | (AE000654) outer membrane protein [Helicobacter pylori] | 283 | 2.70E-48 |
| EF006-2 | gi 2196996 | lipoprotein homolog [Treponema pallidum] >gi 2108234 29K protein | 267 | 4.40E-47 |
| EF006-2 | gnl PID e118435 | similar to hypothetical proteins [Bacillus subtilis] | 359 | 1.80E-44 |
| EF006-2 | gi 349531 | lipoprotein [Pasteurella haemolytica] >pir JN0752 JN0752 outer | 218 | 3.80E-41 |
| EF006-2 | gi 294071 | lipoprotein 3 [Pasteurella haemolytica] | 220 | 2.30E-38 |
| EF006-2 | gi 146649 | lipoprotein-28 precursor [Escherichia coli] >gi 290510 | 193 | 2.60E-38 |
| EF006-2 | gi 294070 | lipoprotein 2 [Pasteurella haemolytica] | 218 | 1.20E-36 |
| EF006-2 | gi 148838 | 28 kDa membrane protein [Haemophilus influenzae] | 112 | 8.50E-34 |
| EF006-2 | gi 1573614 | 28 kDa membrane protein (hlpA) [Haemophilus influenzae] | 112 | 1.50E-33 |
| EF006-2 | gi 349530 | lipoprotein [Pasteurella haemolytica] >gi 150508 lipoprotein | 114 | 4.30E-29 |
| EF006-2 | gi 294069 | lipoprotein 1 [Pasteurella haemolytica] | 114 | 1.30E-27 |
| EF006-2 | gi 1336657 | lipoprotein [Bacillus subtilis] | 202 | 2.10E-26 |
| EF006-2 | gnl PID e233873 | hypothetical protein [Bacillus subtilis] >gnl PID e1182900 | 200 | 6.50E-25 |
| EF008-2 | gi 493017 | endocarditis specific antigen [Enterococcus faecalis] | 1590 | 2.70E-211 |
| EF008-2 | gi 393269 | adhesion protein [Streptococcus pneumoniae] | 986 | 1.80E-129 |
| EF008-2 | gi 153834 | adhesin specific for salivary pellicle of dental surfaces | 973 | 1.00E-127 |
| EF008-2 | gi 1575030 | surface adhesin A precursor [Streptococcus pneumoniae] | 934 | 2.90E-126 |
| EF008-2 | gi 153826 | adhesin B [Streptococcus sanguis] >pir A43583 A43583 adhesin B | 916 | 3.90E-126 |
| EF008-2 | gi 1184932 | ScbA [Streptococcus crista] | 915 | 3.40E-125 |
| EF008-2 | gi 1117994 | surface antigen A variant precursor [Streptococcus pneumoniae] | 917 | 5.60E-124 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|-----------------|----------------------------------------------------------------------|-----|-----------|
| EF008-2 | gi 310633 | adhesin [Streptococcus gordonii] | 891 | 6.00E-122 |
| EF008-2 | gnl PID e255529 | lipoprotein [Staphylococcus epidermidis] | 476 | 1.20E-99 |
| EF008-2 | gi 1573330 | adhesin B precursor (fimA) [Haemophilus influenzae] | 380 | 1.60E-68 |
| EF008-2 | gi 1245464 | YfeA [Yersinia pestis] >gi 1245464 YfeA [Yersinia pestis] | 355 | 1.20E-64 |
| EF008-2 | gi 755075 | periplasmic-binding protein [Synechocystis sp.] >gnl PID d1018652 Mn | 321 | 1.70E-62 |
| EF008-2 | gi 1335912 | EwIA [Erysipelothrix rhusiopathiae] | 232 | 4.40E-42 |
| EF008-2 | gnl PID e118595 | similar to ABC transporter (membrane protein) [Bacillus] | 204 | 4.10E-38 |
| EF008-2 | gi 1777933 | TroA [Treponema pallidum] | 181 | 2.40E-35 |
| EF009-2 | gi 349531 | lipoprotein [Pasteurella haemolytica] >pir JN0752 JN0752 outer | 391 | 4.00E-64 |
| EF009-2 | gi 1552773 | hypothetical [Escherichia coli] >gnl PID d1012634 hypothetical 29.4 | 359 | 1.90E-63 |
| EF009-2 | gi 294070 | lipoprotein 2 [Pasteurella haemolytica] | 391 | 6.40E-63 |
| EF009-2 | gi 349532 | lipoprotein [Pasteurella haemolytica] >pir JN0753 JN0753 outer | 386 | 1.10E-61 |
| EF009-2 | gi 148838 | 28 kDa membrane protein [Haemophilus influenzae] | 286 | 5.60E-60 |
| EF009-2 | gi 1573614 | 28 kDa membrane protein (hlpA) [Haemophilus influenzae] | 286 | 7.60E-60 |
| EF009-2 | gi 294069 | lipoprotein 1 [Pasteurella haemolytica] | 122 | 4.70E-59 |
| EF009-2 | gi 146649 | lipoprotein-28 precursor [Escherichia coli] >gi 290510 | 326 | 2.20E-58 |
| EF009-2 | gi 349530 | lipoprotein [Pasteurella haemolytica] >gi 150508 lipoprotein | 239 | 7.80E-57 |
| EF009-2 | gi 294071 | lipoprotein 3 [Pasteurella haemolytica] | 344 | 4.90E-56 |
| EF009-2 | gi 2314748 | (AE000654) outer membrane protein [Helicobacter pylori] | 319 | 4.20E-53 |
| EF009-2 | gi 2196996 | lipoprotein homolog [Treponema pallidum] >gi 2108234 29K protein | 312 | 2.60E-41 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|-------------------------------------------------------------------------|-----|-----------|
| EF009-2 | gi 1336657 | lipoprotein [Bacillus subtilis] | 234 | 4.00E-32 |
| EF009-2 | gnl PID e233873 | hypothetical protein [Bacillus subtilis] >gnl PID e1182900 | 242 | 1.40E-31 |
| EF009-2 | gnl PID e118435 | similar to hypothetical proteins [Bacillus subtilis] | 102 | 6.80E-22 |
| EF011-2 | gnl PID d10096 5 | ferric anguibactin-binding protein precursor FatB of V. | 579 | 3.10E-98 |
| EF011-2 | gnl PID d10096 5 | ferric anguibactin-binding protein precursor FatB of V. | 579 | 3.10E-98 |
| EF011-2 | gnl PID e185374 | ceuE gene product [Campylobacter coli] | 284 | 1.30E-89 |
| EF011-2 | gnl PID e185374 | ceuE gene product [Campylobacter coli] | 284 | 1.30E-89 |
| EF011-2 | gi 150756 | 40 kDa protein [Plasmid pJM1] >pir A29928 A29928 membrane-associated | 222 | 2.80E-52 |
| EF011-2 | gi 150756 | 40 kDa protein [Plasmid pJM1] >pir A29928 A29928 membrane-associated | 222 | 2.80E-52 |
| EF012-2 | gi 309662 | pheromone binding protein [Plasmid pCF10] >pir B53309 B53309 | 266 | 8.70E-116 |
| EF012-2 | gi 388269 | traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding | 252 | 1.10E-109 |
| EF012-2 | gnl PID d10118 5 | TRAC [Enterococcus faecalis] | 281 | 3.60E-103 |
| EF012-2 | gnl PID d10065 5 | TraC [Enterococcus faecalis] | 277 | 2.30E-102 |
| EF012-2 | gi 312940 | threonine kinase [Streptococcus equisimilis] >pir S28153 S28153 | 227 | 1.90E-67 |
| EF012-2 | gi 48808 | dciAE [Bacillus subtilis] | 228 | 1.70E-46 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|-------------------------------------------------------------------------------|-----|----------|
| EF012-2 | pir S1665 S166 | dciAE protein - <i>Bacillus subtilis</i> | 228 | 1.00E-45 |
| EF012-2 | gnl PID e118149 | (AJ002571) DppE [<i>Bacillus subtilis</i>] >gnl PID e1183316 | 228 | 3.80E-45 |
| EF012-2 | gi 40005 | OppA gene product [<i>Bacillus subtilis</i>] | 281 | 3.90E-44 |
| EF012-2 | gi 143603 | sporulation protein [<i>Bacillus subtilis</i>] >gnl PID e1183163 | 281 | 7.70E-44 |
| EF012-2 | gnl PID d10156 3 | Periplasmic oligopeptide-binding protein precursor. | 152 | 2.20E-43 |
| EF012-2 | gi 1574679 | oligopeptide binding protein (oppA) [<i>Haemophilus influenzae</i>] | 178 | 2.20E-42 |
| EF012-2 | gi 47802 | Opp A (AA1-542) [<i>Salmonella typhimurium</i>] >gi 47808 precursor | 128 | 1.00E-37 |
| EF012-2 | gi 882550 | ORF_f535 [<i>Escherichia coli</i>] >gi 1789397 (AE000384) f535; This 535 aa | 228 | 5.30E-36 |
| EF014-2 | pir D70070 D70 0 | transcriptional regulator homolog ywtF - <i>Bacillus subtilis</i> | 101 | 1.40E-27 |
| EF014-2 | gnl PID e116988 | capsular polysaccharide synthesis protein [<i>Streptococcus</i>] | 121 | 9.50E-27 |
| EF014-2 | gi 2804769 | (AF030373) putative regulatory protein [<i>Streptococcus pneumoniae</i>] | 121 | 9.50E-27 |
| EF014-2 | gnl PID e289126 | unknown [<i>Streptococcus pneumoniae</i>] | 121 | 1.00E-24 |
| EF014-2 | gi 2267239 | ORF1 [<i>Staphylococcus epidermidis</i>] | 234 | 1.50E-24 |
| EF014-2 | gi 485275 | putative regulatory protein [<i>Streptococcus pneumoniae</i>] | 121 | 3.90E-24 |
| EF014-2 | gi 2804735 | (AF030367) putative regulatory protein [<i>Streptococcus pneumoniae</i>] | 121 | 3.90E-24 |
| EF014-2 | gi 2804747 | (AF030369) putative regulatory protein [<i>Streptococcus pneumoniae</i>] | 121 | 3.90E-24 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|--------------------|---------------------------------------------------------------------|-----|----------|
| EF014-2 | gi 1762327 | putative transcriptional regulator [Bacillus subtilis] | 185 | 2.80E-22 |
| EF014-2 | gi 143156 | membrane bound protein [Bacillus subtilis] >gn PID e1184471 | 116 | 1.10E-21 |
| EF014-2 | gn PID d10189 5 | membrane bound protein LytR [Synechocystis sp.] | 113 | 6.20E-20 |
| EF014-2 | gi 1276874 | EpsA [Streptococcus thermophilus] | 103 | 4.00E-17 |
| EF016-2 | gn PID e118566 | similar to amino acid ABC transporter (binding protein) | 194 | 3.70E-35 |
| EF016-2 | gi 40934 | arginine binding protein [Escherichia coli] >gi 769794 artJ | 121 | 1.60E-31 |
| EF016-2 | gn PID d10152 7 | Arginine-binding periplasmic protein 2 precursor [Escherichia] | 121 | 4.80E-31 |
| EF016-2 | gi 687652 | FlhY [Escherichia coli] >gn PID d1016464 FlhY protein precursor. | 160 | 5.70E-31 |
| EF016-2 | gi 2650410 | (AE001090) glutamine ABC transporter, periplasmic glutamine-binding | 122 | 3.30E-29 |
| EF016-2 | gi 1649035 | high-affinity periplasmic glutamine binding protein [Salmonella] | 104 | 1.80E-27 |
| EF016-2 | gi 1574634 | glutamine-binding periplasmic protein (glnH) [Haemophilus] | 174 | 2.50E-27 |
| EF016-2 | gi 41569 | GlnH precursor (AA -22 to 226) [Escherichia coli] >gn PID d1015250 | 106 | 4.70E-27 |
| EF016-2 | gn PID d10152 7 | Arginine-binding periplasmic protein 1 precursor [Escherichia] | 109 | 3.70E-26 |
| EF016-2 | gi 769791 | artI [Escherichia coli] >gi 769791 artI [Escherichia coli] | 127 | 2.30E-25 |
| EF016-2 | gn PID d10089 2 | homologous to Gln-binding periplasmic proteins [Bacillus] | 117 | 8.50E-24 |
| EF016-2 | gi 154125 | J protein [Salmonella typhimurium] >gi 47718 reading frame | 118 | 2.10E-23 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|--------------------|--------------------------------------------------------------------|-----|-----------|
| EF016-2 | gn PID d10168 8 | hisJ HISTIDINE-BINDING PERIPLASMIC PROTEIN PRECURSOR (HBP). | 117 | 4.50E-23 |
| EF016-2 | gi 1166636 | histidine-binding periplasmic protein HisJ [Escherichia coli] | 117 | 6.60E-23 |
| EF017-2 | gi 388269 | traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding | 421 | 4.50E-128 |
| EF017-2 | gn PID d10118 5 | TRAC [Enterococcus faecalis] | 417 | 5.10E-124 |
| EF017-2 | gn PID d10065 5 | TraC [Enterococcus faecalis] | 414 | 4.40E-123 |
| EF017-2 | gi 309662 | pheromone binding protein [Plasmid pCF10] >pir B53309 B53309 | 415 | 2.40E-119 |
| EF017-2 | gi 40005 | OppA gene product [Bacillus subtilis] | 294 | 6.20E-82 |
| EF017-2 | gi 143603 | sporulation protein [Bacillus subtilis] >gn PID e1183163 | 290 | 2.80E-79 |
| EF017-2 | gi 312940 | threonine kinase [Streptococcus equisimilis] >pir S28153 S28153 | 241 | 2.40E-71 |
| EF017-2 | gi 48808 | dciAE [Bacillus subtilis] | 270 | 1.10E-61 |
| EF017-2 | gn PID e118149 | (AJ002571) DppE [Bacillus subtilis] >gn PID e1183316 | 270 | 1.50E-61 |
| EF017-2 | pir S16651 S166 | dciAE protein - Bacillus subtilis | 270 | 3.10E-60 |
| EF017-2 | gi 304925 | periplasmic oligopeptide binding protein [Escherichia coli] | 171 | 2.60E-57 |
| EF017-2 | gi 147014 | oligopeptide binding protein precursor [Escherichia coli] | 171 | 8.70E-56 |
| EF017-2 | gi 47802 | Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor | 154 | 1.30E-52 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|-----------------|-------------------------------------------------------------------------|-----|-----------|
| EF017-2 | gi 882550 | ORF_f535 [Escherichia coli] >gi 1789397 (AE000384) f535; This 535 aa | 135 | 5.50E-52 |
| EF017-2 | gi 1574679 | oligopeptide binding protein (oppA) [Haemophilus influenzae] | 168 | 2.90E-43 |
| EF019-2 | gi 438458 | likely N-terminal signal sequence; mature protein probably | 104 | 2.30E-17 |
| EF021-2 | gnl PID e311492 | unknown [Bacillus subtilis] >gnl PID e1184232 similar to ABC | 317 | 2.50E-103 |
| EF021-2 | bbs 173803 | CD4+ T cell-stimulating antigen [Listeria monocytogenes, 85EO-1167, | 476 | 2.80E-81 |
| EF021-2 | gi 581809 | tmbC gene product [Treponema pallidum] >pir A43595 A43595 membrane | 152 | 3.20E-71 |
| EF021-2 | gi 2688280 | (AE001143) basic membrane protein C (bmpC) [Borrelia burgdorferi] | 101 | 5.50E-27 |
| EF021-2 | gnl PID e117283 | membrane protein A [Borrelia garinii] | 142 | 6.50E-22 |
| EF021-2 | gnl PID e117283 | membrane protein A [Borrelia burgdorferi] | 141 | 9.20E-22 |
| EF021-2 | gnl PID e117283 | membrane protein A [Borrelia burgdorferi] >gi 516592 membrane | 141 | 9.20E-22 |
| EF021-2 | gnl PID e117283 | bmpA(p39,ORF1) [Borrelia burgdorferi] | 141 | 1.70E-21 |
| EF021-2 | gi 508421 | antigen P39 [Borrelia burgdorferi] >gi 2688281 (AE001143) basic | 141 | 1.70E-21 |
| EF021-2 | gi 1753225 | BmpA protein [Borrelia burgdorferi] | 141 | 2.70E-20 |
| EF021-2 | gnl PID e117282 | membrane protein A [Borrelia afzelii] | 141 | 8.60E-20 |
| EF021-2 | gnl PID e117283 | membrane protein A [Borrelia afzelii] | 141 | 8.60E-20 |
| EF021-2 | gnl PID e117283 | membrane protein A [Borrelia afzelii] | 141 | 8.60E-20 |
| EF021-2 | gnl PID e117282 | bmpA(p39,ORF1) [Borrelia burgdorferi] | 141 | 1.50E-19 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|------------------------------------------------------------------------|-----|----------|
| EF022-2 | gi 312940 | threonine kinase [Streptococcus equisimilis] >pir S28153 S28153 | 324 | 5.90E-66 |
| EF022-2 | gi 309662 | pheromone binding protein [Plasmid pCF10] >pir B53309 B53309 | 307 | 5.60E-60 |
| EF022-2 | gnl PID d10118 5 | TRAC [Enterococcus faecalis] | 301 | 4.80E-59 |
| EF022-2 | gnl PID e118149 | (AJ002571) DppE [Bacillus subtilis] >gnl PID e1183316 | 170 | 5.10E-59 |
| EF022-2 | gi 48808 | dciAE [Bacillus subtilis] | 170 | 5.20E-59 |
| EF022-2 | gnl PID d10065 5 | TraC [Enterococcus faecalis] | 299 | 2.80E-58 |
| EF022-2 | pir S16651 S166 | dciAE protein - Bacillus subtilis | 170 | 1.60E-57 |
| EF022-2 | gi 388269 | traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding | 280 | 2.70E-53 |
| EF022-2 | gi 40005 | OppA gene product [Bacillus subtilis] | 154 | 7.30E-48 |
| EF022-2 | gi 143603 | sporulation protein [Bacillus subtilis] >gnl PID e1183163 | 154 | 3.10E-47 |
| EF022-2 | gi 2688227 | (AE001139) oligopeptide ABC transporter, periplasmic | 215 | 1.00E-36 |
| EF022-2 | gi 2281458 | (AF000366) oligopeptide permease homolog Ali [Borrelia burgdorferi] | 215 | 1.00E-36 |
| EF022-2 | gi 304925 | periplasmic oligopeptide binding protein [Escherichia coli] | 131 | 1.30E-35 |
| EF022-2 | gi 147014 | oligopeptide binding protein precursor [Escherichia coli] | 131 | 1.80E-34 |
| EF022-2 | gi 47802 | Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor | 138 | 4.90E-34 |
| EF023-2 | gi 309662 | pheromone binding protein [Plasmid pCF10] | 231 | 4.70E-66 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | >pir B53309 B53309 | | |
|---------|---------------------|----------------------------------------------------------------------|-----|----------|
| EF023-2 | gi 388269 | traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding | 223 | 4.80E-62 |
| EF023-2 | gnl PID d10118 5 | TRAC [Enterococcus faecalis] | 226 | 1.00E-58 |
| EF023-2 | gnl PID d10065 5 | TraC [Enterococcus faecalis] | 226 | 4.40E-58 |
| EF023-2 | gi 48808 | dciAE [Bacillus subtilis] | 157 | 1.20E-57 |
| EF023-2 | gnl PID e118149 | (AJ002571) DppE [Bacillus subtilis] >gnl PID e1183316 | 157 | 1.20E-57 |
| EF023-2 | pir S16651 S166 | dciAE protein - Bacillus subtilis | 157 | 3.80E-56 |
| EF023-2 | gi 40005 | OppA gene product [Bacillus subtilis] | 137 | 2.30E-53 |
| EF023-2 | gi 143603 | sporulation protein [Bacillus subtilis] >gnl PID e1183163 | 133 | 6.90E-53 |
| EF023-2 | gi 47802 | Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor | 135 | 2.00E-41 |
| EF023-2 | gi 2688227 | (AE001139) oligopeptide ABC transporter, periplasmic | 187 | 9.40E-41 |
| EF023-2 | gi 2281458 | (AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi] | 187 | 1.90E-40 |
| EF023-2 | gi 882550 | ORF_f535 [Escherichia coli] >gi 1789397 (AE000384) f535; This 535 aa | 155 | 1.30E-38 |
| EF023-2 | gi 304925 | periplasmic oligopeptide binding protein [Escherichia coli] | 130 | 9.00E-37 |
| EF023-2 | gi 147014 | oligopeptide binding protein precursor [Escherichia coli] | 130 | 3.70E-34 |
| EF026-2 | gi 2352482 | (AF005097) unknown [Lactococcus lactis] | 141 | 1.10E-23 |
| EF027-2 | gi 309662 | pheromone binding protein [Plasmid pCF10] | 198 | 6.20E-71 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | | |
|---------|---------------------|---------------------------------------------------------------------|-----|--|-----------|
| | | >pir B53309 B53309 | | | |
| EF027-2 | gnl PID d10065 5 | TraC [Enterococcus faecalis] | 202 | | 1.50E-68 |
| EF027-2 | gnl PID d10118 5 | TRAC [Enterococcus faecalis] | 202 | | 1.50E-68 |
| EF027-2 | gi 388269 | traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding | 213 | | 8.30E-68 |
| EF027-2 | gnl PID e118149 | (AJ002571) DppE [Bacillus subtilis] >gnl PID e1183316 | 222 | | 3.70E-41 |
| EF027-2 | gi 48808 | dciAE [Bacillus subtilis] | 222 | | 4.90E-41 |
| EF027-2 | pir S16651 S166 | dciAE protein - Bacillus subtilis | 222 | | 1.10E-39 |
| EF027-2 | gi 40005 | OppA gene product [Bacillus subtilis] | 251 | | 4.10E-39 |
| EF027-2 | gi 143603 | sporulation protein [Bacillus subtilis] >gnl PID e1183163 | 247 | | 5.80E-39 |
| EF027-2 | gi 312940 | threonine kinase [Streptococcus equisimilis] >pir S28153 S28153 | 233 | | 8.90E-33 |
| EF027-2 | gi 2688227 | (AE001139) oligopeptide ABC transporter, periplasmic | 131 | | 2.40E-24 |
| EF027-2 | gi 2281458 | (AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi] | 131 | | 2.40E-24 |
| EF027-2 | gi 2281468 | (AF000948) OppAIV [Borrelia burgdorferi] >gi 2689891 (AE000792) | 117 | | 3.00E-20 |
| EF027-2 | gi 1574679 | oligopeptide binding protein (oppA) [Haemophilus influenzae] | 130 | | 3.50E-20 |
| EF028-2 | gnl PID d10204 7 | B. subtilis alkaline phosphatase IIIA; P19405 secretory | 996 | | 3.60E-131 |
| EF028-2 | pir B39096 B39 | alkaline phosphatase (EC 3.1.3.1) III precursor - Bacillus | 982 | | 2.90E-129 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | 0 | | | |
|---------|-----------------|-------------------------------------------------------------------|-----|-----------|
| EF028-2 | gi 470383 | alkaline phosphatase A [Bacillus subtilis] >gnl PID e1182942 | 803 | 4.80E-119 |
| EF028-2 | gi 143324 | APase I [Bacillus licheniformis] >pir A44828 A44828 alkaline | 184 | 3.00E-54 |
| EF028-2 | gi 147243 | alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli] | 183 | 8.30E-54 |
| EF028-2 | gi 147237 | alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli] | 178 | 4.40E-53 |
| EF028-2 | gi 147239 | alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli] | 178 | 4.40E-53 |
| EF028-2 | gi 147241 | alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli] | 178 | 4.40E-53 |
| EF028-2 | gi 1277127 | phoA gene product [Cloning vector pFW_phoA1] >gi 1277130 | 174 | 4.90E-53 |
| | | phoA gene | | |
| EF028-2 | gi 147229 | alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli] | 178 | 8.40E-53 |
| EF028-2 | gi 818851 | alkaline phosphatase [synthetic construct] | 174 | 1.10E-52 |
| EF028-2 | gi 147245 | alkaline phosphatase (phoA) (EC 3.1.3.1) [Escherichia fergusonii] | 177 | 1.20E-52 |
| | | | | |
| EF028-2 | gi 147231 | alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli] | 174 | 1.60E-52 |
| EF028-2 | gi 147235 | alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli] | 174 | 1.60E-52 |
| EF028-2 | gi 1016010 | alkaline phosphatase with N-terminal PelB-leader and C-terminal | 174 | 1.60E-52 |
| | | | | |
| EF029-2 | gi 1750126 | YncB [Bacillus subtilis] >gnl PID e1183421 similar to micrococcal | 257 | 3.50E-55 |
| | | | | |
| EF029-2 | gnl PID e118360 | similar to hypothetical proteins [Bacillus subtilis] | 263 | 7.80E-53 |
| EF029-2 | gi 673492 | nuclease [Staphylococcus aureus] >pir A00790 NCSAF micrococcal | 320 | 2.20E-39 |
| | | | | |
| EF029-2 | gi 532653 | thermonuclease [Staphylococcus hyicus] | 155 | 9.10E-39 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|------------------------------------------------------------------------|-----|----------|
| EF029-2 | gi 47146 | thermonuclease [Staphylococcus intermedius] >pir S26079 S26079 | 145 | 4.90E-32 |
| EF030-2 | gi 48808 | dciAE [Bacillus subtilis] | 149 | 1.10E-66 |
| EF030-2 | gnl PID e118149 | (AJ002571) DppE [Bacillus subtilis] >gnl PID e1183316 | 149 | 1.50E-66 |
| EF030-2 | pir S16651 S166 | dciAE protein - Bacillus subtilis | 149 | 5.90E-66 |
| EF030-2 | gi 309662 | pheromone binding protein [Plasmid pCF10] >pir B53309 B53309 | 227 | 7.40E-52 |
| EF030-2 | gnl PID d10118 5 | TRAC [Enterococcus faecalis] | 237 | 7.40E-52 |
| EF030-2 | gnl PID d10065 5 | TraC [Enterococcus faecalis] | 233 | 9.70E-51 |
| EF030-2 | gi 388269 | traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding | 229 | 3.00E-48 |
| EF030-2 | gi 312940 | threonine kinase [Streptococcus equisimilis] >pir S28153 S28153 | 277 | 3.00E-45 |
| EF030-2 | gi 47802 | Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor | 125 | 8.50E-34 |
| EF030-2 | gi 2688227 | (AE001139) oligopeptide ABC transporter, periplasmic | 211 | 4.80E-31 |
| EF030-2 | gi 2281458 | (AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi] | 211 | 4.80E-31 |
| EF030-2 | gi 40005 | OppA gene product [Bacillus subtilis] | 148 | 1.20E-30 |
| EF030-2 | gi 143603 | sporulation protein [Bacillus subtilis] >gnl PID e1183163 | 144 | 4.80E-30 |
| EF030-2 | gi 2281468 | (AF000948) OppAIV [Borrelia burgdorferi] >gi 2689891 (AE000792) | 210 | 2.10E-29 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|-------------------------------------------------------------------------|-----|----------|
| EF030-2 | gi 1574679 | oligopeptide binding protein (oppA) [Haemophilus influenzae] | 148 | 6.00E-29 |
| EF033-2 | gnl PID e118439 | similar to iron-binding protein [Bacillus subtilis] | 164 | 2.60E-14 |
| EF033-2 | pir S54437 S544 | hemin binding protein - Yersinia enterocolitica | 108 | 1.40E-11 |
| EF033-2 | gi 1619623 | hemin binding protein [Yersinia enterocolitica] | 108 | 2.00E-11 |
| EF036-2 | gnl PID d10102 2 | ORF108 [Bacillus subtilis] >gnl PID e1185766 alternate gene | 544 | 1.20E-96 |
| EF036-2 | gi 2622858 | (AE000929) phosphate-binding protein PstS [Methanobacterium] | 183 | 1.40E-45 |
| EF036-2 | gi 2622859 | (AE000929) phosphate-binding protein PstS homolog [Methanobacterium] | 158 | 2.40E-41 |
| EF036-2 | gi 2688115 | (AE001132) phosphate ABC transporter, periplasmic phosphate-binding | 117 | 1.10E-12 |
| EF037-2 | gi 2352482 | (AF005097) unknown [Lactococcus lactis] | 141 | 1.10E-23 |
| EF040-2 | gi 1657516 | hypothetical protein [Escherichia coli] >gi 1786511 (AE000139) | 208 | 1.90E-29 |
| EF040-2 | gi 293265 | 2-5A-dependent RNase [Mus musculus] >pir B45771 B45771 | 105 | 1.00E-17 |
| EF040-2 | gi 287865 | G9a [Homo sapiens] >pir S30385 S30385 G9a protein - human | 143 | 8.30E-14 |
| EF040-2 | gi 311817 | erythroid ankyrin [Mus musculus] >pir S37771 S37771 ankyrin, | 119 | 4.80E-13 |
| EF040-2 | gi 191940 | ankyrin [Mus musculus] >pir 49502 49502 ankyrin - mouse | 119 | 4.90E-13 |
| EF040-2 | gi 747710 | alt. ankyrin (variant 2.2) [Homo sapiens] | 120 | 1.50E-12 |
| EF040-2 | gi 178646 | ankyrin [Homo sapiens] | 120 | 1.80E-12 |
| EF040-2 | gi 1845265 | ankyrin [Homo sapiens] | 120 | 1.80E-12 |
| EF040-2 | pir A35049 A35 0 | ankyrin 1, erythrocyte splice form 2 - human | 120 | 1.80E-12 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|-----------------|--------------------------------------------------------------------------|-----|----------|
| EF040-2 | pir B35049 B350 | ankyrin 1, erythrocyte splice form 3 - human | 120 | 1.80E-12 |
| EF040-2 | gi 28702 | ankyrin (variant 2.1) [Homo sapiens] >pir S08275 SJHUK | 120 | 1.80E-12 |
| EF041-2 | gi 388269 | ankyrin 1, traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding | 670 | 1.40E-87 |
| EF041-2 | gnl PID d100655 | TraC [Enterococcus faecalis] | 662 | 1.50E-85 |
| EF041-2 | gnl PID d101185 | TRAC [Enterococcus faecalis] | 662 | 1.50E-85 |
| EF041-2 | gi 309662 | pheromone binding protein [Plasmid pCF10] >pir B53309 B53309 | 648 | 1.20E-83 |
| EF041-2 | gi 48808 | dciAE [Bacillus subtilis] | 218 | 1.20E-57 |
| EF041-2 | gnl PID e118149 | (AJ002571) DppE [Bacillus subtilis] >gnl PID e1183316 | 218 | 1.40E-57 |
| EF041-2 | pir S16651 S166 | dciAE protein - Bacillus subtilis | 218 | 2.10E-56 |
| EF041-2 | gi 882550 | ORF_f535 [Escherichia coli] >gi 1789397 (AE000384) f535; This 535 aa | 146 | 7.30E-40 |
| EF041-2 | gi 143603 | sporulation protein [Bacillus subtilis] >gnl PID e1183163 | 278 | 1.00E-34 |
| EF041-2 | gi 40005 | OppA gene product [Bacillus subtilis] | 279 | 1.00E-34 |
| EF041-2 | gi 47802 | Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor | 141 | 6.60E-30 |
| EF041-2 | gi 304925 | periplasmic oligopeptide binding protein [Escherichia coli] | 160 | 1.90E-29 |
| EF041-2 | gi 1574679 | oligopeptide binding protein (oppA) [Haemophilus influenzae] | 163 | 1.00E-28 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|----------------|--------------------------------------------------------------------------|-----|-----------|
| EF041-2 | gi 147014 | oligopeptide binding protein precursor [Escherichia coli] | 160 | 1.50E-28 |
| EF041-2 | gi 2253286 | (AF005657) plasminogen binding protein [Borrelia burgdorferi] | 134 | 5.00E-27 |
| EF045-2 | gi 308854 | oligopeptide binding protein [Lactococcus lactis] >pir[E53290 E53290] | 437 | 3.20E-125 |
| EF045-2 | gi 495181 | oligopeptide binding protein [Lactococcus lactis] | 426 | 9.70E-124 |
| EF045-2 | gi 677945 | AppA [Bacillus subtilis] >gnl PID e1183158 oligopeptide ABC | 154 | 2.30E-31 |
| EF045-2 | gi 293014 | peptide-binding protein [Lactococcus lactis] >pir[B47098 B47098] | 158 | 2.40E-14 |
| EF048-2 | gi 1574060 | hypothetical [Haemophilus influenzae] >pir 64164 64164 | 250 | 2.30E-41 |
| EF048-2 | dbj AB001488_2 | (AB001488) SIMILAR TO C4-DICARBOXYLATE-BINDING PERIPLASMIC | 208 | 3.60E-34 |
| EF048-2 | gi 466717 | No definition line found [Escherichia coli] >gi 1790004 (AE000435) | 199 | 1.30E-30 |
| EF048-2 | gi 46006 | periplasmic C4-dicarboxylate binding-protein [Rhodobacter capsulatus] | 162 | 1.40E-25 |
| EF048-2 | gi 1573102 | hypothetical [Haemophilus influenzae] >pir H64143 H64143 | 244 | 3.80E-25 |
| EF048-2 | gi 2182530 | (AE000085) Y4mM [Rhizobium sp. NGR234] | 114 | 5.60E-18 |
| EF048-2 | gi 1572999 | hypothetical [Haemophilus influenzae] >pir E64141 E64141 | 116 | 5.90E-15 |
| EF049-2 | gi 149581 | maturation protein [Lactobacillus paracasei] >pir A44858 A44858 | 241 | 2.40E-55 |
| EF049-2 | gi 47198 | ORF (AA 1 to 299) [Lactococcus lactis cremoris] >pir S08083 S08083 | 239 | 1.00E-54 |
| EF049-2 | gi 432402 | maturation protein [Lactococcus lactis] >gi 623055 proteinase | 239 | 6.20E-54 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|-------------------------------------------------------------------------|------|-----------|
| EF049-2 | gi 472835 | ORF1 [Lactococcus lactis cremoris] | 241 | 1.50E-53 |
| EF049-2 | gi 39782 | 33kDa lipoprotein [Bacillus subtilis] >gnl PID e325181 33kDa | 128 | 8.90E-40 |
| EF051-2 | gnl PID d10114 2 | molybdate-binding periplasmic protein [Synechocystis sp.] | 173 | 3.20E-50 |
| EF051-2 | gnl PID e118602 | alternate gene name: yvsD; similar to molybdate-binding | 314 | 5.90E-50 |
| EF051-2 | gi 1574546 | lsg locus hypothetical [Haemophilus influenzae] >pir A64175 A64175 | 161 | 2.20E-43 |
| EF051-2 | gi 504498 | periplasmic molybdate-binding protein [Escherichia coli] >gi 1147817 | 148 | 1.40E-30 |
| EF051-2 | gi 148939 | ORF 8 [Haemophilus influenzae] >pir S27583 S27583 hypothetical | 150 | 8.10E-28 |
| EF054-2 | gi 150556 | surface protein [Plasmid pCF10] >pir A41826 A41826 probable | 1490 | 1.80E-192 |
| EF054-2 | gnl PID e236571 | cell wall anchoring signal [Enterococcus faecalis] | 515 | 8.10E-64 |
| EF054-2 | gi 45738 | ORFC [Enterococcus faecalis] >pir JH0204 JH0204 hypothetical 30.5K | 372 | 1.60E-58 |
| EF054-2 | gi 496520 | orf iota [Streptococcus pyogenes] >pir S68125 S45091 hypothetical | 362 | 1.30E-43 |
| EF054-2 | gi 160693 | sporozoite surface protein [Plasmodium yoelii] >pir A45559 A45559 | 286 | 4.30E-33 |
| EF054-2 | gi 1813523 | PbTRAP [Plasmodium berghei] | 305 | 1.30E-32 |
| EF054-2 | gnl PID e225687 | zinc finger protein [Mus musculus] >gnl PID e225688 zinc | 246 | 3.60E-26 |
| EF054-2 | gi 2290394 | IgG and IgE immunoreactive antigen recognized by sera from patients | 242 | 1.40E-25 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|-----------------------------------------------------------------------|-----|----------|
| EF054-2 | gi 2290392 | IgG and IgE immunoreactive antigen recognized by sera from patients | 237 | 7.80E-25 |
| EF054-2 | gi 46523 | B antigen [Streptococcus agalactiae] | 232 | 2.80E-23 |
| EF054-2 | pir S15330 FCS O | IgA Fc receptor precursor - Streptococcus agalactiae | 228 | 1.00E-22 |
| EF054-2 | gi 1620100 | Pro- and Glu-rich, PENPEV (10x); similar to Streptococcus B | 210 | 3.10E-21 |
| EF054-2 | gi 63686 | NF-M c-terminus [Gallus gallus] | 222 | 6.90E-21 |
| EF054-2 | gi 63689 | NF-M protein [Gallus gallus] >pir S15762 S15762 neurofilament triplet | 222 | 8.50E-21 |
| EF054-2 | gi 757867 | TATA-box like sequence (Us11) [Human herpesvirus 1] >gi 291493 18 | 194 | 4.10E-19 |
| EF059-2 | gml PID e236571 | cell wall anchoring signal [Enterococcus faecalis] | 418 | 5.60E-95 |
| EF059-2 | gi 150556 | surface protein [Plasmid pCF10] >pir A41826 A41826 probable | 606 | 3.70E-87 |
| EF059-2 | gi 45738 | ORFC [Enterococcus faecalis] >pir JH0204 JH0204 hypothetical 30.5K | 366 | 9.30E-50 |
| EF059-2 | gi 496520 | orf iota [Streptococcus pyogenes] >pir S68125 S45091 hypothetical | 367 | 5.90E-44 |
| EF059-2 | gi 160693 | sporozoite surface protein [Plasmodium yoelii] >pir A45559 A45559 | 344 | 1.10E-38 |
| EF059-2 | gi 1813523 | PbTRAP [Plasmodium berghei] | 295 | 2.50E-32 |
| EF059-2 | gi 2290394 | IgG and IgE immunoreactive antigen recognized by sera from patients | 251 | 3.00E-29 |
| EF059-2 | gi 2290392 | IgG and IgE immunoreactive antigen recognized by sera from patients | 251 | 3.40E-29 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|-----------------------------------------------------------------------|-----|-----------|
| EF059-2 | gi 1620100 | Pro- and Glu-rich, PENPEV (10x); similar to Streptococcus B | 253 | 6.40E-27 |
| EF059-2 | gi 46521 | Fc receptor [Streptococcus agalactiae] >pir A60234 A60234 IgA Fc | 197 | 2.70E-26 |
| EF059-2 | gi 46523 | B antigen [Streptococcus agalactiae] | 232 | 9.30E-26 |
| EF059-2 | pir S15330 FCS O | IgA Fc receptor precursor - Streptococcus agalactiae | 232 | 9.30E-26 |
| EF059-2 | gnl PID e225687 | zinc finger protein [Mus musculus] >gnl PID e225688 zinc | 234 | 1.40E-22 |
| EF059-2 | gi 425356 | zona pellucida protein [Pseudopleuronectes americanus] | 229 | 1.00E-21 |
| EF059-2 | gi 457769 | Collagen [Bombyx mori] >pir S42886 S42886 collagen - silkworm | 209 | 7.60E-19 |
| EF061-2 | gnl PID e236571 | cell wall anchoring signal [Enterococcus faecalis] | 925 | 8.10E-118 |
| EF061-2 | gi 150556 | surface protein [Plasmid pCF10] >pir A41826 A41826 probable | 350 | 1.50E-107 |
| EF061-2 | gi 496520 | orf iota [Streptococcus pyogenes] >pir S68125 S45091 hypothetical | 308 | 1.40E-58 |
| EF061-2 | gi 45738 | ORFC [Enterococcus faecalis] >pir JH0204 JH0204 hypothetical 30.5K | 322 | 6.40E-50 |
| EF061-2 | gi 1813523 | PbTRAP [Plasmodium berghei] | 263 | 1.00E-26 |
| EF061-2 | gi 160693 | sporozoite surface protein [Plasmodium yoelii] >pir A45559 A45559 | 241 | 9.00E-25 |
| EF061-2 | gi 63686 | NF-M c-terminus [Gallus gallus] | 232 | 2.10E-22 |
| EF061-2 | gi 63689 | NF-M protein [Gallus gallus] >pir S15762 S15762 neurofilament triplet | 232 | 2.60E-22 |
| EF061-2 | gi 2290392 | IgG and IgE immunoreactive antigen recognized by sera from | 176 | 2.40E-21 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | patients | | |
|---------|--------------------|----------------------------------------------------------------------|------|----------|
| EF061-2 | gi 1620100 | Pro- and Glu-rich, PENPEV (10x); similar to Streptococcus B | 165 | 2.70E-20 |
| EF061-2 | gn PID e225687 | zinc finger protein [Mus musculus] >gn PID e225688 zinc | 197 | 7.80E-19 |
| EF061-2 | gi 160355 | interspersed repeat antigen [Plasmodium falciparum] | 199 | 8.20E-18 |
| EF061-2 | gi 410750 | interspersed repeat antigen [Plasmodium falciparum] | 199 | 8.90E-18 |
| EF061-2 | gi 2290388 | IgG and IgE immunoreactive antigen recognized by sera from patients | 182 | 1.40E-17 |
| EF061-2 | gi 2290394 | IgG and IgE immunoreactive antigen recognized by sera from patients | 180 | 2.80E-17 |
| EF062-2 | gi 47049 | asa1 gene product (AA 1-1296) [Enterococcus faecalis] | 3716 | 0 |
| EF062-2 | gi 43324 | aggregation substance (ASP1) [Enterococcus faecalis] | 4003 | 0 |
| EF062-2 | gi 2109266 | aggregation substance [Enterococcus faecium] | 5523 | 0 |
| EF062-2 | gi 150555 | aggregation substance [Plasmid pCF10] >pir H41662 H41662 150K mating | 6338 | 0 |
| EF062-2 | gi 1100973 | SspB precursor [Streptococcus gordonii] | 110 | 9.90E-39 |
| EF062-2 | gi 47248 | Pac protein precursor (AA -38 to 1527) [Streptococcus mutans] | 107 | 1.70E-38 |
| EF062-2 | gn PID d10150 7 | surface protein antigen precursor [Streptococcus sobrinus] | 132 | 5.00E-36 |
| EF062-2 | gi 47267 | cell surface antigen I/II [Streptococcus mutans] >pir S06839 S06839 | 107 | 6.50E-36 |
| EF062-2 | bbs 148453 | SpaA=endocarditis immunodominant antigen [Streptococcus sobrinus, | 132 | 1.20E-35 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|-----------------|----------------------------------------------------------------------|------|----------|
| EF062-2 | gi 47620 | antigen I /II [Streptococcus sobrinus] >pir A60338 A60338 surface | 132 | 2.90E-35 |
| EF062-2 | pir A35186 A351 | salivary agglutinin receptor precursor - Streptococcus | 109 | 2.10E-34 |
| EF062-2 | gi 1100971 | SspA [Streptococcus gordonii] | 110 | 3.80E-32 |
| EF062-2 | gi 1100975 | SspA [Streptococcus gordonii] | 110 | 2.30E-21 |
| EF063-2 | gi 47049 | asa1 gene product (AA 1-1296) [Enterococcus faecalis] | 3716 | 0 |
| EF063-2 | gi 43324 | aggregation substance (ASP1) [Enterococcus faecalis] | 4003 | 0 |
| EF063-2 | gi 2109266 | aggregation substance [Enterococcus faecium] | 5523 | 0 |
| EF063-2 | gi 150555 | aggregation substance [Plasmid pCF10] >pir H41662 H41662 150K mating | 6338 | 0 |
| EF063-2 | gi 1100973 | SspB precursor [Streptococcus gordonii] | 110 | 9.90E-39 |
| EF063-2 | gi 47248 | P Ac protein precursor (AA -38 to 1527) [Streptococcus mutans] | 107 | 1.70E-38 |
| EF063-2 | gnl PID d101507 | surface protein antigen precursor [Streptococcus sobrinus] | 132 | 5.00E-36 |
| EF063-2 | gi 47267 | cell surface antigen I/II [Streptococcus mutans] >pir S06839 S06839 | 107 | 6.50E-36 |
| EF063-2 | bbs 148453 | SpaA=endocarditis immunodominant antigen [Streptococcus sobrinus, | 132 | 1.20E-35 |
| EF063-2 | gi 47620 | antigen I /II [Streptococcus sobrinus] >pir A60338 A60338 surface | 132 | 2.90E-35 |
| EF063-2 | pir A35186 A351 | salivary agglutinin receptor precursor - Streptococcus | 109 | 2.10E-34 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|-------------------------------------------------------------------------|------|----------|
| EF063-2 | gi 1100971 | SspA [Streptococcus gordonii] | 110 | 3.80E-32 |
| EF063-2 | gi 1100975 | SspA [Streptococcus gordonii] | 110 | 2.30E-21 |
| EF064-2 | gi 47049 | asaI gene product (AA 1-1296) [Enterococcus faecalis] | 3716 | 0 |
| EF064-2 | gi 43324 | aggregation substance (ASP1) [Enterococcus faecalis] | 4003 | 0 |
| EF064-2 | gi 2109266 | aggregation substance [Enterococcus faecium] | 5523 | 0 |
| EF064-2 | gi 150555 | aggregation substance [Plasmid pCF10] >pir H41662 H41662 150K mating | 6338 | 0 |
| EF064-2 | gi 1100973 | SspB precursor [Streptococcus gordonii] | 110 | 9.90E-39 |
| EF064-2 | gi 47248 | Pac protein precursor (AA -38 to 1527) [Streptococcus mutans] | 107 | 1.70E-38 |
| EF064-2 | gn PID d10150 7 | surface protein antigen precursor [Streptococcus sobrinus] | 132 | 5.00E-36 |
| EF064-2 | gi 47267 | cell surface antigen I/II [Streptococcus mutans] >pir S06839 S06839 | 107 | 6.50E-36 |
| EF064-2 | bbs 148453 | SpaA=endocarditis immunodominant antigen [Streptococcus sobrinus, | 132 | 1.20E-35 |
| EF064-2 | gi 47620 | antigen I/II [Streptococcus sobrinus] >pir A60338 A60338 surface | 132 | 2.90E-35 |
| EF064-2 | pir A35186 A35 1 | salivary agglutinin receptor precursor - Streptococcus | 109 | 2.10E-34 |
| EF064-2 | gi 1100971 | SspA [Streptococcus gordonii] | 110 | 3.80E-32 |
| EF064-2 | gi 1100975 | SspA [Streptococcus gordonii] | 110 | 2.30E-21 |
| EF068-2 | gi 790398 | T06D8.1 [Caenorhabditis elegans] | 137 | 8.50E-17 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|--------------------|----------------------------------------------------------------------|-----|----------|
| EF068-2 | gn PID d10208 4 | membrane glycoprotein [Equine herpesvirus 1] | 210 | 5.80E-16 |
| EF068-2 | gi 2286204 | (AF011339) unknown [Acinetobacter calcoaceticus] | 121 | 8.40E-16 |
| EF068-2 | gi 330862 | membrane glycoprotein [Equine herpesvirus 1] >pir H36802 VGBEX1 | 208 | 1.10E-15 |
| EF068-2 | gi 1707247 | partial CDS [Caenorhabditis elegans] | 131 | 3.70E-15 |
| EF068-2 | gn PID d10208 4 | membrane glycoprotein [Equine herpesvirus 1] | 203 | 6.20E-15 |
| EF068-2 | gi 213392 | antifreeze glycoprotein [Notothenia coriiceps] >pir A38420 A38420 | 102 | 4.60E-13 |
| EF068-2 | gn PID e125464 | (AL022022) PGRS-family protein [Mycobacterium tuberculosis] | 145 | 1.50E-12 |
| EF068-2 | gi 951460 | FIM-C.1 gene product [Xenopus laevis] >pir A45155 A45155 mucin | 109 | 2.70E-12 |
| EF069-2 | gi 790398 | T06D8.1 [Caenorhabditis elegans] | 137 | 8.50E-17 |
| EF069-2 | gn PID d10208 4 | membrane glycoprotein [Equine herpesvirus 1] | 210 | 5.80E-16 |
| EF069-2 | gi 2286204 | (AF011339) unknown [Acinetobacter calcoaceticus] | 121 | 8.40E-16 |
| EF069-2 | gi 330862 | membrane glycoprotein [Equine herpesvirus 1] >pir H36802 VGBEX1 | 208 | 1.10E-15 |
| EF069-2 | gi 1707247 | partial CDS [Caenorhabditis elegans] | 131 | 3.70E-15 |
| EF069-2 | gn PID d10208 4 | membrane glycoprotein [Equine herpesvirus 1] | 203 | 6.20E-15 |
| EF069-2 | gi 213392 | antifreeze glycoprotein [Notothenia coriiceps] | 102 | 4.60E-13 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | | |
|---------|-----------------|-------------------------------------------------------------|-----|----------|--|
| | | >pir A38420 A38420 | | | |
| EF069-2 | gnl PID e125464 | (AL022022) PGRS-family protein [Mycobacterium tuberculosis] | 145 | 1.50E-12 | |
| EF069-2 | gi 951460 | FIM-C.1 gene product [Xenopus laevis] >pir A45155 A45155 | 109 | 2.70E-12 | |
| | | mucin | | | |
| EF070-2 | gi 790398 | T06D8.1 [Caenorhabditis elegans] | 137 | 8.50E-17 | |
| EF070-2 | gnl PID d10208 | membrane glycoprotein [Equine herpesvirus 1] | 210 | 5.80E-16 | |
| | 4 | | | | |
| EF070-2 | gi 2286204 | (AF011339) unknown [Acinetobacter calcoaceticus] | 121 | 8.40E-16 | |
| EF070-2 | gi 330862 | membrane glycoprotein [Equine herpesvirus 1] | 208 | 1.10E-15 | |
| | | >pir H36802 VGBEX1 | | | |
| EF070-2 | gi 1707247 | partial CDS [Caenorhabditis elegans] | 131 | 3.70E-15 | |
| EF070-2 | gnl PID d10208 | membrane glycoprotein [Equine herpesvirus 1] | 203 | 6.20E-15 | |
| | 4 | | | | |
| EF070-2 | gi 213392 | antifreeze glycoprotein [Notothenia coriiceps] | 102 | 4.60E-13 | |
| | | >pir A38420 A38420 | | | |
| EF070-2 | gnl PID e125464 | (AL022022) PGRS-family protein [Mycobacterium tuberculosis] | 145 | 1.50E-12 | |
| EF070-2 | gi 951460 | FIM-C.1 gene product [Xenopus laevis] >pir A45155 A45155 | 109 | 2.70E-12 | |
| | | mucin | | | |
| EF071-2 | gnl PID e306428 | unnamed protein product [Bacteriophage r1t] >gil 353566 | 127 | 2.00E-37 | |
| | | Lysin | | | |
| EF071-2 | gi 853751 | N-acetylmuramoyl-L-alanine amidase [Bacteriophage A511] | 273 | 2.60E-36 | |
| EF073-2 | gi 143830 | xpaC [Bacillus subtilis] >gnl PID d1005803 hydrolysis of | 173 | 7.10E-16 | |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|-----------------|-------------------------------------------------------------------|-----|-----------|
| EF074-2 | gi 1256698 | chitinase [Serratia marcescens] >gi 1256698 chitinase [Serratia | 618 | 2.60E-104 |
| EF074-2 | gi 1763985 | chitinase A [Vibrio harveyi] | 526 | 2.80E-84 |
| EF075-2 | gi 143156 | membrane bound protein [Bacillus subtilis] >gnl PID e1184471 | 593 | 1.70E-91 |
| EF075-2 | pir D70070 D700 | transcriptional regulator homolog ywtF - Bacillus subtilis | 118 | 1.90E-59 |
| EF075-2 | gi 1762327 | putative transcriptional regulator [Bacillus subtilis] | 148 | 9.60E-53 |
| EF075-2 | gi 1276874 | EpsA [Streptococcus thermophilus] | 239 | 2.20E-33 |
| EF075-2 | gnl PID e289126 | unknown [Streptococcus pneumoniae] | 150 | 1.20E-27 |
| EF075-2 | gi 485275 | putative regulatory protein [Streptococcus pneumoniae] | 150 | 2.50E-27 |
| EF075-2 | gi 2804735 | (AF030367) putative regulatory protein [Streptococcus pneumoniae] | 150 | 2.50E-27 |
| EF075-2 | gi 2804747 | (AF030369) putative regulatory protein [Streptococcus pneumoniae] | 150 | 2.50E-27 |
| EF075-2 | gnl PID e116988 | capsular polysaccharide synthesis protein [Streptococcus | 148 | 5.30E-27 |
| EF075-2 | gi 2804769 | (AF030373) putative regulatory protein [Streptococcus pneumoniae] | 148 | 5.30E-27 |
| EF075-2 | gi 1147744 | PSR [Enterococcus hirae] | 109 | 2.10E-23 |
| EF075-2 | gi 790435 | PSR [Enterococcus faecium] >pir S54177 S54177 PSR protein - | 102 | 4.40E-19 |
| EF075-2 | gi 2267239 | ORF1 [Staphylococcus epidermidis] | 109 | 8.50E-19 |
| EF075-2 | gnl PID d10189 | membrane bound protein LytR [Synechocystis sp.] | 121 | 2.80E-16 |
| EF077-2 | gnl PID d10113 | cadmium-transporting ATPase [Synechocystis sp.] | 396 | 2.30E-113 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|------------------------------------------------------------------------|-----|-----------|
| EF077-2 | gi 150719 | cadmium resistance protein [Plasmid p1258] >pir A32561 A32561 | 373 | 8.60E-112 |
| EF077-2 | gi 143753 | cadmium-efflux ATPase [Bacillus firmus] >pir D42707 D42707 probable | 361 | 8.10E-111 |
| EF077-2 | gi 152978 | E1-E2 cadmium efflux adenosine triphosphatase [Staphylococcus] | 381 | 4.30E-110 |
| EF077-2 | gnl PID e248808 | unknown [Mycobacterium tuberculosis] | 298 | 3.50E-107 |
| EF077-2 | gi 495646 | ATPase [Transposon Tn5422] | 361 | 2.10E-106 |
| EF077-2 | gnl PID e118497 | similar to heavy metal-transporting ATPase [Bacillus] | 286 | 3.50E-104 |
| EF077-2 | gi 1699049 | cadmium resistance protein [Lactococcus lactis] | 352 | 3.60E-100 |
| EF077-2 | gnl PID e118603 | similar to heavy metal-transporting ATPase [Bacillus] | 254 | 9.90E-100 |
| EF077-2 | gnl PID e306540 | unknown [Mycobacterium tuberculosis] | 352 | 5.20E-88 |
| EF077-2 | gnl PID e263525 | P-type ATPase [Mycobacterium tuberculosis] >gnl PID e249413 | 199 | 5.50E-86 |
| EF077-2 | gnl PID e264090 | unknown [Mycobacterium tuberculosis] | 250 | 3.00E-84 |
| EF077-2 | gnl PID d10113 5 | cadmium-transporting ATPase [Synechocystis sp.] | 260 | 1.00E-81 |
| EF077-2 | gi 1773166 | probable copper-transporting atpase [Escherichia coli] >gi 1786691 | 212 | 4.70E-80 |
| EF077-2 | gi 1354935 | probable copper-transporting atpase [Escherichia coli] | 212 | 8.50E-79 |
| EF078-2 | gi 143331 | alkaline phosphatase regulatory protein [Bacillus subtilis] | 257 | 5.50E-58 |
| EF078-2 | gi 410142 | ORFX18 [Bacillus subtilis] >gnl PID e1185580 two-component sensor | 235 | 8.20E-51 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|---------------------------------------------------------------------|------|-----------|
| EF078-2 | gnl PID d10119 6 | homologous to sp:PHOR_BACSU [Bacillus subtilis] | 219 | 4.20E-44 |
| EF078-2 | gi 1575578 | histidine protein kinase [Thermotoga maritima] | 191 | 7.10E-44 |
| EF078-2 | gi 2182990 | histidine kinase [Lactococcus lactis cremoris] | 169 | 6.40E-40 |
| EF078-2 | gi 2182992 | histidine kinase [Lactococcus lactis cremoris] | 152 | 1.10E-39 |
| EF078-2 | gnl PID d10113 4 | sensory transduction histidine kinase [Synechocystis sp.] | 259 | 3.90E-38 |
| EF078-2 | gi 149296 | phosphate regulatory protein phoR (gtg start codon) [Klebsiella | 228 | 7.60E-33 |
| EF078-2 | gi 581188 | phoR gene product (AA 1-431) [Escherichia coli] >gi 1657596 | 226 | 1.60E-32 |
| EF078-2 | gnl PID d10108 7 | sensory transduction histidine kinase [Synechocystis sp.] | 138 | 3.70E-32 |
| EF078-2 | gnl PID e266592 | unknown [Mycobacterium tuberculosis] | 232 | 1.10E-31 |
| EF078-2 | gi 2182996 | histidine kinase [Lactococcus lactis cremoris] | 206 | 1.30E-31 |
| EF078-2 | gnl PID d10113 5 | sensory transduction histidine kinase [Synechocystis sp.] | 256 | 1.30E-31 |
| EF078-2 | gi 294893 | phosphate regulatory protein phoR (gtg start codon) [Shigella | 225 | 1.60E-31 |
| EF078-2 | gi 288420 | drug sensory protein A [Synechocystis PCC6803] >gnl PID d1017420 | 106 | 2.50E-31 |
| EF079-2 | gi 2098719 | putative fimbrial-associated protein [Actinomyces naeslundii] | 183 | 8.60E-26 |
| EF081-2 | gi 467806 | penicillin-binding protein [Enterococcus faecalis] | 1356 | 2.10E-178 |
| EF081-2 | gi 790429 | low affinity penicillin-binding protein 5 (PBPS) [Enterococcus | 607 | 1.00E-78 |
| EF081-2 | gnl PID e208365 | penicillin-binding protein 5 [Enterococcus faecium] | 604 | 1.10E-78 |
| EF081-2 | gi 790433 | low affinity penicillin-binding protein 5 (PBPS) [Enterococcus | 604 | 2.70E-78 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|--------------------------------------------------------------------|-----|-----------|
| EF081-2 | gi 790437 | low affinity penicillin-binding protein 5 (PBP5) [Enterococcus | 602 | 5.10E-78 |
| EF081-2 | gi 790431 | low affinity penicillin-binding protein 5 (PBP5) [Enterococcus | 591 | 2.60E-77 |
| EF081-2 | gi 43342 | D-alanyl-D-alanine carboxypeptidase [Enterococcus hirae] | 587 | 9.30E-77 |
| EF081-2 | gi 49000 | D-alanyl-D-alanine carboxypeptidase [Enterococcus hirae] | 572 | 5.20E-74 |
| EF081-2 | gnl PID d10079 4 | penicillin-binding protein 2 [Bacillus subtilis] | 149 | 7.40E-24 |
| EF081-2 | gnl PID e315088 | MecA1 [Staphylococcus sciuri] | 111 | 4.40E-19 |
| EF081-2 | gnl PID e286651 | MecA protein [Staphylococcus sciuri] | 106 | 2.90E-18 |
| EF081-2 | gnl PID e316581 | MecA protein [Staphylococcus sciuri] | 111 | 2.90E-18 |
| EF081-2 | gnl PID e316607 | MecA2 protein [Staphylococcus sciuri] | 101 | 3.70E-14 |
| EF081-2 | gnl PID e316613 | MecA protein [Staphylococcus sciuri] >gi 46613 mecA gene | 101 | 3.70E-14 |
| EF083-2 | gi 496283 | lysine [Bacteriophage Tuc2009] | 436 | 6.20E-176 |
| EF083-2 | gi 530798 | LysB [Bacteriophage phi-LC3] | 421 | 3.00E-175 |
| EF083-2 | gi 166183 | muramidase [Bacteriophage CP-7] | 186 | 1.20E-21 |
| EF083-2 | gi 166188 | muramidase [Bacteriophage CP-9] >pir JQ0438 MUBPC9 | 188 | 5.00E-21 |
| EF083-2 | gi 623084 | muramidase; muramidase [Bacteriophage LL-H] | 193 | 8.40E-20 |
| EF083-2 | gi 166175 | muramidase [Bacteriophage CP-1] | 175 | 3.40E-19 |
| EF083-2 | gnl PID e221272 | lysozyme [Bacteriophage CP-1] >pir A31086 MUBPCP | 175 | 3.40E-19 |
| EF083-2 | pir JQ0437 MU BP | N-acetyl-muramoyl-L-alanine amidase (EC 3.5.1.28) - phage | 171 | 9.50E-19 |
| EF083-2 | gi 410502 | LysA [Bacteriophage mv4] >pir S38477 S38477 lytic enzyme lysA - | 187 | 8.90E-17 |
| EF083-2 | gi 793850 | lysine [Lactobacillus bacteriophage phi adh] >gnl PID e1217314 | 117 | 5.60E-15 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|-------------------------------------------------------------------------------|------|-----------|
| EF084-2 | gi 2293312 | lysine (AF008220) YtfP [Bacillus subtilis] >gnl PID e1185879 similar to | 438 | 1.70E-140 |
| EF084-2 | gi 2367234 | (AE000425) hypothetical 43.8 kD protein in rhsB-pit intergenic | 167 | 2.20E-51 |
| EF084-2 | gi 912464 | No definition line found [Escherichia coli] | 167 | 6.00E-51 |
| EF084-2 | gnl PID d10112 7 | hypothetical protein [Synecocystis sp.] >pir S76678 S76678 | 151 | 6.10E-42 |
| EF084-2 | gi 1573954 | hypothetical [Haemophilus influenzae] >pir G64161 G64161 | 142 | 2.90E-40 |
| EF085-2 | gi 1209527 | protein histidine kinase [Enterococcus faecalis] | 2023 | 8.00E-279 |
| EF085-2 | gi 467057 | phoR; B2168_C3_247 [Mycobacterium leprae] >pir S72905 S72905 | 226 | 8.80E-23 |
| EF085-2 | gnl PID e119229 | SenX3 [Mycobacterium bovis BCG] | 222 | 3.10E-22 |
| EF085-2 | gnl PID e255152 | unknown [Mycobacterium tuberculosis] >gnl PID e321546 SenX3 | 222 | 3.10E-22 |
| EF085-2 | gi 1778485 | PcoS homolog [Escherichia coli] >gi 1786783 (AE000162) f480; This | 111 | 3.80E-16 |
| EF085-2 | gi 149296 | phosphate regulatory protein phoR (gtg start codon) [Klebsiella] | 110 | 1.40E-14 |
| EF085-2 | gi 581188 | phoR gene product (AA 1-431) [Escherichia coli] >gi 1657596 | 103 | 5.30E-14 |
| EF085-2 | gi 143331 | alkaline phosphatase regulatory protein [Bacillus subtilis] | 118 | 4.90E-13 |
| EF085-2 | gi 537239 | alternate gene name phoM; CG Site No. 395 [Escherichia coli] | 126 | 9.50E-13 |
| EF085-2 | gi 147251 | phoM [Escherichia coli] >gi 809670 phoM protein (1 is 3rd base in | 126 | 9.50E-13 |
| EF085-2 | gi 2182992 | histidine kinase [Lactococcus lactis cremoris] | 109 | 5.90E-12 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|------------|--------------------------------------------------------------------------|-----|----------|
| EF086-2 | gi 437706 | alternative truncated translation product from E.coli [Streptococcus] | 221 | 3.00E-54 |
| EF086-2 | gi 437705 | hyaluronidase [Streptococcus pneumoniae] | 221 | 1.60E-53 |
| EF086-2 | gi 595847 | hyaluronate lyase [Streptococcus agalactiae] >pir A55137 A55137 | 203 | 3.30E-44 |
| EF086-2 | gi 705406 | hyaluronate lyase [Staphylococcus aureus] | 191 | 3.40E-42 |
| EF086-2 | gi 562086 | hyaluronidase [Propionibacterium acnes] | 198 | 6.00E-27 |
| EF087-2 | gi 437706 | alternative truncated translation product from E.coli [Streptococcus] | 221 | 3.00E-54 |
| EF087-2 | gi 437705 | hyaluronidase [Streptococcus pneumoniae] | 221 | 1.60E-53 |
| EF087-2 | gi 595847 | hyaluronate lyase [Streptococcus agalactiae] >pir A55137 A55137 | 203 | 3.30E-44 |
| EF087-2 | gi 705406 | hyaluronate lyase [Staphylococcus aureus] | 191 | 3.40E-42 |
| EF087-2 | gi 562086 | hyaluronidase [Propionibacterium acnes] | 198 | 6.00E-27 |
| EF088-2 | gi 437706 | alternative truncated translation product from E.coli [Streptococcus] | 221 | 3.00E-54 |
| EF088-2 | gi 437705 | hyaluronidase [Streptococcus pneumoniae] | 221 | 1.60E-53 |
| EF088-2 | gi 595847 | hyaluronate lyase [Streptococcus agalactiae] >pir A55137 A55137 | 203 | 3.30E-44 |
| EF088-2 | gi 705406 | hyaluronate lyase [Staphylococcus aureus] | 191 | 3.40E-42 |
| EF088-2 | gi 562086 | hyaluronidase [Propionibacterium acnes] | 198 | 6.00E-27 |
| EF091-2 | gi 556016 | similar to plant water stress proteins; ORF2 [Bacillus subtilis] | 198 | 5.50E-21 |
| EF091-2 | gi 2353333 | (AF016513) Ce-LEA [Caenorhabditis elegans] | 189 | 2.40E-17 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|-----------------|--------------------------------------------------------------------|-----|----------|
| EF091-2 | gn PID e353216 | seed maturation protein homolog [Arabidopsis thaliana] | 146 | 3.60E-11 |
| EF091-2 | gi 1161171 | late embryogenesis abundant protein [Picea glauca] | 132 | 5.70E-11 |
| EF091-2 | pir S04909 S049 | embryonic protein DC8 (clone 8/10) - carrot | 127 | 6.50E-11 |
| EF092-2 | gi 2689898 | (AE000792) PTS system, cellobiose-specific IIB component (celA) | 145 | 4.00E-27 |
| EF092-2 | gn PID d102048 | B. subtilis, cellobiose phosphotransferase system, celA; | 116 | 1.40E-26 |
| EF096-2 | gi 147329 | transport protein [Escherichia coli] >gn PID d1015409 | 532 | 2.10E-91 |
| EF096-2 | gi 1573475 | spermidine/putrescine-binding periplasmic protein precursor (potD) | 527 | 1.10E-79 |
| EF096-2 | gi 1574803 | spermidine/putrescine-binding periplasmic protein precursor (potD) | 468 | 1.60E-75 |
| EF096-2 | gi 1142681 | Lpp38 [Pasteurella haemolytica] | 446 | 4.40E-72 |
| EF096-2 | gn PID d101526 | Putrescine transport protein PotF [Escherichia coli] | 216 | 1.50E-54 |
| EF096-2 | gi 147334 | periplasmic putrescine binding protein [Escherichia coli] | 216 | 2.10E-53 |
| EF096-2 | gi 2688565 | (AE001165) spermidine/putrescine ABC transporter, | 240 | 2.00E-48 |
| EF096-2 | gi 1881733 | PotD [Salmonella typhimurium] | 253 | 2.70E-28 |
| EF096-2 | gn PID d101926 | spermidine/putrescine-binding periplasmic protein | 243 | 4.20E-26 |
| EF096-2 | gn PID e152543 | potF gene product [Clostridium perfringens] | 204 | 3.30E-21 |
| EF097-2 | gi 622991 | mannitol transport protein [Bacillus stearothermophilus] | 547 | 4.90E-93 |
| EF097-2 | gi 42034 | mannitol permease [Escherichia coli] >gi 466737 mannitol- | 535 | 5.50E-85 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | specific | | |
|---------|---------------------|-------------------------------------------------------------------------|-----|----------|
| EF097-2 | gi 633650 | enzyme II(mannitol) [Staphylococcus carnosus] >pir S68193 S22385 | 516 | 2.10E-82 |
| EF097-2 | gi 882462 | protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia | 509 | 3.00E-76 |
| EF097-2 | gi 312763 | protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia | 357 | 7.50E-70 |
| EF097-2 | gnl PID d10096 6 | homologue of mannitol transport protein of B. | 492 | 3.10E-62 |
| EF097-2 | gnl PID d10079 2 | mannitol-specific phosphotransferase enzyme II [Bacillus | 484 | 5.20E-61 |
| EF097-2 | gi 1673855 | (AE000020) Mycoplasma pneumoniae, PTS system mannitol- specific | 232 | 3.50E-59 |
| EF097-2 | gnl PID d10065 1 | phosphotransferase enzymell, mannitol-specific [Mycoplasma | 158 | 8.20E-18 |
| EF097-2 | pir S77757 S777 | phosphotransferase system enzyme II (EC 2.7.1.69), | 103 | 2.00E-13 |
| EF100-2 | gi 2058546 | Com YC [Streptococcus gordonii] | 193 | 7.30E-27 |
| EF100-2 | gi 2058546 | Com YC [Streptococcus gordonii] | 193 | 7.30E-27 |
| EF100-2 | gi 142708 | comG3 gene product [Bacillus subtilis] >gnl PID e1185739 comGC | 150 | 2.90E-22 |
| EF100-2 | gi 142708 | comG3 gene product [Bacillus subtilis] >gnl PID e1185739 comGC | 150 | 2.90E-22 |
| EF100-2 | gi 148437 | secretory component [Erwinia chrysanthemi] >pir E47021 E47021 pectic | 134 | 4.40E-15 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|-------------------------------------------------------------------------|------|-----------|
| EF100-2 | gi 148437 | secretory component [Erwinia chrysanthemi] >pir E47021 E47021 peptic | 134 | 4.40E-15 |
| EF100-2 | gi 606262 | ORF_o145 [Escherichia coli] >gi 693706 HopG [Escherichia coli] | 136 | 9.10E-13 |
| EF100-2 | gi 606262 | ORF_o145 [Escherichia coli] >gi 693706 HopG [Escherichia coli] | 136 | 9.10E-13 |
| EF100-2 | gi 38828 | ExeG gene product [Aeromonas hydrophila] >pir S22910 I49905 protein | 132 | 3.50E-12 |
| EF100-2 | gi 38828 | ExeG gene product [Aeromonas hydrophila] >pir S22910 I49905 protein | 132 | 3.50E-12 |
| EF100-2 | gnl PID e117259 | etpG [Escherichia coli] | 131 | 5.10E-12 |
| EF100-2 | gnl PID e117259 | etpG [Escherichia coli] | 131 | 5.10E-12 |
| EF100-2 | gi 42189 | outG gene product [Erwinia carotovora] >pir S32861 S32861 outG | 130 | 9.90E-12 |
| EF100-2 | gi 42189 | outG gene product [Erwinia carotovora] >pir S32861 S32861 outG | 130 | 9.90E-12 |
| EF100-2 | gi 609628 | putative [Vibrio cholerae] | 128 | 1.60E-11 |
| EF100-2 | gi 609628 | putative [Vibrio cholerae] | 128 | 1.60E-11 |
| EF101-2 | gnl PID d10257 3 | bacG [Enterococcus faecalis] | 106 | 3.60E-17 |
| EF101-2 | gnl PID e321943 | hypothetical protein [Enterococcus faecalis] >gnl PID e321943 | 105 | 1.80E-16 |
| EF101-2 | gnl PID e118502 | similar to hypothetical proteins from B. subtilis [Bacillus] | 113 | 1.80E-15 |
| EF110-2 | gi 43338 | Staphylococcal serine proteinase homologue [Enterococcus faecalis] | 1462 | 2.30E-195 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|---------------------|------------------------------------------------------------------------------|-----|----------|
| EF110-2 | gnl PID d10010 8 | glutamic acid specific protease prepropeptide [Staphylococcus aureus] | 106 | 3.70E-14 |
| EF110-2 | gi 46687 | preproenzyme (AA -68 to 268) [Staphylococcus aureus] | 106 | 6.70E-14 |
| EF111-2 | gi 606018 | ORF_o783 [Escherichia coli] >gi 1789462 (AE000390) | 477 | 8.10E-80 |
| | | hypothetical 88.3 | | |
| EF121-2 | gi 2626826 | YfkN [Bacillus subtilis] >gnl PID e1182774 similar to | 143 | 1.30E-96 |
| EF121-2 | gi 2313187 | (AE000532) 2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) | 413 | 2.60E-82 |
| EF121-2 | gi 48453 | 5'-nucleotidase [Vibrio parahaemolyticus] >gnl PID d1001218 | 279 | 8.50E-47 |
| EF121-2 | gi 757842 | UDP-sugar hydrolase [Escherichia coli] | 239 | 1.60E-44 |
| EF121-2 | gi 1773162 | UDP-sugar hydrolase precursor [Escherichia coli] >gi 1786687 | 239 | 1.60E-44 |
| EF121-2 | gi 47950 | precursor polypeptide (AA -25 to 525) [Salmonella typhimurium] | 229 | 2.10E-41 |
| EF121-2 | gi 747913 | 2',3'-cyclic-nucleotide 2'-phosphodiesterase [Yersinia enterocolitica] | 115 | 4.70E-36 |
| EF121-2 | gi 62772 | 5'-nucleotidase [Discopyge ommata] >pir S19564 S19564 5'-nucleotidase | 137 | 5.80E-35 |
| EF121-2 | gi 1573573 | 2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) [Haemophilus influenzae] | 114 | 8.90E-34 |
| EF121-2 | gi 537054 | 2',3'-cyclic-nucleotide 2'-phosphodiesterase [Escherichia coli] | 110 | 1.10E-31 |
| EF121-2 | bbs 135915 | 5'-nucleotidase=glycosylphosphatidylinositol-anchored protein {EC 3.1.3.5} | 128 | 7.70E-29 |
| EF121-2 | gi 1737443 | 5'-nucleotidase [Boophilus microplus] | 104 | 1.60E-28 |
| EF121-2 | gi 202551 | 5'-nucleotidase precursor (EC 3.1.3.5) [Rattus norvegicus] | 138 | 6.10E-28 |
| EF121-2 | gi 349783 | ecto-5'-nucleotidase [Mus musculus] >pir JC2001 JC2001 | 136 | 1.10E-27 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|------------|----------------------------------------------------------------------------------------------------------------------|-----|----------|
| EF121-2 | gi 23897 | 5'-nucleotidase [Homo sapiens] >pir S11032 S11032 5'-nucleotidase (EC) | 133 | 1.60E-27 |
| EF122-2 | gi 2626826 | YfkN [Bacillus subtilis] >gnl PID e1182774 similar to (AE000532) 2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) | 143 | 1.30E-96 |
| EF122-2 | gi 2313187 | 5'-nucleotidase [Vibrio parahaemolyticus] >gnl PID d1001218 | 413 | 2.60E-82 |
| EF122-2 | gi 48453 | UDP-sugar hydrolase [Escherichia coli] | 279 | 8.50E-47 |
| EF122-2 | gi 757842 | UDP-sugar hydrolase precursor [Escherichia coli] >gi 1786687 | 239 | 1.60E-44 |
| EF122-2 | gi 1773162 | precursor polypeptide (AA -25 to 525) [Salmonella typhimurium] | 239 | 1.60E-44 |
| EF122-2 | gi 47950 | 2',3'-cyclic-nucleotide 2'-phosphodiesterase [Yersinia] | 229 | 2.10E-41 |
| EF122-2 | gi 747913 | 5'-nucleotidase [Discopyge ommata] >pir S19564 S19564 5'-nucleotidase | 115 | 4.70E-36 |
| EF122-2 | gi 62772 | 2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) [Haemophilus] | 137 | 5.80E-35 |
| EF122-2 | gi 1573573 | 2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) [Haemophilus] | 114 | 8.90E-34 |
| EF122-2 | gi 537054 | 2',3'-cyclic-nucleotide 2'-phosphodiesterase [Escherichia coli] | 110 | 1.10E-31 |
| EF122-2 | bbs 135915 | 5'-nucleotidase=glycosylphosphatidylinositol-anchored protein {EC} | 128 | 7.70E-29 |
| EF122-2 | gi 1737443 | 5'-nucleotidase [Boophilus microplus] | 104 | 1.60E-28 |
| EF122-2 | gi 202551 | 5'-nucleotidase precursor (EC 3.1.3.5) [Rattus norvegicus] | 138 | 6.10E-28 |
| EF122-2 | gi 349783 | ecto-5'-nucleotidase [Mus musculus] >pir JC2001 JC2001 | 136 | 1.10E-27 |
| EF122-2 | gi 23897 | 5'-nucleotidase [Homo sapiens] >pir S11032 S11032 5'-nucleotidase (EC) | 133 | 1.60E-27 |
| EF129-2 | gi 43334 | P54 protein [Enterococcus faecium] >pir S05542 S05542 | 630 | 9.40E-79 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | hypothetical | | |
|---------|---------------------|-------------------------------------------------------------------------|------|-----------|
| EF129-2 | gi 512521 | usp 45 gene product [Lactococcus lactis] >pir JN0097 JN0097 secreted | 374 | 1.30E-42 |
| EF129-2 | gi 149525 | secreted protein [Lactococcus lactis] | 371 | 3.60E-42 |
| EF129-2 | gnl PID e313022 | hypothetical protein [Bacillus subtilis] >gnl PID e1186168 | 317 | 2.30E-33 |
| EF130-2 | gi 488339 | alpha-amylase [unidentified cloning vector] | 621 | 6.70E-81 |
| EF130-2 | gi 488336 | ORF [unidentified cloning vector] | 242 | 8.00E-27 |
| EF130-2 | bbs 112518 | alpha-amylase {N-terminal region} [Artificial sequence, Peptide] | 237 | 4.80E-26 |
| EF130-2 | gnl PID e289144 | ywpE [Bacillus subtilis] >gnl PID e1184540 ywpE [Bacillus] | 129 | 5.40E-11 |
| EF131-2 | gnl PID e118528 | penicillin-binding protein [Bacillus subtilis] | 277 | 7.40E-43 |
| EF131-2 | gi 488330 | alpha-amylase [unidentified cloning vector] | 280 | 1.30E-31 |
| EF131-2 | gi 509249 | No definition line found [Lactobacillus plantarum] | 274 | 1.10E-30 |
| EF131-2 | gnl PID d10249 1 | (AB009635) Fmt [Staphylococcus aureus] | 170 | 5.60E-20 |
| EF131-2 | gi 515050 | DD-peptidase precursor [Streptomyces lividans] >pir S48220 S48220 | 131 | 2.30E-14 |
| EF131-2 | gi 153448 | serine DD-peptidase [Streptomyces lividans] | 131 | 1.20E-12 |
| EF132-2 | gi 153826 | adhesin B [Streptococcus sanguis] >pir A43583 A43583 adhesin B | 1257 | 2.30E-166 |
| EF132-2 | gi 1184932 | ScbA [Streptococcus crista] | 1248 | 3.70E-165 |
| EF132-2 | gi 310633 | adhesin [Streptococcus gordonii] | 1247 | 5.10E-165 |
| EF132-2 | gi 393269 | adhesion protein [Streptococcus pneumoniae] | 1204 | 3.40E-163 |
| EF132-2 | gi 1575030 | surface adhesin A precursor [Streptococcus pneumoniae] | 1220 | 2.40E-161 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| EF132-2 | gi 153834 | adhesin specific for salivary pellicle of dental surfaces | 1203 | 4.80E-159 |
|---------|---------------------|----------------------------------------------------------------------|-------------|---------------|
| EF132-2 | gi 1117994 | surface antigen A variant precursor [Streptococcus pneumoniae] | 1191 | 2.00E-157 |
| EF132-2 | gi 493017 | endocarditis specific antigen [Enterococcus faecalis] | 931 | 3.70E-122 |
| EF132-2 | gnl PID e255529 | lipoprotein [Staphylococcus epidermidis] | 453 | 3.20E-92 |
| EF132-2 | gi 1245464 | YfeA [Yersinia pestis] >gi 1245464 YfeA [Yersinia pestis] | 364 | 3.60E-64 |
| EF132-2 | gi 1573330 | adhesin B precursor (fimA) [Haemophilus influenzae] | 349 | 3.50E-63 |
| EF132-2 | gi 755075 | periplasmic-binding protein [Synechocystis sp.] >gnl PID d1018652 Mn | 326 | 6.80E-62 |
| EF132-2 | gnl PID e118595 | similar to ABC transporter (membrane protein) [Bacillus | 174 | 3.10E-32 |
| EF132-2 | gi 1777933 | TroA [Treponema pallidum] | 171 | 3.40E-32 |
| EF132-2 | gi 790546 | Tromp1 [Treponema pallidum] | 171 | 5.10E-32 |
| Query | Derwent Access. No. | Derwent Gene Description | BLAST Score | BLAST P-Value |
| EF003-2 | W20909 | H. pylori outer membrane protein 14ge10705orf5. | 268 | 4.20E-39 |
| EF003-2 | W20166 | Helicobacter pylori outer membrane protein, 16225006.aa. | 241 | 3.00E-27 |
| EF006-2 | W20909 | H. pylori outer membrane protein 14ge10705orf5. | 283 | 1.20E-48 |
| EF006-2 | W20166 | Helicobacter pylori outer membrane protein, 16225006.aa. | 266 | 1.10E-30 |
| EF008-2 | R37495 | Pneumococcal fimbrial protein A. | 967 | 1.20E-127 |
| EF008-2 | W26367 | Staphylococcus aureus saliva binding protein. | 467 | 7.50E-100 |
| EF008-2 | R79722 | ROM precursor TROMP1. | 181 | 8.00E-36 |
| EF008-2 | W22134 | Treponema pallidum rare outer membrane protein (TROMP-1). | 181 | 8.00E-36 |
| EF009-2 | W20909 | H. pylori outer membrane protein 14ge10705orf5. | 319 | 1.40E-53 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|--------|----------------------------------------------------------------------|-----|----------|
| EF009-2 | W20166 | Helicobacter pylori outer membrane protein, 16225006.aa. | 278 | 2.50E-32 |
| EF012-2 | R48035 | Hyaluronic acid synthase of Streptococcus equisimilis. | 227 | 3.20E-69 |
| EF014-2 | W14070 | S.thermophilus exopolysaccharide biosynthesis protein EpsR. | 103 | 5.90E-19 |
| EF014-2 | W22169 | S.thermophilus exopolysaccharide synthesis operon epsA gene product. | 103 | 7.30E-18 |
| EF016-2 | W15799 | Adherence factor 104R of Lactobacillus fermentum. | 157 | 9.60E-22 |
| EF016-2 | W15793 | Adherence factor consensus sequence. | 103 | 1.00E-11 |
| EF017-2 | R48035 | Hyaluronic acid synthase of Streptococcus equisimilis. | 241 | 8.90E-71 |
| EF021-2 | R31013 | P39-alpha. | 141 | 1.60E-19 |
| EF021-2 | R33280 | P39-beta. | 134 | 7.00E-14 |
| EF022-2 | R48035 | Hyaluronic acid synthase of Streptococcus equisimilis. | 324 | 2.20E-65 |
| EF023-2 | R48035 | Hyaluronic acid synthase of Streptococcus equisimilis. | 155 | 9.90E-33 |
| EF023-2 | R70152 | Streptococcus pneumoniae strain SPRU98 P1pA. | 125 | 5.90E-17 |
| EF027-2 | R48035 | Hyaluronic acid synthase of Streptococcus equisimilis. | 233 | 2.20E-34 |
| EF028-2 | W17830 | Thermophilic alkaline phosphatase. | 202 | 7.70E-59 |
| EF028-2 | W11568 | E.coli alkaline phosphatase mutant D153H/Q329A. | 182 | 7.90E-56 |
| EF028-2 | W11570 | E.coli alkaline phosphatase mutant D153H/K328H/Q329A. | 182 | 7.90E-56 |
| EF028-2 | W26300 | E.coli alkaline phosphatase mutant D153H/K328H/Q329A/D330H. | 182 | 1.10E-55 |
| EF028-2 | W11565 | E.coli alkaline phosphatase mutant D153H/K328H/D330A. | 182 | 3.10E-55 |
| EF028-2 | W11557 | E.coli alkaline phosphatase mutant D153H/D330N. | 182 | 4.30E-55 |
| EF028-2 | W11561 | E.coli alkaline phosphatase mutant D153H/D330A. | 182 | 4.30E-55 |
| EF028-2 | W11555 | E.coli alkaline phosphatase mutant D153H/K328H/D330N. | 182 | 4.70E-55 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|--------|-----------------------------------------------------------------------|-----|----------|
| EF028-2 | W11566 | E.coli alkaline phosphatase mutant D153H/K328H/D330L. | 182 | 1.20E-54 |
| EF028-2 | W11569 | E.coli alkaline phosphatase mutant K328H/Q329A. | 180 | 1.70E-54 |
| EF028-2 | W11562 | E.coli alkaline phosphatase mutant D153H/D330L. | 182 | 1.70E-54 |
| EF028-2 | R26980 | Fv(FRP5)-phoA recombinant antibody. | 174 | 1.90E-54 |
| EF028-2 | W11567 | E.coli alkaline phosphatase mutant Q329A. | 179 | 2.30E-54 |
| EF028-2 | W11558 | E.coli alkaline phosphatase mutant K328H/D330N. | 176 | 6.40E-54 |
| EF028-2 | W11563 | E.coli alkaline phosphatase mutant K328H/D330A. | 176 | 6.40E-54 |
| EF029-2 | R10044 | Plasmid pOW360 encoded Human Growth Hormone (HGH) - nuclease A | 320 | 3.50E-40 |
| EF029-2 | R10041 | Plasmid pOW350 nuclease A product. | 320 | 4.30E-40 |
| EF029-2 | R73997 | Staphylococcus aureus (Foggi) nuclease signal and mature sequences. | 320 | 5.60E-40 |
| EF029-2 | R10043 | Plasmid pOW360 encoding Human Growth Hormone (HGH) - nuclease | 320 | 2.90E-38 |
| EF030-2 | R48035 | Hyaluronic acid synthase of Streptococcus equisimilis. | 277 | 6.10E-47 |
| EF040-2 | R59077 | 2-5A-dependent RNA-ase. | 105 | 1.90E-18 |
| EF040-2 | W12703 | Mouse 2-5A-dependent RNase. | 105 | 1.90E-18 |
| EF040-2 | R82661 | Partial murine 2-5A-dependent RNase. | 105 | 1.90E-18 |
| EF041-2 | R48035 | Hyaluronic acid synthase of Streptococcus equisimilis. | 225 | 6.30E-26 |
| EF054-2 | R26042 | P. yoelii SSP2 antigen. | 286 | 8.00E-34 |
| EF054-2 | R85782 | Group B Streptococcal mutant beta antigen without IgA binding domain. | 232 | 3.30E-24 |
| EF054-2 | R85781 | Group B Streptococcal wild-type beta antigen. | 232 | 5.20E-24 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|--------|-----------------------------------------------------------------------|-----|----------|
| EF054-2 | P91941 | Sequence of preprospasmolysin. | 204 | 3.10E-19 |
| EF054-2 | W32519 | Collagen-like polypeptide SEQ ID NO:2. | 180 | 7.50E-18 |
| EF054-2 | W12324 | Silver halide emulsion protein monomeric repeat unit #2. | 180 | 7.50E-18 |
| EF054-2 | W32522 | Collagen-like polypeptide SEQ ID NO:5. | 192 | 1.60E-17 |
| EF054-2 | W12327 | Silver halide emulsion protein monomeric repeat unit #5. | 192 | 1.60E-17 |
| EF054-2 | W32520 | Collagen-like polypeptide SEQ ID NO:3. | 189 | 2.40E-17 |
| EF054-2 | W32532 | Collagen-like polypeptide SEQ ID NO:15. | 189 | 2.40E-17 |
| EF054-2 | W12325 | Silver halide emulsion protein monomeric repeat unit #3. | 189 | 2.40E-17 |
| EF054-2 | W12337 | Silver halide emulsion protein monomeric repeat unit #15. | 189 | 2.40E-17 |
| EF054-2 | W12341 | Silver halide emulsion FLAG(RTM)-tagged protein #2. | 189 | 2.60E-17 |
| EF054-2 | W02098 | S. mutans antigen I/II. | 161 | 5.40E-15 |
| EF054-2 | W02096 | S. mutans antigen I/II fragment (aa803-1114). | 161 | 1.90E-13 |
| EF059-2 | R26042 | P. yoelii SSP2 antigen. | 344 | 1.90E-39 |
| EF059-2 | R85782 | Group B Streptococcal mutant beta antigen without IgA binding domain. | 232 | 1.10E-26 |
| EF059-2 | R85781 | Group B Streptococcal wild-type beta antigen. | 232 | 1.70E-26 |
| EF059-2 | P91941 | Sequence of preprospasmolysin. | 200 | 1.50E-18 |
| EF059-2 | P60570 | Sequence of the Falciparum Interspersed Repeat Antigen | 186 | 4.60E-18 |
| EF059-2 | W02096 | S. mutans antigen I/II fragment (aa803-1114). | 167 | 8.20E-16 |
| EF059-2 | W02098 | S. mutans antigen I/II. | 167 | 4.90E-15 |
| EF059-2 | R79625 | Endocarditis specific antigen region. | 147 | 4.40E-12 |
| EF059-2 | R26049 | MSF precursor. | 143 | 1.30E-11 |
| EF059-2 | R28150 | Sugar beet chitinase 1. | 148 | 1.70E-11 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|--------|-----------------------------------------------------------------------|-----|----------|
| EF059-2 | R26842 | Protease from <i>S. Aureus</i> ATCC12600. | 147 | 2.10E-11 |
| EF059-2 | R79643 | Immunodominant antigen of <i>Streptococcus sobrinus</i> . | 151 | 2.10E-11 |
| EF059-2 | W07539 | Collagen like protein (CLP). | 146 | 3.00E-11 |
| EF061-2 | R26042 | <i>P. yoelii</i> SSP2 antigen. | 241 | 1.70E-25 |
| EF061-2 | P60570 | Sequence of the Falciparum Interspersed Repeat Antigen | 199 | 1.60E-18 |
| EF061-2 | R85782 | Group B Streptococcal mutant beta antigen without IgA binding domain. | 153 | 2.40E-14 |
| EF061-2 | R85781 | Group B Streptococcal wild-type beta antigen. | 153 | 3.60E-14 |
| EF061-2 | P91941 | Sequence of preprospasmolysin. | 163 | 9.70E-14 |
| EF061-2 | P83194 | Sequence of a bioadhesive precursor protein encoded by cDNA clone | 156 | 7.90E-13 |
| EF061-2 | R28150 | Sugar beet chitinase 1. | 156 | 9.10E-13 |
| EF061-2 | W02096 | <i>S. mutans</i> antigen I/II fragment (aa803-1114). | 148 | 1.20E-12 |
| EF061-2 | P82971 | Bioadhesive precursor protein from cDNA 52. | 148 | 9.70E-12 |
| EF061-2 | W02098 | <i>S. mutans</i> antigen I/II. | 148 | 1.50E-11 |
| EF062-2 | W02098 | <i>S. mutans</i> antigen I/II. | 107 | 1.20E-36 |
| EF062-2 | R79643 | Immunodominant antigen of <i>Streptococcus sobrinus</i> . | 132 | 3.00E-36 |
| EF063-2 | W02098 | <i>S. mutans</i> antigen I/II. | 107 | 1.20E-36 |
| EF063-2 | R79643 | Immunodominant antigen of <i>Streptococcus sobrinus</i> . | 132 | 3.00E-36 |
| EF064-2 | W02098 | <i>S. mutans</i> antigen I/II. | 107 | 1.20E-36 |
| EF064-2 | R79643 | Immunodominant antigen of <i>Streptococcus sobrinus</i> . | 132 | 3.00E-36 |
| EF071-2 | R85294 | Phage R1-t LytR lysin. | 127 | 3.70E-38 |
| EF071-2 | R91515 | Listeria phage lysin PLY511. | 273 | 4.70E-37 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|--------|----------------------------------------------------------------------|-----|----------|
| EF075-2 | W14070 | S.thermophilus exopolysaccharide biosynthesis protein EpsR. | 239 | 4.20E-36 |
| EF075-2 | W22169 | S.thermophilus exopolysaccharide synthesis operon epsA gene product. | 239 | 4.00E-34 |
| EF077-2 | R97280 | Helicobacter-specific ATPase 439. | 258 | 4.10E-74 |
| EF077-2 | R48036 | Mycobacterium BCG immunogen. | 192 | 2.20E-67 |
| EF077-2 | W06712 | Helicobacter-specific ATPase 948 (ORF-4). | 220 | 2.50E-67 |
| EF077-2 | R70419 | Rat homologue of human Wilson disease gene ATP7B. | 186 | 9.80E-54 |
| EF077-2 | R72343 | Wilson disease protein ATP7B. | 176 | 6.70E-40 |
| EF077-2 | R06376 | Product of the ssc1 gene. | 166 | 3.10E-28 |
| EF077-2 | R75396 | Flea sodium pump alpha subunit. | 146 | 2.40E-25 |
| EF077-2 | W20891 | H. pylori transporter protein, 14ce20219orf1. | 156 | 8.60E-14 |
| EF078-2 | R56667 | Bacteroides fragilis RprX regulatory response protein. | 148 | 8.30E-18 |
| EF078-2 | R74630 | Tomato TGETR1 ethylene response protein. | 130 | 7.80E-13 |
| EF078-2 | R69849 | Ethylene response (ETR) gene product. | 128 | 1.70E-11 |
| EF078-2 | R69850 | Ethylene response (ETR) mutant protein etr1-1. | 128 | 1.70E-11 |
| EF078-2 | R69851 | Ethylene response (ETR) mutant protein etr1-2. | 128 | 1.70E-11 |
| EF078-2 | R69852 | Ethylene response (ETR) mutant protein etr1-3. | 128 | 1.70E-11 |
| EF078-2 | R69853 | Ethylene response (ETR) mutant protein etr1-4. | 128 | 1.70E-11 |
| EF078-2 | R24296 | Regulatory protein VanS involved in glycopeptide resistance. | 142 | 2.70E-11 |
| EF081-2 | R27253 | Penicillin binding protein PBP2A-epi. | 101 | 4.70E-16 |
| EF081-2 | R27256 | Penicillin binding protein PBP2A-27R. | 101 | 6.00E-15 |
| EF081-2 | R27257 | Penicillin binding protein derivative #1. | 101 | 6.20E-15 |
| EF081-2 | R27258 | Penicillin binding protein derivative #2. | 101 | 6.20E-15 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|--------|------------------------------------------------|------|-----------|
| EF081-2 | R27259 | Penicillin binding protein derivative #3. | 101 | 6.20E-15 |
| EF081-2 | R27260 | Penicillin binding protein derivative #4. | 101 | 6.20E-15 |
| EF081-2 | R27261 | Penicillin binding protein derivative #5. | 101 | 6.20E-15 |
| EF081-2 | R27263 | Penicillin binding protein derivative #7. | 101 | 6.20E-15 |
| EF081-2 | R27264 | Penicillin binding protein derivative #8. | 101 | 6.20E-15 |
| EF081-2 | R27262 | Penicillin binding protein derivative #6. | 101 | 6.50E-15 |
| EF081-2 | R30845 | Sequence encoded by the mec A gene. | 101 | 6.90E-15 |
| EF081-2 | R27255 | Penicillin binding protein PBP2A-27R. | 101 | 6.90E-15 |
| EF081-2 | R31216 | Penicillin binding protein PBP2A-27R. | 101 | 7.00E-15 |
| EF110-2 | R91042 | V8 mature protease (aal-213). | 106 | 6.60E-16 |
| EF110-2 | R91043 | V8 mature protease (aal-214). | 106 | 7.20E-16 |
| EF110-2 | R91044 | V8 mature protease (aal-215). | 106 | 7.80E-16 |
| EF110-2 | R26842 | Protease from <i>S. Aureus</i> ATCC12600. | 106 | 6.70E-15 |
| EF110-2 | R29644 | Protease from <i>S. Aureus</i> . | 106 | 1.20E-14 |
| EF110-2 | W22218 | Protein encoded by pV8RPT(-) construct. | 106 | 7.60E-14 |
| EF110-2 | R91033 | Beta-galactosidase-V8 protease fusion protein. | 106 | 7.60E-14 |
| EF110-2 | R91034 | Beta-galactosidase-V8 protease fusion protein. | 106 | 1.70E-13 |
| EF110-2 | W22219 | Protein encoded by pV8D construct. | 106 | 7.60E-13 |
| EF110-2 | R91035 | Recombinant V8 protease V8D fusion protein. | 106 | 7.60E-13 |
| EF110-2 | W22220 | Protein encoded by pV8F construct. | 106 | 7.90E-13 |
| EF129-2 | R14530 | Usp45 protein. | 374 | 2.40E-43 |
| EF129-2 | R14150 | MSP encoded by pUCRS (DSM 5803). | 372 | 4.70E-43 |
| EF131-2 | R37495 | Pneumococcal fimbrial protein A. | 1185 | 6.80E-163 |

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

| | | | | |
|---------|--------|-----------------------------------------------------------|-----|----------|
| EF131-2 | W26367 | Staphylococcus aureus saliva binding protein. | 418 | 3.70E-85 |
| EF131-2 | R79722 | ROM precursor TROMPI. | 171 | 9.00E-31 |
| EF131-2 | W22134 | Treponema pallidum rare outer membrane protein (TROMP-1). | 171 | 9.00E-31 |

TABLE 3. Conservative Amino Acid Substitutions.

| | |
|-------------|---------------------------------------------------------|
| Aromatic | Phenylalanine Tryptophan Tyrosine |
| Hydrophobic | Leucine Isoleucine Valine |
| Polar | Glutamine Asparagine |
| Basic | Arginine Lysine Histidine |
| Acidic | Aspartic Acid Glutamic Acid |
| Small | Alanine Serine Threonine Methionine Glycine |

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

| | |
|---------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| EF001-2 | from about Asp-150 to about Lys-152, from about Ser-256 to about Tyr-259, from about Lys-360 to about Lys-363, from about Asn-406 to about Asp-408. |
| EF002-2 | from about Asp-80 to about Asp-83, from about Asp-281 to about Gly-283. |
| EF003-2 | from about Asn-263 to about Gly-266. |
| EF004-2 | from about Asn-23 to about Asn-26, from about Lys-83 to about Ser-87, from about Tyr-154 to about Asp-159. |
| EF005-2 | from about Lys-249 to about Glu-252. |
| EF006-2 | from about Gly-23 to about Asp-28. |
| EF008-2 | from about Thr-92 to about Gly-94, from about Pro-161 to about Asp-165, from about Gly-287 to about Thr-289. |
| EF010-2 | from about Pro-129 to about Asn-131. |
| EF012-2 | from about Asp-77 to about Asp-79, from about Asp-94 to about Lys-98, from about Asp-256 to about Thr-258, from about Glu-461 to about Asn-468. |
| EF013-2 | from about Thr-30 to about Asp-32, from about Glu-73 to about Ala-75, from about Gln-164 to about Asn-166, from about Lys-193 to about Gly-195. |
| EF014-2 | from about Ser-203 to about Asp-206, from about Gln-314 to about Gly-316 |
| EF015-2 | from about Pro-66 to about Gly-69. |
| EF016-2 | from about Lys-236 to about Asn-239. |
| EF017-2 | from about Ser-90 to about Gly-93, from about Thr-197 to about Lys-199, from about Lys-230 to about Asn-233, from about Ser-428 to about Gly-431. |
| EF018-2 | from about Lys-159 to about Tyr-161, from about Asn-165 to about Ser-167, from about Asn-250 to about Arg-256, from about Asn-392 to about Gly-395, from about Lys-416 to about Tyr-418, from about Asn-428 to |

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

| | |
|---------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| | about Arg-430. |
| | |
| EF019-2 | from about Arg-209 to about Ser-211, from about Lys-287 to about Ser-290. |
| | |
| EF020-2 | from about Lys-57 to about Asn-62. |
| | |
| EF021-2 | from about Ser-33 to about Gly-35, from about Glu-77 to about Gly-81, from about Asp-139 to about Lys-141, from about Glu-255 to about Ser-258, from about Gln-271 to about Tyr-277. |
| | |
| EF023-2 | from about Lys-232 to about Asp-234, from about Arg-304 to about Gly-306, from about Thr-453 to about Arg-456, from about Ser-478 to about Thr-480. |
| | |
| EF025-2 | from about Arg-183 to about Asp-185. |
| | |
| EF026-2 | from about Ser-25 to about Asp-30, from about Asp-90 to about Asp-94, from about Gln-107 to about Asn-110. |
| | |
| EF027-2 | from about Gln-72 to about Lys-74, from about Lys-229 to about Asp-231. |
| | |
| EF028-2 | from about Asp-186 to about Gln-188. |
| | |
| EF029-2 | from about Asp-118 to about Lys-122, from about Asp-124 to about Tyr-126. |
| | |
| EF031-2 | from about Glu-30 to about Gly-33. |
| | |
| EF034-2 | from about Glu-25 to about Gly-27, from about Glu-75 to about Thr-77. |
| | |
| | |
| EF36-2 | from about Gln-177 to about Ser-179. |
| | |
| EF037-2 | from about Ser-25 to about Asp-30, from about Asp-90 to about Asp-94, from about Gln-107 to about Asn-110. |
| | |
| EF038-2 | from about Asn-77 to about Lys-79, from about Tyr-88 to about Asn-92. |
| | |
| EF040-2 | from about Lys-167 to about Gly-172, from about Lys-240 to about Asn-242. |
| | |

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

| | |
|---------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| EF044-2 | from about Arg-192 to about Gly-194, from about Asn-200 to about Asn-203. |
| | |
| EF045-2 | from about Asp-159 to about Asn-161, from about His-172 to about Gly-174, from about Tyr-261 to about Gly-264, from about Lys-305 to about Glu-308. |
| | |
| EF046-2 | from about Ser-18 to about Gly-23, from about Gln-41 to about Ser-47, from about Thr-76 to about Asp-78. |
| | |
| EF047-2 | from about Asn-28 to about Asp-30, from about Asp-273 to about Asn-277. |
| | |
| EF048-2 | from about Asp-138 to about Lys-141, from about Asp-152 to about Gly-154. |
| | |
| EF051-2 | from about Asp-73 to about Gly-76. |
| | |
| EF053-2 | from about Ser-79 to about Gly-82. |
| | |
| EF055-2 | from about Asp-26 to about Gly-28, from about Gln-67 to about Asp-69, from about Arg-71 to about Gly-74, from about Arg-87 to about Gly-89. |
| | |
| EF056-2 | from about Arg-71 to about Gly-74, from about Arg-87 to about Gly-89. |
| | |
| | |
| EF058-2 | from about Lys-129 to about Gly-133, from about Gln-571 to about Tyr-573, from about Pro-586 to about Gly-591. |
| | |
| EF065-2 | from about Ser-236 to about Tyr-239, from about Asp-350 to about Gly-352, from about Lys-415 to about Asn-418, from about Arg-446 to about Asp-448, from about Asn-489 to about Lys-491, from about Ser-516 to about Asp-518, from about Glu-639 to about Lys-642. |
| | |
| EF066-2 | from about Ser-236 to about Tyr-239, from about Asp-350 to about Gly-352, from about Lys-415 to about Asn-418, from about Arg-446 to about Asp-448, from about Asn-489 to about Lys-491, from about Ser-516 to about Asp-518, from about Glu-639 to about Lys-642. |
| | |
| EF067-2 | from about Ser-236 to about Tyr-239, from about Asp-350 to about Gly-352, from about Lys-415 to about Asn-418, from about Arg-446 to about Asp-448, from about Asn-489 to about Lys-491, from about Ser-516 to about Asp-518, from about Glu-639 to about Lys-642. |

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

| | |
|---------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| EF073-2 | from about Met-98 to about Arg-100, from about Arg-110 to about Asp-112. |
| EF074-2 | from about Ser-53 to about Tyr-59, from about Ser-86 to about Gly-88, from about Pro-97 to about Gln-100, from about Gln-230 to about Gly-232. |
| EF076-2 | from about Asn-38 to about Tyr-40, from about Asp-48 to about Asn-53, from about Lys-79 to about Gly-81. |
| EF077-2 | from about Arg-411 to about Gly-413. |
| EF078-2 | from about Thr-294 to about Gly-296, from about Asp-366 to about Gln-368, from about Glu-524 to about Gly-526. |
| EF080-2 | from about Glu-164 to about Gly-166, from about Ser-206 to about Tyr-208, from about Lys-239 to about Gly-243. |
| EF081-2 | from about Asn-7 to about Ser-11, from about Lys-77 to about Tyr-80, from about Lys-112 to about Asn-114, from about Gly-162 to about Asp-164, from about Arg-181 to about Gly-183. |
| EF083-2 | from about Gln-38 to about Arg-40. |
| EF084-2 | from about Lys-140 to about Asp-142, from about Gly-164 to about Arg-166, from about Arg-262 to about Gly-264. |
| EF085-2 | from about Asn-95 to about Asp-97, from about Arg-112 to about Asp-114, from about Asp-258 to about Ser-260, from about Arg-401 to about Ser-403. |
| EF086-2 | from about Pro-112 to about Gly-115, from about Ser-222 to about Ser-224, from about Asn-296 to about Gly-299, from about Thr-346 to about Lys-348, from about Asp-428 to about Ser-432. |
| EF087-2 | from about Pro-112 to about Gly-115, from about Ser-222 to about Ser-224, from about Asn-296 to about Gly-299, from about Thr-346 to about Lys-348, from about Asp-428 to about Ser-432. |
| EF088-2 | from about Pro-112 to about Gly-115, from about Ser-222 to about Ser-224, from about Asn-296 to about Gly-299, from about Thr-346 to about Lys-348, from about Asp-428 to about Ser-432. |

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

| | |
|---------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| | |
| EF090-2 | from about Arg-2 to about Arg-5. |
| | |
| EF091-2 | from about Gln-40 to about Asp-43. |
| | |
| EF093-2 | from about Lys-95 to about Gly-97. |
| | |
| EF094-2 | from about Asp-314 to about Asp-316. |
| | |
| EF095-2 | from about Ser-328 to about Thr-330, from about Asp-359 to about Asp-363, from about Glu-637 to about Gly-639, from about Asn-744 to about Gly-746. |
| | |
| EF096-2 | from about Pro-128 to about Asn-130, from about Ser-193 to about Asp-196. |
| | |
| EF097-2 | from about Val-357 to about Gly-359. |
| | |
| EF099-2 | from about Glu-44 to about Asp-47, from about Lys-154 to about Gly-156, from about Asn-286 to about Asp-289. |
| | |
| EF101-2 | from about Lys-40 to about Asp-42, from about Pro-255 to about Asn-258, from about Lys-288 to about Gly-290. |
| | |
| EF102-2 | from about Asp-314 to about Asp-316. |
| | |
| EF103-2 | from about Asn-46 to about Gly-48. |
| | |
| EF104-2 | from about Pro-232 to about Lys-237, from about Ala-362 to about Asn-366, from about Ser-421 to about Gly-423, from about Lys-488 to about Ser-490, from about Asp-550 to about Asn-552, from about Pro-637 to about Lys-640, from about Asp-727 to about Gly-729, from about Asn-751 to about Ser-754, from about Lys-771 to about Asn-774, from about Ile-835 to about Asn-837, from about Pro-851 to about Gly-853. |
| | |
| EF105-2 | from about Ser-40 to about Gly-43, from about Asn-94 to about Gln-97, from about Gln-220 to about Gly-222, from about Asn-263 to about Gly-265. |
| | |
| EF106-2 | from about Asp-72 to about Gly-75, from about Thr-274 to about Asp-277, from about Asn-310 to about Arg-313. |
| | |
| EF107-2 | from about Thr-155 to about Asn-157, from about Thr-189 to about Asp- |

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

| | |
|---------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| | 191, from about Arg-270 to about Gly-272, from about Thr-330 to about Lys-335, from about Asp-365 to about Asp-368, from about Pro-451 to about Asp-453, from about Gly-485 to about Thr-488. |
| EF108-2 | from about Lys-142 to about Trp-145, from about Thr-147 to about Tyr-150, from about Arg-212 to about Gly-214, from about Ser-248 to about Asp-251, from about Asp-384 to about Asp-387, from about Pro-481 to about Arg-483, from about Lys-491 to about Gly-494, from about Thr-619 to about Gly-624, from about Asp-656 to about Asp-659, from about Lys-717 to about Asn-721, from about Ser-822 to about Gly-824, from about Tyr-1137 to about Thr-1141. |
| EF110-2 | from about Pro-123 to about Gly-127, from about Thr-223 to about Gly-225. |
| EF111-2 | from about Lys-207 to about Asn-209, from about Asp-245 to about Asn-248, from about Lys-396 to about Asp-398, from about Glu-429 to about Ser-432, from about Thr-470 to about His-474. |
| EF119-2 | from about Asp-90 to about Asn-92, from about Gln-142 to about Gly-144. |
| EF121-2 | from about Asn-159 to about Asp-161, from about Asn-351 to about Lys-353, from about Pro-658 to about Gly-660, from about Lys-786 to about Ser-789. |
| EF122-2 | from about Asn-159 to about Asp-161, from about Asn-351 to about Lys-353, from about Pro-658 to about Gly-660, from about Lys-786 to about Ser-789. |
| EF123-2 | from about Asn-331 to about Arg-336, from about Asp-634 to about Gly-636, from about Glu-780 to about Ser-782, from about Tyr-909 to about Asn-911, from about Lys-939 to about Glu-942, from about Asp-1074 to about Gly-1076, from about Asp-1367 to about Gly-1369, from about Pro-1433 to about Lys-1435, from about Gly-1516 to about Asp-1518, from about Lys-1656 to about Asp-1660, from about Lys-1860 to about Gln-1863, from about Ser-1916 to about Gln-1919, from about Pro-1940 to about Gly-1942. |
| EF124-2 | from about Asn-331 to about Arg-336, from about Asp-634 to about Gly-636, from about Glu-780 to about Ser-782, from about Tyr-909 to about Asn-911, from about Lys-939 to about Glu-942, from about Asp-1074 to about Gly-1076, from about Asp-1367 to about Gly-1369, from about Pro-1433 to about Lys-1435, from about Gly-1516 to about Asp-1518, |

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

| | |
|---------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| | from about Lys-1656 to about Asp-1660, from about Lys-1860 to about Gln-1863, from about Ser-1916 to about Gln-1919, from about Pro-1940 to about Gly-1942. |
| EF125-2 | from about Asn-331 to about Arg-336, from about Asp-634 to about Gly-636, from about Glu-780 to about Ser-782, from about Tyr-909 to about Asn-911, from about Lys-939 to about Glu-942, from about Asp-1074 to about Gly-1076, from about Asp-1367 to about Gly-1369, from about Pro-1433 to about Lys-1435, from about Gly-1516 to about Asp-1518, from about Lys-1656 to about Asp-1660, from about Lys-1860 to about Gln-1863, from about Ser-1916 to about Gln-1919, from about Pro-1940 to about Gly-1942. |
| EF126-2 | from about Ser-236 to about Tyr-239, from about Asp-350 to about Gly-352, from about Lys-415 to about Asn-418, from about Arg-446 to about Asp-448, from about Asn-489 to about Lys-491, from about Ser-516 to about Asp-518, from about Glu-639 to about Lys-642. |
| EF127-2 | from about Ser-236 to about Tyr-239, from about Asp-350 to about Gly-352, from about Lys-415 to about Asn-418, from about Arg-446 to about Asp-448, from about Asn-489 to about Lys-491, from about Ser-516 to about Asp-518, from about Glu-639 to about Lys-642. |
| EF128-2 | from about Ser-236 to about Tyr-239, from about Asp-350 to about Gly-352, from about Lys-415 to about Asn-418, from about Arg-446 to about Asp-448, from about Asn-489 to about Lys-491, from about Ser-516 to about Asp-518, from about Glu-639 to about Lys-642. |
| EF129-2 | from about Asn-300 to about Gly-302, from about Ser-316 to about Gly-319, from about Asn-385 to about His-387 |
| EF131-2 | from about Lys-201 to about Tyr-204, from about Glu-263 to about Ser-266. |
| EF132-2 | from about Thr-26 to about Ser-28. |

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

| | |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------|
| A. The indications made below relate to the microorganism referred to in the description on page <u>10</u> , line <u>12</u> | |
| B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/> | |
| Name of depositary institution <u>American Type Culture Collection</u> | |
| Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u> | |
| Date of deposit <u>May 2, 1997</u> | Accession Number <u>55969</u> |
| C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/> | |
| | |
| D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States) | |
| | |
| E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) | |
| The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit") | |
| | |

| | |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 5px;"><input checked="" type="checkbox"/> This sheet was received with the international application</div> <div style="text-align: center; margin-bottom: 5px;"></div> <div style="border-top: 1px solid black; margin-top: 5px;">Authorized officer</div> | <div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; margin-top: 5px;">Authorized officer</div> |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence selected from the group consisting of:
 - (a) a nucleotide sequence encoding any one of the amino acid sequences of the polypeptides shown in Table 1; or
 - (b) a nucleotide sequence complementary to any one of the nucleotide sequences in (a).
 - (c) a nucleotide sequence at least 95% identical to any one of the nucleotide sequences shown in Table 1; or,
 - (d) a nucleotide sequence at least 95% identical to a nucleotide sequence complementary to any one of the nucleotide sequences shown in Table 1.
2. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide having a nucleotide sequence identical to a nucleotide sequence in (a) or (b) of claim 1.
3. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which encodes an epitope-bearing portion of a polypeptide in (a) of claim 1.
4. The isolated nucleic acid molecule of claim 3, wherein said epitope-bearing portion of a polypeptide comprises an amino acid sequence listed in Table 4.
5. A method for making a recombinant vector comprising inserting an isolated nucleic acid molecule of claim 1 into a vector.
6. A recombinant vector produced by the method of claim 5.
7. A host cell comprising the vector of claim 6.
8. A method of producing a polypeptide comprising:
 - (a) growing the host cell of claim 7 such that the protein is expressed by the cell; and
 - (b) recovering the expressed polypeptide.
9. An isolated polypeptide comprising a polypeptide selected from the group consisting of:
 - (a) a polypeptide consisting of one of the complete amino acid sequences of Table 1;
 - (b) a polypeptide consisting of one the complete amino acid sequences of Table 1 except the N-terminal residue;

- (c) a fragment of the polypeptide of (a) having biological activity; and
- (d) a fragment of the polypeptide of (a) which binds to an antibody specific for the polypeptide of (a).

10. An isolated antibody specific for the polypeptide of claim 9.

11. A polypeptide produced according to the method of claim 8.

12. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of an amino acid sequence of any one of the polypeptides in Table 1.

13. An isolated polypeptide antigen comprising an amino acid sequence of an *E. faecalis* epitope shown in Table 4.

14. An isolated nucleic acid molecule comprising a polynucleotide with a nucleotide sequence encoding a polypeptide of claim 9.

15. A hybridoma which produces an antibody of claim 10.

16. A vaccine, comprising:

(1) one or more *E. faecalis* polypeptides selected from the group consisting of a polypeptide of claim 9; and

(2) a pharmaceutically acceptable diluent, carrier, or excipient;

wherein said polypeptide is present, in an amount effective to elicit protective antibodies in an animal to a member of the *Enterococcus* genus.

17. A method of preventing or attenuating an infection caused by a member of the *Enterococcus* genus in an animal, comprising administering to said animal a polypeptide of claim 9, wherein said polypeptide is administered in an amount effective to prevent or attenuate said infection.

18. A method of detecting *Enterococcus* nucleic acids in a biological sample comprising:

(a) contacting the sample with one or more nucleic acids of claim 1, under conditions such that hybridization occurs, and

(b) detecting hybridization of said nucleic acids to the one or more *Enterococcus* nucleic acid sequences present in the biological sample.

19. A method of detecting *Enterococcus* nucleic acids in a biological sample obtained from an animal, comprising:

- (a) amplifying one or more *Enterococcus* nucleic acid sequences in said sample using polymerase chain reaction, and
- (b) detecting said amplified *Enterococcus* nucleic acid.

20. A kit for detecting *Enterococcus* antibodies in a biological sample obtained from an animal, comprising

- (a) a polypeptide of claim 9 attached to a solid support; and
- (b) detecting means.

21. A method of detecting *Enterococcus* antibodies in a biological sample obtained from an animal, comprising

- (a) contacting the sample with a polypeptide of claim 9; and
- (b) detecting antibody-antigen complexes.